WHOLE GENOME BASED CHARACTERIZATION OF INDIGENOUS CHICKEN POPULATIONS IN ETHIOPIA

THESIS SUBMITTED TO THE DEPARTMENT OF MICROBIAL, CELLULAR AND MOLECULAR BIOLOGY IN PARTIAL FULFILMENT OF THE REQUIREMENTS FOR THE AWARD OF THE DEGREE OF DOCTOR OF PHILOSOPHY IN APPLIED GENETICS

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This is to certify that the dissertation prepared by Adebabay Kebede Belew entitled: "**WHOLE GENOME BASED CHARACTERIZATION OF INDIGENOUS CHICKEN POPULATIONS IN ETHIOPIA submitted in fulfilment of the requirements for the Degree of Doctor of Philosophy in Applied Genetics**" complies with the regulations of the University and meets the accepted standards with respect to originality and quality.

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DECLARATION

I, Adebabay Kebede Belew, hereby declare that this dissertation and its entirety is my own original work and no part of this has been previously presented or submitted for examination anywhere else. All assistance towards the synthesis of this thesis and entire references of others contained herein have been duly acknowledged.

“The chicken that digs for food will not sleep hungry”. ~Bayombe Proverb

December, 2018

DEDICATION

This thesis is dedicated to the memory of my late mother Mrs. Alaminie Tarekegn Mersha and father Sergeant Kebede Belew Mengesha.

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LIST OF ACRONYMS AND ABBREVIATIONS

AA	Amino Acid
AAF	Alternate Allele Frequency
AATI	Agilent Formerly Advanced Analytical
AEZ	Agro-Ecological Zone
AF	Allele Frequency
AFLP	Amplified Fragment Length Polymorphism
AMOVA	Analysis of Molecular Variance
ANOVA	Analysis of Variance
AR	Allelic Richness
BAM	Binary Alignment Map
bp	Base pair
BQSR	Base Quality Score Recalibration
BWA	Burrows Wheeler Aligner
CLUMPAK	CLUstering Markov Packager Across K
cM	Centi Morgan
CP	Crude Protein
DAVID	Database for Annotation, Visualization, and Integrated Discovery
dbsnp	Data base Single Nucleotide Polimorphism
DNA	Deoxyribose Nucleic Acid
DnaSP	DNA Sequence Polymorphism
DZARC	Debre Zeit Agricultural Research Center

He	Expected heterozygosity
FAO	Food and Agricultural Organization of the United Nations
gerp	Genomic Evolutionary Rate Profiling
gDNA	Genomic DNA
GGA	*Gallus gallus* (chicken) Autosome
GO	Gene Ontology
gVCF	Genomic Variant Format
HWE	Hardy-Weinberg Equilibrium
IBS	Identity By Decent
IC	Ethiopian indigenous chicken
Kb	Kilo base (1000 bases)
Kcal	Kilo Calorie
Kg	Kilo gram
ME	Metabolizable energy
KEGG	Kyoto Encyclopedia of Genes and Genomes
LD	Linkage Disequilibrium
LSM	Least Square Means
LTR	Long Terminal Repeats
MAEZ	Major Agro-ecological Zones
M	Molar
masl	Meter above sea level
MCMC	Markov Chain Monte Carlo
MEGA	Molecular Evolutionary Genetics Analysis

MHC	Major Histocompatibility Complex
MNA	Mean Number of alleles
MOA	Ministry of Agriculture
NCBI	National Center of Biotechnology Information
ncRNA	Non-coding Ribonucleic Acid
NGS	Next Generation Sequencing
NJ	Neighbor joining
^{o}C	Degree centigrade
Ho	Observed heterozygosity
PA	Private Allele
PCA	Principal Components Analysis
PCR	Polymerase Chain Reaction
PIC	Polymorphic Information Content
QC	Quality control
QTL	Quantitative Trait Loci
RFLP	Restriction Fragment Length Polymorphism
RAPD	Random Amplification of Polymorphic DNA
RNA	Ribonucleic Acid
SAM	Sequence Alignment MAP
SIFT	Sorting Intolerant from Tolerant
SMART	Simple Molecular Architecture Research tools
SNP	Single Nucleotide Polymorphism
UPGMA	Unweighted Pair-Group Method with Arithmetic mean

USA	United States of America
UTR	Untranslated Region
UV	Ultra-violate Light
µl	Micro litre
VCF	Variant Calling Format
VEP	Variant Effect Predictor
VQSR	Variant Quality Score Recalibration

GENERAL ABSTRACT

WHOLE GENOME BASED CHARACTERIZATION OF INDIGENOUS CHICKEN POPULATIONS IN ETHIOPIA

Adebabay Kebede

Addis Ababa University, 2018

Indigenous chicken are locally adapted to environmental challenges and provide subsistence to millions of farmers in Africa. Their productivity remains low compared to exotic chicken strains. Efforts are being made to combine the local adaptation of indigenous chicken with productivity traits of exotic chicken. Understanding the link between diversity and adaptability is opening the door to marker-assisted breed improvement programs. Selective breeding for genetic improvement is expected to leave distinctive selection signatures within genomes. The identification of selection signatures can help to elucidate the mechanisms of selection and accelerate genetic improvement. Ethiopia has several chicken ecotypes which evolved in different agro-ecologies. This study aims to characterize the genomic diversity of indigenous chicken populations from Ethiopia. The first part of this study addresses the characterization of the LEI0258 microsatellite loci in the MHC region with previous study supporting links of the locus with infectious diseases resistance/susceptibility in commercial chicken. Here, we report diversity of LEI0258 in 236 chicken from 24 Ethiopian indigenous chicken populations from different agro-ecological zones using gel electrophoresis and sequencing.

The number of alleles, allele frequency, and heterozygosity levels were used to measure diversity within populations whilst the Wright's fixation indices were used to analyze the level of population structuring. Twenty-nine LEI0258 allele sizes were observed using capillary electrophoresis. Allele sizes ranged from 185 to 569 bp with no significant difference in allele frequencies between populations ($P < 0.01$). Allele frequencies were in Hardy and Weinberg Equilibrium in all population except in improved Horro and Dara chicken ($P < 0.05$). Excluding the tandemly repeated motif, the number of monomorphic and polymorphic sites are 412 and 35, respectively. Number of point mutation and indels are 33 and 17, respectively. The number of R12 CTTTCCTTCTTT repeats ranged from 2 to 18, while R13 was found monomorphic with a single motif CTATGTCTTCTTT. Sequences relationships reveal two distinct groups of alleles. The high diversity at microsatellite LEI0258 at Ethiopian indigenous village chicken populations supports the importance of the MHC region in relation to the disease challenges diversity faced by smallholder poultry production within and across Ethiopian agro-ecologies. We recommend that breed improvement programs ensure the maintenance of this diversity by selecting breeding stock as diverse as possible at the LEI0258 locus. The part of the thesis reports the genomic diversity of Ethiopian indigenous chicken through discovery and characterization of 21 million SNPs (72% novel) from 27 indigenous chicken populations (n = 260 birds) using whole genome sequencing. In each population, around 10 to 12 million SNPs are present, of which, 40-47% are a heterozygote. The mean SNP density across all population is 21 (±5) per kb, although it is much lower on the sex chromosomes (W = 0.4, Z = 11). Principal component and admixture analyses suggest the presence of four ancestral gene pools across the populations. Over 46% of the SNPs are located within genes, of which exonic and intronic SNPs account for 1.59% and 43.94%, respectively; while 31% of the exonic SNPs are non-synonymous. A large proportion of SNPs has low

alternative allele frequency (AAF < 10%), although this proportion is higher for potentially harmful categories like missense and stop gain/loss (> 60%) than neutral ones (40-45%). Genes with deleterious missense variants are included within several important biological pathways like innate immunity. Our results confirm the existence of significant genomic diversity in indigenous chicken populations of Ethiopia, with most of the variants previously undescribed in commercial breeds. The last part of the thesis assesses the footprints of candidate signatures of positive selection from whole genome autosomal sequences, comprising 14,857,039 SNPs, in Improved Horro, Local Horro, Hugub, Arabo and Jarso chicken populations of Ethiopia. We identified selection signals in 20 Kb windows size with 10 Kb sliding steps based on estimators of pooled heterozygosity (*Hp* and F-statistics (*Fst*) within and between those populations. Selective sweep analysis using *Hp* and *Fst* methods identified genomic regions associated with production and reproduction traits. A total of 595 candidate genes showed high evidence of positive selection in indigenous chicken populations. These genes were related to traits such as growth and egg production. Gene ontology analysis displayed several biological processes and KEGG pathways involved in oestrogen biosynthetic and nervous system development processes, calcium signaling and biosynthesis of unsaturated fatty acids. The regions identified in this study are expected to provide a genome landmark to enhance the ongoing breed improvement operations in improved Horro and other four chicken populations. In general, this study revealed the huge genomic diversity and taped the genomic regions under strong selection in indigenous chicken populations of Ethiopia

Keywords: Chicken, Diversity, Ethiopia, Genomic, Indigenous, Population

CHAPTER 1. INTRODUCTION

1.1. Background and Justification

In the last 50 years, the world human population was increasing dramatically and its growth is projected to reach 9.73 billion by 2050 and 11.2 billion by 2100 which makes the greater confront for agriculture to meet the growing food demand (FAO, 2017). More than a billion people around the world live in extreme poverty. Moreover, as of 2009 there have been marked increases in hunger, and the Food and Agriculture Organization of the United Nations(FAO) estimated that 1.02 billion people are undernourished (FAO, 2010) and most of these people are found in sub-Saharan Africa. 30% or more of children under 5 years of age are malnourished in many parts of this region. Similarly, Cicia *et al*. (2003) indicated that the profound changes that have taken place in agriculture in the past 50 years in both developed and developing countries have caused severe and undesirable impacts on the environment.

Particularly, Ethiopia is known to have an estimated human population of over 82.64 million, growing at a rate of 2.4% per annum at which 85% the population relies on agriculture (45% of GDP and 85% of export earnings) (CSA, 2012) including livestock production. Livestock production is an integral part of the country's agricultural production system and has a profound contribution to the national effort to ensure food self-sufficiency both at the national and household level (Dessie, 2011). In particular, chicken production is playing a fundamental role in its considerable potential to improve the livelihoods of rapidly increasing populations of Ethiopia since long time ago. Numerous indigenous chicken populations are reported to adapt to different

circumstances of various regions of the country. These chickens are being kept mainly by smallholders under backyard poultry farming mainly as a livelihood source of income.

Padhi *et al*. (2016) mentioned that commercial chicken production is world widely increasing because of its better efficiency, leaving indigenous breeds to hardly compete with. However, under normal circumstance, it is usually suggested that rare or endangered breeds are often highly adapted and their performances should be measured comparatively, within their own environmental conditions than comparing with other breeds under improved or modified conditions or under intensive management (Dessie, 2011). In other words, examining these breeds with respect to the products for which they were selected and valued in the conditions under which they evolved very meaningful. Azage *et al*. (2006) have in their remark stated that many occasions where growth rate, prolificacy, or milk production have been measured and used as criteria to point up the inferiority of purebred indigenous stock over that of exotic imported breeds or their crosses.

Needless to say, indigenous breeds are known to possess occasionally unique alleles pertinent to their adaptation (diseases resistance and climate) and breeding goals (quality egg and meat) (Zanetti, 2009). Moreover, they have also enormous use for scientific, cultural and economic use that urges us to conserve and improve for the use of the future (Koehler-Rollefson, 2014). Many scholars also advocate that utilization of indigenous genotypes by improving their competitiveness under the socioeconomic circumstances of their production environments is one of the practical options to ensure the conservation of genetic diversity.

Despite these beneficial roles, indigenous chicken genetic resources are not getting greater

attention for further improvement in the country. For instance, regardless of breed type, FAO (2007) reported that chicken population and an average number of chickens per household in Ethiopia have declined by 64% and 37% over the last 50 and 20 years, respectively. In Ethiopia, the Growth and Transformation Plan (GTP) of the government, has put ambitious targets to double the chicken meat production from the total meat production by 2030 as part of a broader and integrated livestock productivity improvement program (MOFED, 2010). However, due to the limited fundamental information on the genetic diversity of nationally acquired chicken populations, the absence of well-managed conservation genetics programmes and the uncontrolled genetic introgression between indigenous as well as exotic breeds are seriously threatening the future of many indigenous chicken populations of the country.

1.2. Statement of the problem

Genetic diversity is seriously suffering from genetic erosion in several fields of genetic resources especially in farm Animal genetic resources (Zanetti, 2009). This is especially true for the chicken industry where very few genotypes provide the breeding basis for the industrialized production (Romanov and Weigend, 2001). Weigend and Romanov (2002) stated that chicken genetic resources are considered to be one of the most endangered. In this regard, since the start of commercial chicken breeding in the middle of the 20th century, chicken genetic diversity has become partitioned among relatively few highly specialized lines. As a consequence, many dual-purpose breeds, resulting from centuries of domestication and breeding, are now at the risk of being lost (Hillel *et al*., 2003).

In a similar way, the issue of chicken genetic resources conservation is also a hotspot topic for Ethiopia, a country facing with major agricultural productivity challenges. For instance, according to IBC (2004), only limited research and development activities on phenotypic and genetic characterization have been conducted on chicken breeds of Ethiopia to conserve, reveal and exploit its genetic potential. As a result, little is known about the genetic diversity, structure, and degree of admixture within and between indigenous chicken populations in Ethiopia. Most breeds/populations may disappear before they have been recognized and exploited for breeding improvement goals. Specifically, in spite of the presence of various reports on the potential of indigenous chicken populations in Ethiopia, there are few studies, e.g. Hassen *et al*. (2009), Alemayehu *et al*. (2003), Mwacharo *et al.* (2007),Wragg *et al*. (2012) and Desta *et al*. (2014), which have reported the diversity of Ethiopian chicken using microsatellites, and SNP markers with no studies so far reporting the analysis of full genome sequences data.

Hence, taking all this facts and figures, understanding the level of genetic diversity at genome level within and among chicken populations is of paramount importance in identifying potential chicken populations for genetic improvement programs.

1.3. Research Questions and Hypotheses

I. Research Questions

The following research questions are addressed in this study:

- Is there any difference in genetic diversity among chicken populations of Ethiopia?
- How is the diversity partitioned within and among chicken populations?
- What is the genetic relationship between the target indigenous chicken populations?

- What are the regions and genes under strong selection pressures in Improved Horro and other indigenous chicken populations of Ethiopia?

II. Research Hypotheses

The following major hypotheses are tested:

- Due to the local preference of chicken genotypes among communities in Ethiopia, low genetic diversity within the population and high genetic variation between populations are expected.
- Chicken populations will show geographic structuring primarily induced by rare long-distance dispersal, followed by mutation and limited gene flow.
- Due to exchange at the local market, genetic distances between chicken populations will follow geographic distances.

1.4. Objectives of the study

The principal objectives of this study are the following:

The principal objectives of this study are the following:

1. To analyse the genetic diversity and population structure of Ethiopian indigenous chicken populations.
2. To analyse the genetic relationship between indigenous chicken populations.
3. To determine the genomic regions under strong positive selection pressure in indigenous chicken populations.

CHAPTER 2. LITERATURE REVIEW

2.1. Origin and history of chicken domestication

Chicken population makes up a large majority (around 30 billion) of avian breeds globally (Jensen, 2005). Chicken domestic genetic resources comprise a wide range of breeds and populations including native, also called indigenous, population, breeds and/or ecotypes, fancy breeds, middle-level food producers, industrial stocks and specialized lines (Weigend and Romanov, 2001). Some archaeological and molecular evidences ascertain that the domesticated chicken (*Gallus gallus*) populations evolved in Asia from a common ancestor, the red jungle fowl *Gallus gallus* (Kanginakudru *et al*., 2008; Nguyen-Phuc and Berres, 2018; Sawai *et al*., 2010; Storey *et al*., 2012). Molecular and archaeological findings also support more multiple maternal origins (Liu *et al*., 2006) with possible contributions from other junglefowl species (Boichard *et al*., 2012; Eriksson *et al*., 2008; Gifford-Gonzalez and Hanotte, 2011; Mwacharo *et al*., 2013). For instance, the yellow skin locus present in several domestic chicken breeds is believed to most likely originate from the grey jungle fowl *Gallus sonneratii* (Eriksson *et al*., 2008).

The time and the geographic center (s) of domestic chicken remain (Liu *et al*., 2006) uncertain. Some evidences confirm that the history of fowl domestication dates back to about 2000 B.C. (Kanginakudru *et al*., 2008; Sawai *et al*., 2010; Yap *et al*., 2010). But, more recent archaeological evidences showed that a much earlier domestication might have occurred around 6000 BC (Gifford-Gonzalez and Hanotte, 2011). Olusij (2010) indicated that the evolutionary history of the domestic fowl occurs in phases starting from the evolution of the genus Gallus, the emergence of

the domestic fowl from its progenitors followed by the appearance of the current breeds, varieties, strains, and lines. During the course of domestication, the chicken has been considerably changed and diversified by natural and artificial selections (Al-Nasser *et al*., 2007). For instance, the ancestor of the domestic chicken, the red jungle fowl, lays 10 to 15 eggs per year in the wild, whereas commercial laying hens are capable of producing more than 300 eggs per year (Weigend and Romanov, 2001) following human selection and the global emergence of the chicken meat and egg industries (Siegel *et al*., 2006; Toro *et al*., 2014). Mwacharo *et al*. (2013) indicated that the history of introduction and dispersal of village chickens across the African continent is a subject of intense argument and speculation among scholars. Socio-cultural, linguistic, archaeological and historic data all suggest the introduction of chickens to Africa is through multiple maritime and/or terrestrial routes over time. Dessie (Alemayhu, 2003) also suggested that chicken could have been introduced into Africa through the Isthmus Suez, the Horn of Africa and through direct sea trading between Asia and Eastern Africa. So far, no molecular genetics study has attempted to understand the genetic diversity and origin of African indigenous chickens at the continental level (Gifford-Gonzalez and Hanotte, 2011).

2.2. Chicken production systems in Ethiopia

The poultry sector in Ethiopia can be characterized into three major production systems(large-scale commercial, small-scale commercial and scavenging) based on some parameters such as breed, flock size, housing, feeding, health, technology and biosecurity (Tadesse, 2015). The most dominant type of poultry production system in Ethiopia is the scavenging production system inherently characterized by low productivity (Alemayhu, 2003; Halima *et al*., 2007). In this system, birds rely on what they are able to pick in the homestead with little or no supplementation

with food leftover waste and a small amount of grains. This system is characterized by a low input, minimal level of biosecurity, high off-take rates and high levels of mortality (Desalew *et al*., 2013). Here, there are little or no inputs for housing, feeding or health care. It does not involve investments beyond the cost of the foundation stock, a few handfuls of local grains, and possibly simple night shades, mostly night time housing in the family dwellings. Over 80-97% are indigenous and raised in small flocks (4-10 hens) and produce a maximum of 40 eggs/hen/year and to achieve a market live-weight of less than 1.5 kg at 6 months (Dessie *et al*., 2011). Still, under this situation, indigenous chicken populations represent an important resource from which improved lines can also be developed. Here, evidences are emanating from well designed, selective breeding programs of indigenous populations showing that significant productivity improvement can be achieved, while maintaining a reasonable level of adaptation, even under scavenging conditions.

For instance, this was manifested by the works on the improvement of Horro chicken populations in Debre Zeit Agricultural Research Centre (Dessie *et al*., 2011). Progress reports showed that survival has improved from less than 50% in the base generation to 98% in generation 6. Similarly, body weight at 16 weeks has increased substantially from 550g to 880g, while egg production per annum has got tripled from 24 to 72. These evidences pinpoint the potential of indigenous chicken populations for productivity improvement. However, these genetic resources are generally under exploited and under leveraged due to lack of effective capacity for local testing, multiplication, and delivery to farmers, followed by continuous genetic improvement. In fact, genetic improvements have been attempted by the government and several development agencies by rather crossbreeding programs of exotic commercial cocks with indigenous chickens than within breed improvement. Selection programs targeting to genetically improve, multiply and distribute

improved indigenous chickens to the farmers are still largely to come. In Ethiopia, much of the chicken improvement efforts have focussed on delivering exotic and more often inappropriate birds to the smallholders' context. For instance, chicken genetic improvement programs in the previous decades focused on the use of White Leghorns, Rhode Island Red, Brown Leghorns, New Hampshire, Cornish, Australoup, Light Sussex and Fayoumi breeds all demanding high input and intensive management (Dana, 2011). These high-yielding breeds are not a sustainable option for improving village poultry so long as the production conditions are not suitable to such genotypes none adapted to the low nutrition input, high disease incidence and weather patterns of a country like Ethiopia. Many scholars advise that breeding programs should be oriented in such a way that it can address the underlying socioeconomic and production circumstances of village chicken production systems.

The second poultry production system in Ethiopia is the small-scale commercial one. In this system, modest flock sizes usually ranging from 20 to 1000 exotic birds are kept for operating on a more commercial basis. Most small-scale poultry farms are located around Debre Zeit town in Oromia region and Addis Ababa. This production system is characterized by a medium level of feed, water and veterinary service inputs and minimal to low biosecurity.

The third type of poultry production system is a large-scale commercial system. This intensive production system involves keeping to 10,000 birds or even more under indoor conditions with a medium to high biosecurity level (Desalew *et al*., 2013). This system heavily depends on imported exotic breeds that require intensive inputs such as feed, housing, health, and modern management system. It is estimated that this sector accounts for nearly 2% of the national poultry population in

Ethiopia. This system is characterized by a higher level of productivity where poultry production is entirely market-oriented to meet the large poultry demand in major cities. The existence of somehow better biosecurity practices has reduced chick mortality rates to merely 5%. Key demographic and production parameters in poultry production systems are presented in Table 1.

Table 1: Key demographic and production parameters in poultry production systems

Parameters	Indigenous	Crossbred (layers)	Crossbred (Broilers)
Overall mortality rate before marketing	50	5	-
Mortality rate young stock	-	-	7
Mortality rate grower	-	-	52
Adult mortality percentage per year	20	3	
Egg production per hen per year(number)	42	308	NA
Kg total feed/kg egg produced/Kg/live weight	NA	2.7 kg/kg of egg	1.8 kg/kg of live weight
No. of animals sold per breeding female per year	1.61	NA	NA
Average weight at slaughter(kg)	1.5	2.4	2.3
Dressing percentage at slaughter (%)	65	6.4	65.2

Source: Livestock Master Plan, 2015

2.3. Description of indigenous chickens in Ethiopia

Indigenous chickens in Ethiopia are found in every corner of the country. They are not exhaustively but are closely related to the jungle fowl. Chicken populations in Ethiopia are non-descriptive which vary in plumage color, comb type, body weight, and body conformation. Under Ethiopian Chicken description context, no chicken was reported as a distinct breed despite some naming of distinct ecotypes. Living in different agro-ecologies they are often also referred as ecotypes. In most of the native flocks, broodiness (maternal instinct) is pronounced. They are characterized by slow growth, late maturity and low production performances (Desalew *et al*., 2013). The productivity of local scavenging chicken is low with high mortality of chicks. Duration of brooding time of a hen is wider with many cycles per year. Moreover, the low productivity of indigenous

stocks partially is attributed to the low management standard of the traditional production systems. Provision of vaccination, improved feeding, clean water, and nighttime enclosure relatively improves the production performance of indigenous chickens (Habte *et al*., 2013).

By and large, studies conducted on indigenous chickens to evaluate their performance usually ignore their unique physiological and behavioral characteristics and their socio-cultural values (Alemayhu, 2003). Due to their high genetic diversity, there is also remarkable variation in the performance of indigenous chickens within and among breeds. This variation is an important genetic attribute of the indigenous chicken, whereby selection can act to improve their performance (Ibid). About sixty million birds (n = 60,505,327) are available in Ethiopia for consumption, sale, breeding and socio-cultural values (CSA, 2016). Smallholder farmers keep birds for its low capital requirement, flexible production systems, and low production risk, taste, flavor and leanness (FAO, 2010; Halima *et al*., 2007). Under Ethiopian context, chickens are considered as the only type of livestock that many poor people can maintain relatively risk-free compared to another type of livestock enterprises (Dessie *et al*., 2011). It is providing a considerable potential to improve the livelihoods of many pro-poor communities of the country. However, low productive chicken genotypes dominate smallholder production systems, mainly owing to the absence of sound long-term chicken genetic improvement, multiplication and delivery systems (Dana, 2011; Padhi, 2016).

Improving chicken productivity is the first step to get out of poverty by improving family nutrition and socio-economic status (Dessie *et al*., 2011). Numerous productivity evaluation elucidates that indigenous chickens have remarkable performance than their improved counterparts under low to

medium input systems. Although indigenous chickens are known to have a number of adaptive traits in hot and humid tropics such as the necked neck, minimum and frizzle feathers, black bones and meats, the potential value of indigenous breeds remain under-estimated (Alemayhu, 2003; Dana, 2011; Fathi *et al*., 2017, 2013). Even though indigenous chickens are not fat growers and poor layers of small-sized eggs(about 45g), they are ideal mothers, good brooder, and excellent scavengers, sturdy and believed to possess better natural immunity against common poultry diseases (Alemayhu, 2003). Berthouly *et al*. (2008) advise the need to explore and properly manage indigenous chicken genetic resources as they represent both a heritage and a reservoir of genetic diversity. Chicken meat offers an attractive lower-carbon alternative to beef. However, chicken consumption is currently low in Ethiopia compared with other countries which are planned to boost to 30% by 2030 aimed to increase the chicken population by 70 million (CRGE, 2011).

2.4. Phenotypic and genotypic characterization of indigenous chicken populations from Ethiopia

2.4.1. Localization of phenotypic and genotypic studies across socio-physical factors

A combined analysis of a dataset of 28 phenotypic and 7 genotypic publications on Ethiopian indigenous chicken across socio-physical (religion, elevation, and agro-ecology) shows the different morphological and morphometric attributes of indigenous chicken (Table S 3, Table S 4, Table S 5). Different factors may affect the production characteristic of indigenous chicken and their phenotypes. For instance, religion may be expected to influence on cultural trait preferences of smallholders in regards to chicken phenotypes. Similarly, elevation and agro-ecology as a proxy of the natural selective forces may have shaped the morphology of the birds at major agro-

ecological zones. Geographic localization across Ethiopia of the various studies examined here is shown in Figure 1.

In term of socio-cultural environment, most of the studies (n = 20) reports the Christian Orthodox faith as the dominant religion in the geographic region of the chicken population reported here, followed by the Muslim one (n = 13), with few studies examining chicken population in Protestant (n = 4) and traditional (n = 3) faith areas (Table S 3). Elevation wise, most of the studies concentrate (n = 25) in elevations ranging from 1800-2400 (Table S 4). A sizable number of (n = 15) phenotypic studies were also carried out in elevations ranging from 1800-2400 masl. There are no studies in elevations less 500 and above 3200 masl. The different studies have variably distributed across agro-ecologies which most of them concentrated in Tepid to cool moist mid highlands (n = 9) and Tepid to cool sub-humid mid highlands (n = 8) (Table S 5). Tepid to cool sub-moist mid highlands (n = 1) and Hot to warm per humid lowlands (n = 1) are least represented.

2.4.2. Morphological diversity and its relationship with socio-physical factors

Various studies reported plumage coloration and pattern, earlobe, shank and skin color variants in flocks of IC of Ethiopia but with inconsistency in color definition between them (Table S 6; Table S 7). Colour is an important feature for most living organisms, having great significance in the wild by affecting the survival and reproductive success of the species. For instance, carotenoid-based ornaments (skin or feathers) in wild birds are considered to be signal of an individual's nutritional status or health, reflecting its foraging efficiency or immune status and are therefore implied to affect sexual attractiveness (Blas *et al*., 2006; Castaneda *et al*., 2005). On top of its advantage in terms of genetic variation, a diversity of colors may serve as a camouflage from

predator attack and in turn boost productivity where a free-range scavenging system is predominant. Apart from other methods, genetic variations in chicken can be described using traits based on pigmentation variants and comb varieties (Dana *et al*., 2010). Accordingly, different scholars consider color diversity of chicken as an important parameter in phenotypic diversity studies. Early color variants were mostly selected for utility reasons or religious practices (Sheppy, 2011). In Ethiopia, chicken plumage has greater economic significance and influences the local breeding strategies (Dana *et al*., 2010). Among others, the most critical color variant considered by farmers is plumage color which is given attention in local market preference and breeding objectives. To this end, a high diversity of Ethiopian IC plumage has been noted in the different phenotypic studies (Table S 10).

The most dominant plumage color variants are red (39.26%), black (39.14%) and white with two or more mixture of the dominant colors reported by different scholars (n = 14; Table S 7). In terms of its relationship with religion, plumage coloration is not significantly different across the dominant religion category ($P < 0.05$; Table S 18). Its relationship was not also significantly to vary across elevation category for all plumages except brown coloration ($P < 0.05$). Apart from the red and black dominant plumages, a diverse spectrum of plumages in variable proportion are reported. Red plumage is the commonest in Tepid to cool sub-humid mid-highlands (SH2; 39.26%) followed by Hot to warm humid lowlands (H1; 24.76%) agro-ecological zones (Table S 28). In contrast, there is no report of red plumage chicken in cold to very cold sub-humid sub-afro alpine to afro-alpine (SH3) agro-ecology. Similarly, black plumage chicken reported predominating in SH2 (39.14%) and H1 (21.93%), respectively. Apart from the red and black

dominant plumages, a diverse spectrum of plumages in variable proportion are reported. Only red, and zagolima plumages significantly vary across agro-ecologies ($P < 0.05$).

Earlobe color is a naturally and artificially selected trait in chicken. In breeding operations, it has been selected as a breed characteristic as a head furnishing trait. White/red earlobe color is a polygenic and sex-linked trait (Luo et al., 2018; Nie et al., 2016). Variable earlobe color variants proportion are also reported from different studies in Ethiopia (Table S 11). Chickens with black (56.46%) and red (41.81%) earlobe variants are the commonest among other comb types. This variant does not vary significantly ($P < 0.05$) across dominant religion demography and elevation for all earlobe color types (Table S 20). Variable earlobe colour variants proportion are also reported across the agro-ecological zones. The highest number of chickens with red earlobe variants (41.81%) is found in (Tepid to cool sub moist mid highlands (SM2) agro-ecological zone (Table S 11). While, chicken with black earlobe variants are the commonest in Tepid to cool moist mid highlands (M2; 56.46%) and it reaches 40.14% in Tepid to cool sub-moist mid highlands (SM2). Unlike chicken with black earlobe colour, chicken with white earlobe colours are found across a wide spectrum of agro-ecological zones. Except for brownish and multi-colour variants, other reported colors vary significantly ($P < 0.05$) in terms of distribution across the respective agro-ecologic zones. Earlobe colour has no significant variation across agro-ecologies for indigenous chickens ($P < 0.05$, Table S 20)

According to Jin *et al*. (2014), in chicken, skin pigmentation such as shank color is related to the levels of carotenoids and melanin. Yellow shanks are the commonest (50.98%) followed by white shank (25.59%) and black (10.59 %) shank color variants in Ethiopian IC (Table S 12). The rest

of the reported shank color variants show the least occurrence across the different reported study sites. To this end, the least occurred shank color across studies is the mottled type (0.14%). Shank color is not significantly variable ($P < 0.05$) across dominant religion demography and elevation category (Table S 22). White shank color variants significantly vary across agro-ecologies unlike yellow and black shank color variants ($P < 0.05$, Table S 29). The presence of feathered shank gene (Pti/pti) in indigenous chicken is also minimal (Table S 17). A variety of skin variants are also documented in different spatiotemporal studies. In this respect, white (48.87%) and yellow (30.86%) skin color variants are the most abundant phenotype across various socio-geographic factors (Table S 12). In contrast, there is little black (0.35%) and green (0.20%) skin color variants in M2 agro-ecology. There was no significant difference in the skin color of indigenous chicken across dominant religion, elevation and agro-ecologies ($P < 0.05$; Table S 23; Table S 32).

Like other coloration variants, eye color variants vary according to the carotenoid pigmentation and blood supply in the eye (Crawford, 1990). Under the context of Ethiopian IC, Eye color variants were only considered in few studies (n = 6, Table S 6; Table S 13). The most prominent eye color variants across these 6 studies are red (36.95%), black (23.80%), while, the least eye color variant is pearl (0.6%). The most prominent eye color variants across these 6 studies are red (36.95%), black (23.80%), while, the least eye color variant is pearl (0.6%). Eye color variants have no any relationship between the different dominant religion demographies and elevation categories (Table S 21). Unlike other plumage and earlobe color variants, eye color variants are only found in a few agro-ecological zones, with a single variant observed for hot to warm humid lowlands (H1) and hot to warm sub-moist lowlands (SM1) agro-ecological zones. Only blue black

and dark brown eye color variants are shown to significantly vary across agro-ecologies ($P < 0.05$, Table S 30).

Feather distribution is reported in Table S 16. The dominant feather distribution is Normal (84.88%) with the least proportion for shank and feet feather distribution (0.6%). Feather distribution is not significant across dominant religion demography, elevation category (Table S 24). The dominant feather morphology is indicated in Table S 16 comprising a major proportion for normal distribution (89.82 %). Feather morphology doesn't have significant variability across dominant religion demography and elevation category (Table S 25). Normal and crest type of feather distribution significantly vary across the variable agro-ecologic zones (Table S 34). Neck feather color variant was also only reported in a couple of studies (n = 2; Table 6 with a predominance of brown (25.18%) followed by white color variants (20.73%). Neck feather variant types do not vary significantly ($P < 0.05$) across dominant religion demography. Neck feather has also no significant variation ($P < 0.05$) with elevation category except for white neck feather type coloration (Table S 26) while white (48.87%) and yellow (30.86%) skin color variants are most widespread across study sites. None of the neck feather color variants are reported to significantly vary across agro-ecologies ($P < 0.05$, Table S 31).

Indigenous chicken (IC) feather genotypes reported in Ethiopia include normal feathered, crested head, frizzle, naked neck, and feathered shank (Table S 16). The naked neck (Na) gene is an autosomal, incompletely dominant gene described as one of the major genes in local chickens of the tropics that has desirable effects on heat tolerance and adult fitness (Fathi *et al.*, 2013). However, to the scope of this review, little proportion of naked neck (2.75%) genes have been

reported and distribute mainly in SH2 (66.57%) and H1 (24.78%) agro-ecology. This might be due to little availability of naked neck chicken (dominant genes) in Ethiopia or due to a single available study by Teketel (1986) as cited by Dana (2010) to exactly define the size and geographic distribution of these chicken. Moreover, this may be due to the fact that naked neck chicken is less preferred and have less aesthetic value to normal feathered and another type of chicken as they are considered ugly. Similarly, shank and feet (0.6%), as well as muff and beard (0.6%) feathered chicken, are available in extremely low frequency (Table S 16). About 97.73% of IC in Ethiopia reported having no shank feather. Another prominent phenotype in chicken is crest which is characterized by a tuft of elongated feathers atop the head. It shows an autosomal incompletely dominant mode of inheritance and is associated with a cerebral hernia (Wang *et al*., 2012). The crested head genotype is considered to be a superior egg producer (Ngeno *et al*., 2014). This gene is also rare in the flocks of Ethiopian IC (4.33%). Fewer proportion of crested birds have been reported and there is no work in birds with mutant phenotypes of the crest, necked nake, feathered shank, and frizzle adaptive genotypes in Ethiopia. The other genotype of Ethiopian IC chicken reported in various studies is frizzle (F) phenotype which is believed to be caused by a single autosomal incomplete dominant gene in which heterozygous individuals show less severe phenotypes than homozygous individuals (Ng *et al*., 2012). The rare abundance of frizzled (1.85 %) IC was also evidenced. The proportion of female chicken with a spur (43.65%) is also indicated in Table S 17. Normal feathered and crested chicken occurrence significantly vary across agro-ecologies ($P < 0.05$, Table S 24).

Comb type is a trait that shows considerable variability among domestic chicken (Shen *et al*., 2016). This variability was also ascertained in Ethiopian IC chicken (Table S 15). The dominant

comb types are single (42%), rose (31%) and pea (21%), while other comb types make the rest (7%). The remaining proportion include Walnut (2.42%), V-shape (2.18%), strawberry (0.34%), Cashion (0.38%), duplex (0.69%), buttercup (0.01%) and unclassified comb types (0.03%). Single comb type variants show a significant difference ($P < 0.05$) across dominant religion demography and elevation category, while, no variation is found for the rest comb type variants (Table S 19). The higher number of these comb type variants predominate in Tepid to cool sub-humid mid-highlands (SH2) followed by Hot to warm humid lowlands (H1) agro-ecology (Table S 33). Only single, rose and duplex comb types significantly vary across agro-ecological zones in contrast to the consistent occurrence for the range of other comb types ($P < 0.05$).

Body shape variants are presented in Table Table S 17 with a high predominance of blocky (59.43%) body shape type. Body shape does not significantly vary ($P < 0.05$) with the dominant religion demography except for blocky body shape (Table S 27).

2.4.3. Morphometric diversity and its relationship with socio-physical factors

Body weight is an important attribute in poultry production as it forms the basis for not only assessing growth and feed efficiency but also making economic and management decisions (Dahloum *et al*., 2016). The body weight of IC chicken ranges from 0.84-1.97 Kg (Table 2). The annual egg production per hen is 47-75 with the lowest (47 ± 5.07) and highest (75 ± 5.07). On top of body weight and egg number, body length and shank length are intensively studied traits involving a higher number of chicken individuals and chicken populations. Various quantitative traits measurements have been also reported in previous studies of Ethiopian IC (Table 2). On top of body weight and egg number, the overall least significant means and their test of significance

is indicated for shank length and other phenotypic traits (Table S 35; Table S 36). Analyses of variance of these traits across dominant religion category shows only wingspan, body length, shank circumference, and body height to significantly vary ($P < 0.05$; Table S 35). Only wattle length was significantly different across elevation category ($P < 0.05$; Table S 35). Body length, wingspan, comb length, keel bone length, neck length, and back length found significantly different ($P < 0.05$) across agro-ecologies (Table S 36).

Our review of phenotypic studies in Ethiopia shows that pelvic width, drum length, tarsus length, tarsus color, thigh circumference, breast width, jaw width wing, and wing length, which are often considered in other country studies not for Ethiopia.

Table 2. Descriptive statistics for morphometric traits of indigenous chicken

Variable	Minimum	Maximum	Mean	Std. deviation
Body weight (Kg)	0.840	1.98	1.26	0.23
No. of eggs/hen/year	47	76	61	11
Body length (cm)	17.75	40.38	33.04	5.68
Wing span (cm)	7.35	77.87	35.17	21.95
Neck length (cm)	10.10	18.93	14.18	3.25
Comb height (cm)	0.58	3.10	1.78	0.76
Comb length (cm)	1.85	5.88	3.37	1.25
Wattle length(cm)	0.59	3.69	2.04	0.97
Shank length(cm)	6.24	12.20	8.47	1.37
Shank circumference (mm)	0.53	3.92	2.01	1.45
Keel bone length (cm)	7.62	16.55	10.32	2.18
Chest circumference (cm)	23.89	30.47	26.26	1.79
Back length (cm)	16.51	21.84	18.97	1.73
Beak length (cm)	1.19	2.70	2.16	0.44
Spur length (cm0	0.08	0.66	0.33	0.23

2.4.4. Genetic diversity

Few genetic studies have been undertaken in IC chicken populations of Ethiopia (Table S 2). Among genetic diversity estimators He (n = 2), Ho (n = 8), MNA (n = 6), PIC (n = 3) and FIS (n = 5) are most studied in diversity studies in indigenous chicken populations of Ethiopia. However, considering the diversity and wide land size of the country, the studies are not representative in terms of sample size and physical coverage. Meta-analysis of results from combined studies indicate the range values for MNA (4.20-6.29), ENA (2.5-6.35), PA (2-3.75), He (0.12-0.63), allele/locus (4.7-5.10), Ho (0.27-0.93), FIS (0.02-0.17) and IBS (0.01-0.02) (Table 3). Only the effective number of alleles vary significantly across the different dominant religious demography ($P < 0.05$; Table S 37). Significant variation was observed between genetic parameters and elevation ($P < 0.05$; Table S 37). Also, mean number of alleles, polymorphic information content, coefficient of inbreeding and alleles per locus show a significant variation with agro-ecologies ($P < 0.05$; Table S 38).

Table 3. Reported genetic parameter values on indigenous chicken across studies

Variable	Minimum	Maximum	Mean	Std. deviation
Mean number of alleles/population	4.20	6.29	5.29	0.57
Allelic richness	4.82	4.95	4.89	0.09
Effective number of alleles	2.53	6.35	4.96	1.65
Alleles/locus	4.70	5.10	4.90	0.19
Private alleles	2.00	3.75	2.96	0.65
Observed heterozygosity	0.27	2.44	0.77	0.55
Expected heterozygosity	0.12	0.63	0.49	0.16
Coefficient of inbreeding	0.02	0.17	0.08	0.04
Mean PIC/population	0.47	0.72	0.59	0.09
Mean number of identity by state	0.01	0.02	0.02	0.00

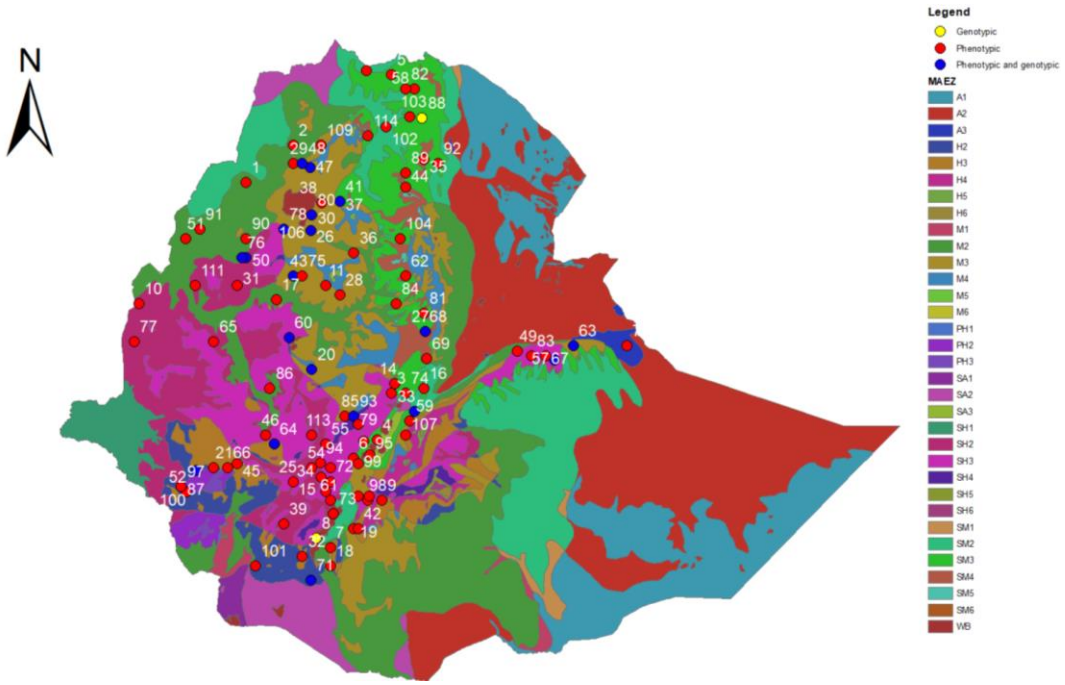


Figure 1. Geographic localization of the phenotypic (red circles), genotypic (yellow circles) and combined phenotypic- genotypic studies (blue circles) against the agro-ecological zones of Ethiopia.

See Table S 1. for sampling sites villages.

A1 = Hot to warm arid lowland plains; A2 = Tepid to cool arid mid highlands; SA1 = Hot to warm semi-arid lowlands; SA2 = Tepid to cool semi-arid mid highlands; SM1 = Hot to warm sub- moist lowlands; SM2 = Tepid to cool sub-moist mid highlands; SM3 = Cold to very cold sub-moist sub-afro-alpine to afro-alpine; M1 = Hot to warm moist lowlands; M2 = Tepid to cool moist mid highlands; M3 = Cold to very cold moist sub-afro alpine to afro-alpine; SH1 = Hot to warm sub-humid lowlands; SH2 = Tepid to cool sub-humid mid highlands; SH3 = Cold to very cold sub-humid sub afro-alpine to afro-alpine; H1 = Hot to warm humid lowlands; H2 = Tepid to cool humid mid highlands; H3 = Cold to very cold humid sub-afro alpine to afro-alpine; Ph1 = Hot to warm per humid lowlands; Ph2 = Tepid to cool per humid mid highlands (MOA, 2000).

2.4.5. Limitations of previous studies

Over all, in the process of reviewing the different phenotypic and molecular studies throughout Ethiopia, huge inconsistencies and less standardization of previous works in describing and addressing different qualitative variants across studies have been noted. For instance, different scholars provided various context of color variant descriptions (Table S 7. Besides, the various studies didn't consider the socio-physical environment in studying the different morphological and molecular diversities. Various scholars have suggested different ecotypes here and there despite little evidence of variation in phenotypic and genetic diversity. To the scope of this review, phenotypic studies that considered effective population size in Ethiopian ICs are not available. Lack of focus in targeting traits having significant socio-cultural and economical importance before designing of their diversity study was also another limitation of previous works. In this regard, the entire phenotypic studies only followed potentiality of chicken production.

Besides, Ethiopian phenotypic studies lack to mention measurement devices and if all measurements were taken by the same individual to avoid individual induced systematic errors. Studies that run PCA and develop a prediction equation for body weight are not reported in this review. No phenotypic studies also attempt to determine the phenotypic diversity indices and quality of distribution of the traits using the Simpson's diversity index and quality of distribution. Dendo-grams through the squared Euclidean distance of hierarchal cluster analysis were not obtained in any kind of phenotypic studies in indigenous chicken populations of Ethiopia based on various physical factors.

2.5. Overview of the chicken genome

The chicken is the first sequenced animal agricultural species with the first of the chicken genome released in 2004 (Burt, 2007, 2004; Jensen, 2005; Tixier-Boichard *et al*., 2011). Chickens are being widely used as a model organism to study human diseases like muscular dystrophy, immunological diseases and thyroid insufficiency to find and investigate candidate genes affecting such traits (Boichard *et al*., 2012; Cogburn *et al*., 2007; Jensen, 2005). The chicken genome contains 15% of repetitive DNA sequences comprised of short tandem repeats and several families of long interspersed elements (Soattin *et al*., 2009; Treangen and Salzberg, 2012; Wicker *et al*., 2004). It comprises 39 pairs of chromosomes including eight pairs of macro-chromosomes, one pair of sex chromosomes (Z and W) and 30 pairs of microchromosomes (Burt, 2007; Rao *et al*., 2007). The size of the chicken genome (Gallus_gallus-5.0; GCA_000002315.3) is estimated to be 1.28×10^9 (1,285,637,921) base pairs (

Table **4**). The chicken genome contains 24,838 genes distributed over 39 pairs of chromosomes plus 34,811,469 LTR elements; 20,000 DNA transposons, 140,000 simple repeats, 571 ncRNA genes and 4,000 satellites (https://www.ensembl.org/Gallus_gallus/Info/Annotation). The chicken genome was also confirmed to possess about 2.8 million genetic polymorphisms (Fulton, 2009) and 5 SNPs per kb unlike the human genome (1 SNPs per Kb) (The 1000 Genomes Project Consortium *et al*., 2015). Simultaneously with the release of the 2004 chicken genome sequence, the Beijing Genome Institute identified and released the 2.8 million single nucleotide polymorphisms (SNP) to the public domain.

Single nucleotide polymorphisms are single nucleotide variants within the DNA sequence. They were identified by comparing the Jungle Fowl genome sequence with partial sequence information

(0.3×) from 4 different chickens: 1 Silkie (Chinese breed), 2 commercial broilers (meat type), and 1 inbred laboratory White Leghorn (egg-layer type). These SNP have formed the basis for all the large SNP genotyping platforms developed to date. The second build was released in 2006 that corrected some of the deficiencies found in the first version. However, even this second build had multiple deficiencies. It was missing many of the gene-rich micro chromosomes. Chromosome 16 contains the major histocompatibility complex (cluster of immune function genes) and was very poorly covered. The Z chromosome is known to be incomplete and to have a considerable number of errors in gene order (Fulton, 2012). A third build of the genome (Gallus_gallus-5.0; GCA_000002315.3) has brought an increase of N50 contig and scaffold size to 252 Kb (460%) and 12.4 Mb, respectively (Warren *et al*., 2016). Gallus Gallus 5.0 shows an increase of 4679 annotated genes (2768 noncoding and 1911 protein-coding) over those in Gallus Gallus 4.0 (Warren *et al*., 2016). A third build of the chicken genome has been produced but has not yet been released for public access.

Table 4. Genome statistics for the chicken reference genome (Gallus Gallus 5.0) assembly.

Statistics	
Assembly	Gallus_gallus-5.0, INSDC Assembly GCA_000002315.3, Dec 2015
Base Pairs	1,285,637,921
Golden Path Length	1,230,258,557
Database version	Ensembl 92.5
Gene counts	
Coding genes	18,346
Noncoding genes	6,492
Small non-coding genes	1,705
Long non-coding genes	4,643
Miscellaneous non-coding genes	144
Pseudogenes	43
Gene transcripts	38,118

Data available from Ensemble genome data base.

(http://www.ensembl.org/Gallus_gallus/Info/Annotation).

2.6. Estimators of genetic diversity between and within chicken populations

Genetic diversity is a result of variations in DNA sequences among organisms due to mutations resulting from the substitution of single nucleotides (SNPs), insertion or deletion of DNA fragments, and duplication or inversion of DNA fragments (Fulton, 2009). It allows farmers to select stocks or develop new breeds in response to changing conditions to ensure food security (Toro *et al*., 2014). Besides, genetic diversity is important as an enormous number of livestock diversity is disappearing globally for a number of reasons to develop conservation and improvement strategies (Barker, 2001; Boettcher *et al*., 2010; Ruane, 1999; Simianer, 2005). A number of estimators of genetic diversity have been reported by different scholars.

2.6.1. Allelic variability

Allelic variability (number of alleles segregating in the population) is one of the estimators used to measure genetic diversity with key relevance in genetic conservation programmes (Barker, 2001; Simianer, 2005; Toro *et al*., 2014). The mean number of alleles (MNA) observed over a range of loci for different populations are a reasonable indicator of genetic variation provided that the populations are at mutational-drift equilibrium and that the sample size is almost equal for each population (Allendorf *et al*., 2010). Breeds with a low MNA have a low genetic variation which might be due to factors like-genetic isolation, historical population bottlenecks or founder effects and a high MNA implies great allelic diversity which could have been influenced by cross-breeding or admixture. The other estimators of allelic variability are the effective number of alleles (ENA) and allelic richness (Ar) (Allendorf *et al*., 2010). These parameters are used when the

sample sizes are not the same for each population under subject. ENA denotes the number of equally frequent alleles it would take to achieve a given level of gene diversity. It allows to compare populations where the number and distribution of alleles differ drastically. Ar is a measure of the number of alleles per locus but allows comparisons to be made between samples of different sizes by using the rarefaction technique or a Bayesian simulation approach to standardize populations to a uniform sample size.

2.6.2. Hardy-Weinberg equilibrium

The other fundamental parameter used to measure genetic diversity between and within populations is Hardy–Weinberg Equilibrium (HWE) (Zhou *et al*., 2009). A population is said to be in HWE when gene and genotype frequencies remain constant from generation to generation without the factors (e.g. selection, migration, and mutation) which can cause changes in these frequencies and in turn non-random union of gametes. Deviation from HWE in a population indicates possible inbreeding, population stratification and sometimes problems with the genotyping (Sha and Zhang, 2011). Allendorf *et al*. (2010) mentioned that the data required to test HWE in a natural population are gene and genotype frequencies and the size of the sample population at each locus. The χ^2-test remains the most popular option (Salanti *et al*., 2005; Shriner, 2011) and tests of HWE are commonly performed using a simple x^2 goodness-of-fit test that compares expected and observed numbers of heterozygotes and homozygotes (Allendorf *et al*., 2010; Allendorf and Luikart, 2007; Wigginton *et al*., 2005).

2.6.3. Linkage disequilibrium

Another estimator of genetic variation is Linkage disequilibrium (LD) which is described as the non-random association between different loci which may arise from admixture of populations with different gene frequencies; chance in small populations (e.g. endangered breeds); selection favouring one combination of alleles over another; the close association between markers in the same linkage group (Lee *et al*., 2012). LD between densely spaced, polymorphic genetic markers in different species contains information about historical events of recombination in a population (Hayes, 2003; Khanyile, 2015). Most measures of LD, such as r^2 and related measures, quantify the association between a pair of loci. The degree of linkage disequilibrium can be estimated directly from the genotypic frequencies in a sample of individuals taken from the population (Hayes, 2003).

2.6.4. Average heterozygosity and inbreeding

The average expected heterozygosity ($H_{e)}$ also called Nei's gene diversity; defined by Nei (1986) at n loci within a population; is the best general measure of genetic diversity within a population (Allendorf and Luikart, 2007). Individual breed average heterozygosity is estimated by summing heterozygosity at each locus and averaging these values over all loci (Hedrick and Kalinowski, 2000). It is often calculated based on the square root of the frequency of the null (recessive) allele as follows: H_e=1-$\sum_i^n$ pi^2, where pi is the frequency of the i^{th} allele (Allendorf *et al*., 2010; Allendorf and Luikart, 2007). The observed heterozygosity (H_O) is defined as the percentage of loci heterozygous per individual or the number of individuals heterozygous per locus. High heterozygosity values for a breed may be due to long-term natural selection for adaptation, to the

mixed nature of the breeds or to historic mixing of strains of different populations. A low level of heterozygosity may be due to isolation with the subsequent loss of unexploited genetic potential.

In genetics, inbreeding is defined as the mating of closest relatives (Allendorf and Luikart, 2007). The inbreeding coefficient (f) is the probability that the two alleles at a locus within an individual are identical by descent as they are derived from the same allele in a common ancestor in a previous generation. It is recommended that inbreeding coefficients should only be estimated for breeds which show significant deviation from the HWE (Curie-Cohen, 1981; Vieira *et al*., 2013). A large value reflects the existence of a small number of heterozygote genotypes and an excess of homozygote genotypes. A small value indicates the occurrence of heterozygote genotypes at a higher proportion than the homozygote genotypes.

2.6.5. Genetic differentiation

When a population is divided into subpopulations, there is less heterozygosity than there would be if the population was undivided (Kanginakudru *et al*., 2008). There are different types of approaches enumerated to quantify the distribution of genetic diversity within and between livestock populations. But, the two commonly used approaches to quantify the distribution of genetic diversity within and between populations include : Wright's F statistics (fixation indices) and AMOVA (Analysis of molecular variance). Computations of Wright's fixation indices (F_{IT}, F_{ST}, and F_{Is}) are pivotal and most widely used for studying the genetic differentiation of populations (Nei, 1986). The fixation index ranges from 0 (indicating no differentiation between the overall population and its subpopulations) to a theoretical maximum of 1. In other words, 0

indicates identical allele frequencies in a pair of populations (no differentiation) and 1.0 indicates alternate fixation for a single unique allele (the absence of any shared alleles) in each population. In practice, however, the observed fixation index is much less than 1 even in highly differentiated populations (Bird *et al*., 2011). The most commonly used programs for performing AMOVA are Arlequin, GDA, and GenAlEx (Excoffier and Smouse, 1992).

2.6.6. Determining genetic relationships between populations

Phylogenetic analysis is the means of inferring or estimating evolutionary relationships among breeds or populations and categorize cattle populations (Brinkman and Leipe, 2002). The evolutionary history inferred from the phylogenetic analysis is usually depicted as branching, treelike diagrams that represent an estimated pedigree of the inherited relationships among molecules, organisms, or both. The commonly used methods of clustering fall into two general categories: hierarchical and non-hierarchical. Hierarchical procedures are the most commonly used in animal diversity studies called phylogenetic analysis. The genetic distance measures are used to construct the dendrograms, also called phylogenetic trees. The two most commonly used methods for constructing the trees are unweighted pair group method (UPGMA) and the neighbor-joining method (NJ) (Backeljau *et al*., 1996). UPGMA trees give an indication of the time of separation (divergence) of breeds. The higher the branch length the longer is the separation period between breeds (Brinkman and Leipe, 2002).

2.7. Molecular markers for assessing chicken genetic diversity

Molecular (genetic) markers are defined as any stable and inherited variation that can be detected by a suitable technique to subsequently detect the presence of a specific genotype or phenotype other than itself (Fulton, 2009). The development of these markers has been created new opportunities for the selection and genetic improvement of livestock. Practically, DNA based polymorphisms are being used for marker-assisted selection strategies, parentage testing, species identification, and population genetic studies (Naqvi, 2007). These polymorphisms also provide the foundation for genetic linkage maps, which are being used to identify loci for economically important variation and speed up the rate of improvement in production traits (Zhang *et al*., 2015). The use of molecular and bio-chemical markers to predict the total genetic merit of livestock to redesign animal breeding and management programs were also appraised (Toro *et al*., 2009). Molecular markers are playing a role in estimating the diversity (Bruford *et al*., 2003; Gibson *et al*., 2006; Teneva, 2009; Weigend and Romanov, 2002), distinctiveness, population structure of animals (Gholizadeh and Mianji, 2007) and aid in the genetic management of small populations, to avoid excessive inbreeding (Zanetti, 2009). Among others, the most pronounced DNA-based molecular techniques that are used to evaluate DNA polymorphism in chickens improvement programs are reviewed as follows:

2.7.1. Restriction Fragment Length Polymorphism

Restriction Fragment Length Polymorphism (RFLP) is the most broadly used hybridization-based molecular marker (Tazeb, 2018). RFLPs are inherited as naturally occurring Mendelian characters and have their DNA rearrangements due to evolutionary processes, point mutations within the

restriction enzyme recognition site, mutations within the fragments, and unequal crossing over. The advantage of RFLPs is that they are co-dominant markers and are very reliable in linkage analysis and breeding. The limitations of the RFLP marker are that a large amount of DNA is required for restriction digestion and Southern blotting. The RFLP is relatively expensive and hazardous due to the requirement of a radioactive isotope. The assay is time-consuming and labor-intensive and only one out of several markers may be polymorphic, which is highly inconvenient especially for crosses between closely-related species which precluded its widespread adoption within the poultry breeding industry (Fulton, 2012). Their inability to detect single base changes restricts their use in detecting point mutations occurring within the regions at which they are detecting polymorphism.

2.7.2. Random Amplification of Polymorphic DNA

Another method for detecting polymorphic markers is the random amplified polymorphic DNA (RAPD) assay. This assay, which is based on the polymerase chain reaction (PCR), uses short oligonucleotide primers of arbitrary sequence to amplify discrete regions of the genome (Kumar and Gurusubramanian, 2011; Tingey and de, 1993). This marker was developed by William and his co-workers in 1990, which employs single primer usually with 10 nucleotide bases as oligo-nucleotide primers and a GC content of at least 50% to amplify discrete fragments of DNA in low stringency of polymerase chain reaction (Smiths *et al*., 1996). RAPD is a quick, rapid, and inexpensive method of studying the DNA polymorphisms within and between populations based on the amplification of random DNA segments with single primers of an arbitrary nucleotide sequence. This dominant marker has also been widely used in poultry research (Shivashankar, 2014). The RAPD markers were used to detect polymorphism among five breeds of chicken i.e.

White Leghorn and Rhodes Island Red (selected for part period egg production and egg mass respectively), Red Cornish and White Plymouth Rock (selected for early body weights) and Kadaknath (native breed) (Sharma *et al*., 2001). It was also used to evaluate genetic diversity and relatedness within and among four breeds of chickens and two turkey populations (Smiths *et al*., 1996). Among the PCR based DNA marker, RAPDs are cost-effective, most versatile and relatively easy to perform. The technique requires no prior knowledge of DNA sequence and utilizes minor quantities of DNA material, therefore, can be applied to even rare plant species. The main limitations encountered with the use of RAPD markers are repeatability of banding patterns and dominant inheritance. The ambiguity of the resulting fingerprint patterns and the fact that heterozygotes cannot be distinguished from homozygotes due to its dominant inheritance mechanism is another limitation of RAPD (Rege and Okeyo, 2006). In addition, how the genetic variation observed is generated is not fully understood, making reconstruction of evolutionary histories from RAPD data difficult.

2.7.3. Microsatellites

Microsatellites are also known as simple sequence repeats SSRs (Bruford *et al*., 2003); short tandem repeats (STRs) or simple sequence length polymorphisms SSLPs are the smallest class of simple repetitive DNA sequences. They are co-dominant, highly polymorphic, and multi-allelic. They are well-dispersed throughout the genome and are presumed to be selectively neutral. Microsatellite polymorphism refers to the differences in allele sizes due to variation in the number of repeats of base sequences that are detected by gel electrophoresis (Rege *et al*., 2006). They are known to be universal in prokaryote and eukaryote genomes and are present both in coding and

non-coding regions. Genetic diversity measures using the highly polymorphic variable number of tandem repeat loci yield reliable and accurate information for the study of genetic relationships between chicken populations (Weigend and Romanov, 2002). In addition, microsatellites are easy to identify and have low mutation rates (Zhang *et al*., 2002). Many microsatellites have recently become available and being exploited in chickens, and have been mapped in reference (Gholizadeh and Mianji, 2007). Based upon sites in which the same short sequence is repeated multiple times, they present a high mutation rate and codominant nature, making them appropriate for the study of both within- and between-breed genetic diversity (Toro *et al*., 2009).

2.7.4. Amplified Fragment Length Polymorphism

Amplified Fragment Length Polymorphism (AFLP) are based on the detection of restriction fragments by PCR amplification. Genomic DNA is restricted with two different restriction endonucleases and then a subset of these are amplified using a modified PCR and visualized using radioactivity, silver staining or fluorescent dyes for use with an automated sequencer (Rege and Okeyo, 2006). Advantages of the AFLP are that no prior sequence information of the genome is required. A large number of polymorphic bands are produced and the technique is highly reproducible and standardized kits are available (Duim *et al*., 2000). According to the narrations of Toro *et al*. (2009), the AFLPs are dominant bi-allelic markers that provide an easy way to carry out a genome-wide screening of variation. AFLPs are reliable informative multi-locus probes and provide high levels of resolution that allows delineation of complex genetic structures (Rege and Okeyo, 2006). They have the disadvantage of a reduced power to analyze within-breed diversity due to the dominant mode of inheritance but could be very useful in analyzing between-breed variation.

2.7.5. Single Nucleotide Polymorphism

Single nucleotide polymorphism (SNP) is a new and very promising molecular marker system which offers opportunities to assess the genetic diversity in farm animal species differently by investigating the mode and extent of changes in specific positions in the genome (Weigend and Romanov, 2002). They can be explained as any polymorphism between two genomes that is based on a single nucleotide exchange (Fulton, 2008). These are the most frequent type of variations found in DNA and their discovery together with insertions/deletions has formed the basis of most differences between alleles (Gu, 2004; Ye *et al*., 2007). SNPs may occur in the coding, non- coding (most frequent in this region) and intergenic regions of the genome. SNPs represent one of the more interesting approaches in animal identification because they are abundant in the genome, genetically stable and amenable to high-throughput automated analysis (Teneva and Petrovic, 2010). On average, SNPs occur every 1000 - 2000 bases and thus could be used as a genetic marker to systematically explore SNP variants for associations with quantitative traits (Gu, 2004; Ye *et al*., 2007). In the chicken genome, SNP has been identified with a frequency of 1 SNP per 225 bp, which is 5 times as many as in humans (Jalving *et al*., 2004; Orsini *et al*., 2011). Toro *et al*. (2009) have indicated their potential to detect both neutral and functional genetic variation because, although most of them are located in non-coding regions, some correspond to mutations inducing changes in expressed genes.

In animal breeding and genetics, SNP offers opportunities to assess the genetic diversity in farm animal species differently by investigating the mode and extent of changes in certain positions in

the genome (Weigend and Romanov, 2002) and for association mapping of genes controlling complex traits and provide the highest map resolution. SNPs offer several advantages over other types of DNA marker systems and are rapidly becoming the markers of choice for many applications in genome analysis due to their abundance (especially important in linkage disequilibrium-based mapping approaches) and also because high throughput genotyping methods are being developed for their analysis. The additional advantage offered by this approach lies in the phylogenetic information gathered through sequence variation analysis that allows drawing inferences on allele and population history that cannot be gathered with any of the other marker systems available. SNPs are also evolutionarily stable (i.e. do not change much from generation to generation) making them easier to follow in population studies (Rege and Okeyo, 2006).

Groenen *et al*. (2011) have affirmed that a high success rate of the SNPs on the Illumina chicken 60k bead chip. Johansson and Nelson, (2015) have used the 60k SNPs to characterize the genetic diversity and map loci associated with a trait that are segregating in both Swedish local chicken breeds. Kranis *et al*. (2013) also developed a very high-density 600k SNP genotyping array for chicken commercial lines. With regard to the mapping of genes of interest in indigenous chickens, so far a single work has been done by Wragg *et al*. (2012) who used 15 randomly selected 5 chicken Ethiopian populations (in Gondar, Konso, Gumuz, Sheka, and Guduro) together with other breeds. They mapped phenotypic traits (skin and egg color) using genome-wide association study and revealed the possibility of fine mapping of non-pedigree chicken populations to characterize Mendelian traits at the molecular level using association analysis. Wragg and his colleagues also recommended that at least 90-110 kb SNPs are required for effective genome-wide associations

study in village chickens. Their study considered a few numbers of samples (three chickens from each population) and it used a 50 K SNP chips.

2.7.6. Mitochondrial DNA

Mitochondria are sub-cellular organelles containing an extra chromosomal genome that is separate and distinct from the nuclear genome. Mitochondrial DNA is maternally inherited, does not undergo recombination, is a valuable molecule in investigating phylogenetic relationships among populations, subspecies, and species, and can be used to evaluate the maternal genetic constitution for a specific population (Shen *et al*., 2002). Shen and his colleagues in their study have made the first attempt to estimate the level of mtDNA diversity in the Chunky broiler and to compare it with some other chicken breeds used for egg production. They have presented new molecular evidence from the entire mitochondrial cytochrome b gene for the Chunky broiler and three other egg-chicken breeds.

2.8. The Major Histocompatibility (MHC) gene in chicken

The Major Histocompatibility Complex (MHC) is a highly conserved gene comprising a cluster of over 80 genes (92 kb) spanning on chromosome 16 (Chazara *et al*., 2011) characterized by high polymorphism and a tight linkage into a single supergene complex (Baelmans *et al*., 2005; Jarosinski *et al*., 2010; Miller *et al*., 2004), which have sought the attention of researchers for their association with disease resistance or susceptibility (Banat *et al*., 2013; Chazara *et al*., 2013, 2011; Gao *et al*., 2015; Hoque *et al*., 2011; Owen *et al*., 2008; Walker *et al*., 2011; Weigend and Romanov, 2001). Particularly, the chicken MHC on GGA16 has long been known as a gene region

contributing significantly genetic resistance to infectious diseases (Hosomichi *et al*., 2010, 2009; Miller and Taylor, 2016; Warren *et al*., 2017). It comprising loci encoding receptors which bind amino acid fragments from foreign pathogens on the surfaces of various immune and non-immune cells (Baelmans *et al*., 2005; Chen *et al*., 2012; Fulton *et al*., 2016; Jarosinski *et al*., 2010; Ncube *et al*., 2014; Nguyen-Phuc *et al*., 2016; Nikbakht and Esmailnejad, 2015; Zheng *et al*., 1999).

LEI0258 is a highly polymorphic microsatellite locus located within the BF region of MHC-B on chromosome 16 and has been reported to have a direct association with chicken performance (Chazara *et al.*, 2011; Figure 2). These include antibody responses to vaccination against Newcastle Disease Virus (NDV), Marek's disease, corona virus and coccidiosis (Baelmans *et al*., 2005; Briles *et al*., 1977; Nikbakht and Esmailnejad, 2015; Hateren *et al*., 2013). Its association with body weight, survival, embryonic mortality, fertilization rate, hatchability, egg production and resistance to worms has also been documented in many studies (Wang *et al*., 2014). Given the high level of polymorphism, LEI0258 marker genotypes have been suggested as good indicator of MHC-B haplotypes and it has become an important genetic marker used in chicken breed improvement program (Nguyen-Phuc *et al*., 2016). This has been confirmed by Chazara *et al*. (2013) who have ascertained that the LEI0258 marker genotypes an excellent predictor of the heterozygosity at the MHC locus. LEI0258 is described as atypical variable number tandem repeat (VNTR) which is composed of 12 bp (CTTTCCTTCTTT) and 13 bp (CTATGTCTTCTTT) conserved sequences which are flanked on both sides by indels and SNPs (Fulton *et al*., 2006). In an association study of MHC haplotypes with Marek's disease, Cole found 96.5% resistant of the birds with B-21 haplotypes were resistant to viral infection while of the birds with the B-19 haplotypes suffered 100% incidence of mortality. Polymorphisms are high at LEI0258. Fulton *et*

al. (2006) observed allele size diversity ranging from 182 bp -552 bp. Lwelamira *et al*. (2008) genotyped two chicken ecotypes from Tanzania and they identified 22 and 23 alleles at LEI0258, respectively. They further report that allele 206 bp had a significant positive correlation ($P < 0.001$) with the elevated antibody responses against NDV vaccine, whereas the allele 307 bp was positively correlated with body weight trait.

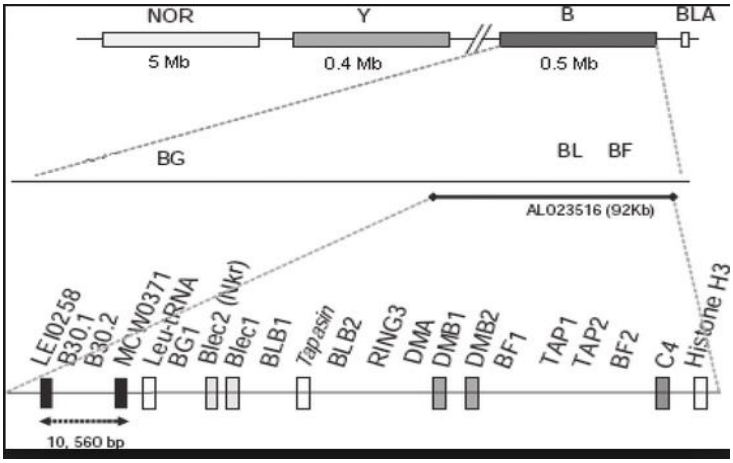


Figure 2. Schematic location of the LEI0258 marker in the chicken MHC map (Fulton, 2006). BF = MHC class 1; BG = MHC class 4; BL = MHC class 2; NOR = nucleolar organizer region; Y = MHC-Y complex; B = MHC-B complex; and BLA = MHC class 2 α gene (Izadi *et al*., 2011).

2.9. Approaches for detecting signatures of selection

The identification of regions that have undergone selection is one of the principal goals of theoretical and applied and evolutionary genetics (Gouveia *et al*., 2014). Such studies can also provide information about the evolutionary processes involved in shaping genomes, as well as physical and functional information about genes/genomic regions (Ibid). Artificial selection is the primary factor in the domestication and breeding history of livestock species. In the genomic era, selection refers to any nonrandom, differential propagation of an allele as a consequence of its phenotypic effect (Vitti *et al*., 2013). Selection may act in a directional manner, in which an allele

is favored and so propagated (positive selection) or disfavored (negative selection, also called purifying selection) (Ibid). Positive selection leaves a more conspicuous footprint on the genome that can be detected using a number of different approaches (Jacobs *et al*., 2016; Pavlidis and Alachiotis, 2017; Ronen *et al*., n.d.; Wollstein and Stephan, 2015). The detection of "signature of selection" is now possible on a genome-wide scale in many plant and animal species and can be performed in a population-specific manner due to a wealth of per population genotype data that is available (Cadzow *et al*., 2014). Identification of the genomic signatures of recent selection may help uncover casual polymorphisms controlling traits relevant to recent decades of selective breeding in livestock (Fu *et al*., 2016) and can contribute to further shaping economically important traits (Ma *et al*., 2018).

The tools used to detect evidence of selection are dependent on the nature of selective signature being investigated, which itself depends on the time scale over which selection occurred (Fu *et al*., 2016; Roosen *et al*., 2016; Tarekegn, 2016; Williams, n.d.). The Fst statistic has been a popular choice for investigation selection by utilizing differences in allelic frequency between populations to infer selective pressure in one population relative to the other and allowing detection of potential selection occurring in the range of 50,000 to 75,000 years prior for human populations (Ibid). A locus that shows significantly highest Fst statistics compared with other loci provides evidence of positive selection (Nielsen, 2005). Tajima's D is also another method suitable for detecting evidence of positive selection in human populations occurring within the past 250,000 years or approximately 10,000 generations and operates by identifying an excess of low to low intermediate frequency variants. Another commonly used measure is Fay and Wu's H (Fay and Wu,2000) which is useful for detecting evidence of more recent positive selection (80,000 years or approximately 3000 generations), particularly for intermediate-high frequency variants and thus

complements Tajima's D and other methods (Baxevanis and Ouellette, 2001). Analysis of haplotypes provides another mechanism for identifying evidence of selection, with a number of methods utilizing the Extended Haplotype Homozygosity (EHH) concept. One of the more popular of these approaches is the Integrated haplotype Homozygosity Score (iHS) methodology, which provides a standard measure of the decay in EHH around a point (e.g., a SNP) from derived allele relative to the central allele (Voight *et al*., 2006). Regions of slowly decaying haplotype Homozygosity in the derived allele (longer than expected haplotypes, relative to the ancestral allele) are thus indicative of selection at that locus (Cadzow *et al*., 2014). Rubin *et al*. (2012), and Elferink *et al*., (2012) have investigated selection signatures in a large number of chicken breeds using Z-transformed pooled Heterozygosity (ZHp) scores. This statistic estimates local heterozygosity depression in chromosomal regions and has been appropriately applied for detecting alleles that have swept to fixation or near fixation for long-term directional selection or during domestication (Fu *et al*., 2016; Rubin *et al*., 2010). Both the Fst statistic and Tajima's D can be calculated using standard genotype data obtained from heterozygous populations must be phased prior to calculation of iHS (Cadzow *et al*., 2014).

Table 5. An overview of common approaches for detecting signatures of selection.

Methods	Intuition	Representative tests
Gene-based	Synonymous substitutions are selectively neutral. If the rate of nonsynonymous substitution differs significantly, it is suggestive of selection	dN/ds(w); McDonald-Kreitman test (MKRT)
Frequency-based	In a selective sweep, a genetic variant reaches high prevalence together with nearby linked variants (high frequency derived alleles). From this homogeneous background, new alleles arise but are initially at low frequency (Surplus of rare alleles).	Ewens-Watterson test; Tajima D and derivatives; Fay and Wu's H
Linkage disequilibrium based	Selective sweeps bring a genetic region to high prevalence in a population, including the casual variant and its neighbors. The associations between these alleles define haplotype, which persists in the population until recombination breaks these	Long-range haplotype (LRH) test; Long range haplotype similarity test; Integrated haplotype score (His); Cross-population extended haplotype homozygosity (XP-EHH); Linkage disequilibrium decay; Identity by descent (IBD) analyses.
Population differentiation	Selection acting on an allele in one population but not in another creates a marked difference in the frequency of that allele between the two populations. This effect of differentiation stands out against the differentiation between the two populations with respect to neutral (i.e., non-selected) alleles.	Leontin-Krakauer test (LKT); Locus specific branch length (LSBL); hapFLK

Source: Vitti *et al*., 2013

CHAPTER 3. DIVERSITY OF LEI0258 MICROSATELLITE IN ETHIOPIAN INDIGENOUS CHICKEN POPULATIONS

Abstract

Indigenous chicken are locally adapted to environmental challenges and provide subsistence to millions of farmers in Africa. However, their productivity remains low compared to exotic chicken strains. Efforts are being made to combine the local adaptation of indigenous chickens with productivity traits of exotic chickens. Understanding the link between genetic diversity and environmental challenges is opening the door to marker-assisted breed improvement programs for sustainable chicken production at smallholder farmer level. Genetic variation at LEI0258 microsatellite found within the MHC region has been linked to infectious diseases resistance/susceptibility in commercial breeds. Here, we report diversity of LEI0258 in 236 chicken from 24 Ethiopian indigenous chicken populations from different agro-ecological zones using gel electrophoresis and sequencing. The MHC polymorphism was ascertained through genotyping the LEI0258 microsatellite locus by PCR-based fragment analysis followed by Sanger sequencing. The number of alleles, allele frequency, and heterozygosity levels were used to measure diversity within populations whilst the Wright's fixation indices were used to analyze the level of population structuring. Twenty nine LEI0258 allele sizes were observed using capillary electrophoresis. Allele sizes ranged from 185 to 569 bp with no significant difference in allele frequencies between populations ($P < 0.01$). Allele frequencies were in Hardy and Weinberg Equilibrium in all population except in Dara chicken ($P > 0.05$). Excluding the tandemly repeated motif, we identified 412 monomorphic and 35 polymorphic sites. The number of point mutation

and indels are 33 and 17, respectively. The number of R12 CTTTCCTTCTTT repeats ranged from 2 to 18, while R13 CTATGTCTTCTTT was found invariant in all populations. Sequences relationships reveal two distinct groups of alleles. The high diversity at microsatellite LEI0258 at Ethiopian indigenous village chicken populations supports the importance of the MHC region in relation to the disease challenges diversity faced by smallholder poultry production within and across Ethiopian agro-ecologies. We recommend that breed improvement programs ensure the maintenance of this diversity by selecting breeding stock as diverse as possible at the LEI0258 locus.

Keywords: Chicken, Genetic Diversity, Ethiopia, LEI0258 microsatellite, MHC

3.1. Introduction

High evolutionary pressures occurred in chicken during the course of domestication and subsequent natural and human selection (Downing *et al.*, 2009). Among others, infectious diseases exert strong selective pressures by affecting genes associated with innate and adaptive disease resistance and susceptibility. According to Salomonson *et al*. (2014), many of the genes involved in immunity are part of multigene families. In some families, each gene is conserved for a specific function dedicated to a particular outcome, in others allelic polymorphism and copy number variation allow rapid evolution in response to new environmental challenges, and other families comprise both kinds of genes (Miller *et al*., 2004). The Major Histocompatibility Complex (MHC) is one of these multigene family comprising loci encoding receptors which bind amino acid fragments from foreign pathogens on the surfaces of various immune and non-immune cells (Baelmans *et al.*, 2005; Chen *et al.*, 2012; Fulton *et al*., 2006; Fulton *et al.*, 2016; Jarosinski *et al*., 2010; Ncube *et al.*, 2014; Nguyen-Phuc *et al.*, 2016; Nikbakht *et al.*, 2013). MHC is a cluster of over 80 genes (92 kb) spanning chromosome 16 (Chazara *et al.*, 2013, 2011; Lima-Rosa *et al.*, 2005; Miller *et al*., 2004; Nikbakht and Esmailnejad, 2015; Walker *et al*., 2011) characterized by high polymorphism and a tight linkage into a single supergene complex (Miller *et al.*, 2004), which have sought the attention of researchers for their association with disease resistance or susceptibility.

LEI0258 is a highly polymorphic microsatellite locus located within the BF region of MHC-B on chromosome 16 (Kannak *et al*., 2017; Miller *et al.*, 2004). It has been reported to have a direct association with chicken performance and diseases tolerance (Nikbakht and Esmailnejad, 2015).

It includes allelic variation in antibody responses to vaccination against Newcastle Disease Virus (NDV) (Baelmans *et al.*, 2005; Nikbakht *et al*., 2013), Marek's disease (Fulton *et al.*, 2016; Wang *et al.*, 2014), corona virus (Hateren *et al.*, 2013) and coccidiosis. Also, its association with body weight, survival, embryonic mortality, fertilization rate, hatchability, egg production and resistance to worms has also been documented in many studies (Owen *et al.*, 2008). Given its high level of polymorphism and linkage disequilibrium association with the MHC-B locus, LEI0258 marker genotypes has been suggested indicator of MHC-B haplotypes, and it has become an important genetic marker used in chicken breed improvement programs *(Banat, 2013; Gao et al*., 2015; Hoque *et al*., 2011; Weigend *et al*., 2001). This has been confirmed by Chazara (2013) who have ascertained that the LEI0258 marker genotypes an excellent predictor of the heterozygosity at the MHC loci.

LEI0258 is described as an atypical variable number tandem repeat (VNTR) locus which is composed of 12 bp (CTTTCCTTCTTT) and 13 bp (CTATGTCTTCTTT) conserved repeat sequences which are flanked on both sides by indels and SNPs (Fulton et al., 2006). In an association study of MHC haplotypes with Marek's disease, Bumstead (1998) found that 96.5% of the birds with B-21 haplotypes were resistant to viral infection while of the birds with the B-19 haplotypes suffered 100% incidence of mortality. Polymorphisms are high at LEI0258. Fulton *et al*. (2006) observed allele size diversity ranging from 182 bp -552 bp. Lwelamira (2008) genotyped two chicken ecotypes from Tanzania and they identified 22 and 23 alleles at LEI0258. They further report that allele of 206 bp length had a significant positive correlation ($P < 0.001$) with elevated antibody responses against NDV vaccine, whereas the allele 307 bp was positively correlated with body weight traits.

Indigenous chicken (IC) (*Gallus gallus domesticus*) are widely distributed in the diverse agro-ecological zones of Ethiopia. Accordingly, they represent ecotypes which may possess unique combinations of alleles in a given gene (Ngeno *et al*., 2015). Relatively, few works have been done so far on the genetic characterization at molecular level Ethiopian indigenous chicken. In particular, no studies have attempted so far to characterize the immune system of Ethiopian chicken. We report here the characterization and diversity of the MHC-linked LEI0258 microsatellite marker in 236 indigenous chickens from 24 distinct populations sampled across Ethiopia.

3.2. Materials and methods

3.2.1. Whole blood sample collection

Blood samples were collected from 24 chicken populations in Ethiopia (Figure 3). Samples included 80 cocks and 156 hens. Except for Tsion Teguaz and Meseret populations, two villages per population were sampled (8-10 chicken from each village). One or two chicken were sampled per household. Photographs and weight of each bird were taken. The average weight of sampled chicken was 1.26 Kg with age ranges of 5 to 36 months. Sampling included chicken from different agro-ecological zones with an altitudes ranges of 730 -3500 meters (Table 6). From the wing vein of each chicken, 50 - 250 µl of whole blood was drawn with syringes using cryo-tubes filled with 1.5 ml absolute ethanol (100%) following the guidelines available at https://www.sheffield.ac.uk/nbaf-s/protocols_list.

Table 6. Sampling sites

No.	Sampling site	Sample size	Agro-ecology	Elevation(meteres absl)
1	Adane	10	Tepid to cool moist mid highlands	2455
2	Alfa Midir	10	Cold to very cold moist sub-afro-alpine to afro-alpine	3404
3	Amesha Shinkuri	10	Tepid to cool moist mid highlands	2464
4	Arabo	10	Tepid to cool moist mid highlands	1521
5	Ashuda	10	Hot to warm sub-moist lowlands	2028
6	Batambe	8	Tepid to cool moist mid highlands	2511
7	Bekele Girisa	10	Tepid to cool sub-humid mid highlands	1643
8	Dikuli	10	Hot to warm sub-moist lowlands	2093
9	Gafera	10	Tepid to cool moist mid highlands	2515
10	Gesses	10	Hot to warm sub-moist lowlands	1192
11	Gijet	10	Hot to warm sub moist lowlands	2050
12	Hadush Adi	10	Hot to warm sub moist lowlands	1494
13	Hugub	10	Hot to warm arid mid highlands	737
14	Kefis	10	Hot to warm moist lowlands	1061
15	Kido	10	Hot to warm sub-moist lowlands	1304
16	Kumato	10	Hot to warm sub-humid lowlands	1728
17	Loya	10	Tepid to cool humid mid highlands	1896
18	Meseret	10	Hot to warm sub moist lowlands	2291
19	Metkilimat	10	Hot to warm sub moist lowlands	1751
20	Mihiquan	9	Tepid to cool sub-moist mid highlands	1316
21	Negasi Amba	10	Cold to very cold moist sub-afro-alpine to afro-alpine	3060
22	Shubi Gemo	10	Tepid to cool sub-humid mid highlands	1555
23	Surta	9	Tepid to cool moist mid-highlands	2529
24	Tsion Teguaz	10	Hot to warm sub moist lowlands	1931

absl = above sea level

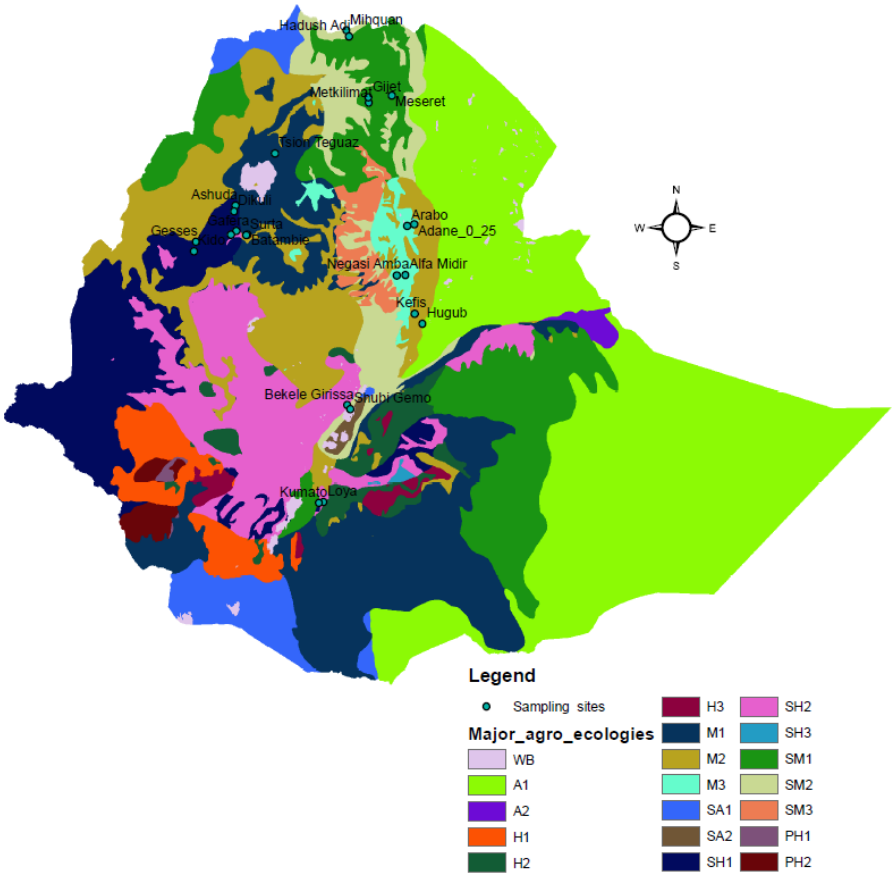


Figure 3. Agro-ecological map of Ethiopia with sampling site (MOA, 2000).

WB = Water body; A1 = Tepid to cool arid mid highlands; Hot to warm semi-arid lowlands; H1 = Hot to warm humid lowlands; H2 = Tepid to cool humid mid highlands; H3 = Cold to very cold humid sub afro-alpine to afro-alpine; M1 = Hot to warm moist lowlands; M2 = Tepid to cool moist mid highlands; M3 = Cold to very cold moist sub-afro alpine to afro-alpine; SA1 = Hot to warm semi-arid lowlands; SA2 = Tepid to cool semi-arid mid highlands; SH1 = Hot to warm sub-humid lowlands; SH2 = Tepid to cool sub-humid mid highlands; SH3 = Cold to very cold sub-humid sub-afro-alpine to afro-alpine; SM1 = Hot to warm sub-moist lowlands; SM2 = Tepid to cool sub-moist mid-highlands; SM3 = Cold to very cold sub moist sub afro-alpine to afro-alpine; PH1 = Hot to warm per humid lowlands; PH2 = Tepid to cool per-humid mid highlands.

3.2.2. DNA isolation

Total DNA was extracted from chicken whole blood at the BecA-ILRI Hub, Nairobi, Kenya facility (http://hub.africabiosciences.org/) using the Qiagen DNeasy blood and tissue kit protocol (Lwelamira *et al*., 2008). To evaluate the DNA concentration a Thermo Scientific NanoDrop spectrophotometer 2000c was used. The integrity of DNA was confirmed by agarose gel electrophoresis whereby 20 ng/µl genomic DNA samples were loaded with 1 µl loading dye (6X) on 1% agarose gel containing 2.5 µl gel red at a voltage of 7/cm for 60 minutes, 3 µl of lambda DNA of size of 48,500 bp and at concentration of 20 ng/µl was used as size marker and the gel was then examined using UV light using a GelDoc-It^2 Imager to check the DNA quality and quantity. The total amount of DNA was normalized to 20 ng/µl using milliQ water for polymerase chain reaction (PCR) and genotyping.

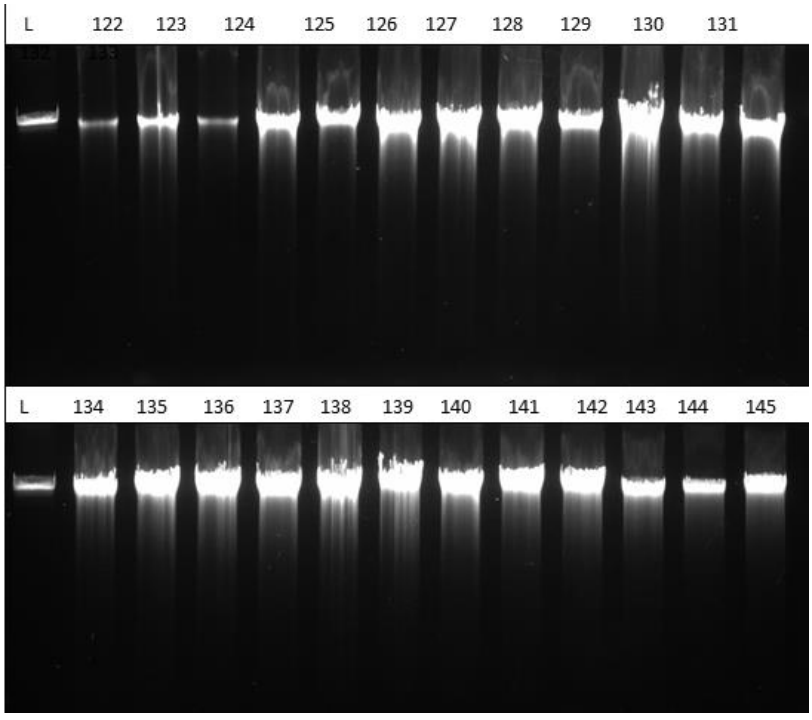


Figure 4. Image of Genomic DNA on 1% agarose gel run at 7/cm for 60 minutes.

3.2.3. MHC genotyping

PCR amplification

PCR amplification was carried out using a thermo-cycler PCR machine ABI PCR 9700 (Applied Biosystems). The primer sequences (GenBank accession number Z83781) for PCR amplification of LEI0258 were: forward 5'-CACGCAGCAGAACTTGGTAAGG -3' (length = 22 bp; GC content 47.6%; Tm = 71.5℃) and reverse-5'-AGCTGTGCTCAGTCCTCAGTGC-3' (length = 22 bp; GC content 46.2%; annealing temperature 69.9℃). The optimal PCR conditions were as described in (Gupta *et al*., n.d.; Han *et al*., 2013; Izadi *et al*., 2011; Nikbakht *et al*., 2013) either in a total volume of 10 µl, including 2 µl of template genomic DNA (20 ng), 5 µl of non-dyed *Taq* DNA Polymerase (1000 U) (Shangai, China), 0.3 µl of PET-labelled forward primer (3 µM), 0.3 µl of reverse primer (3 µM) and 2.4 µl of milliQ water, or a total reaction volume of 50 µl including 3 µl of 20 ng template genomic DNA, 25 µl of Dyed Bioneer Master mix (2x), 3 µl of forward primer (3 µM), 3 µl of reverse primer (3 µM) and 16 µl of milliQ water. The PCR conditions were set with an initial denaturation at 94℃ for 3 minutes; 30 cycles of 94℃ for 45 seconds; annealing temperature of 63℃ for 1 minute; extension of 72℃ for 1 minute; final extension at 72℃ for 20 minutes and final hold at 15℃. 2 µl volume of PCR product were loaded on a 2% agarose gel containing 2.5 µl of gel red and separated by electrophoresis at a voltage of 7/cm for 60 minutes. A 1 Kb ladder DNA from Bioneer was used as a reference to the size of the amplicons (Figure 5). The gel was exposed to UV light using GelDoc-It^2 Imager, to reveal the amplified fragments and their size.

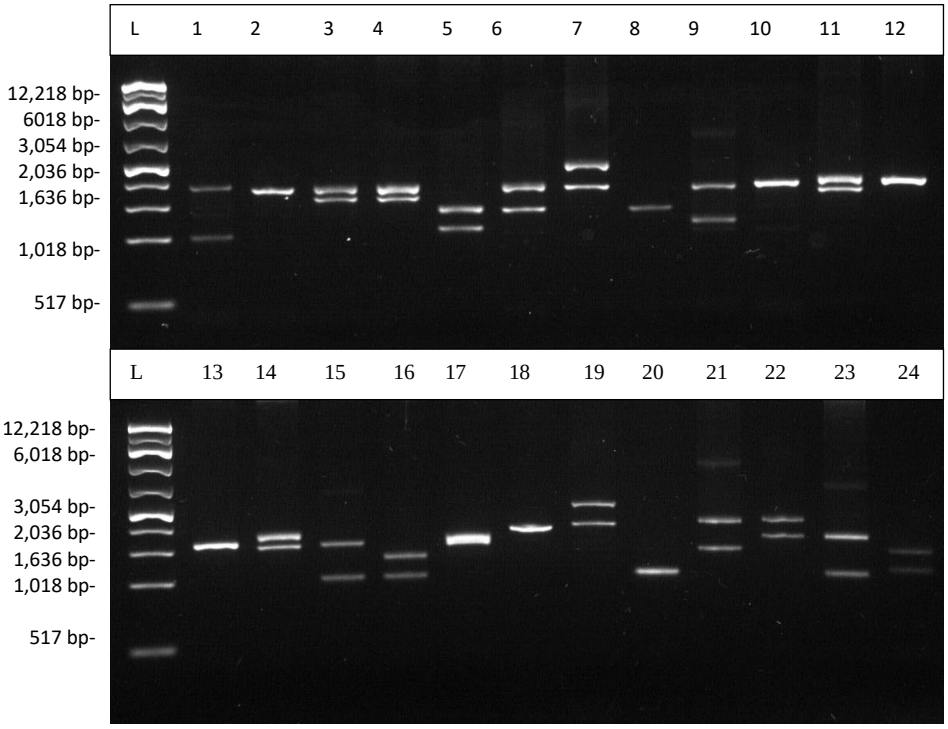


Figure 5. Electrophoretic pattern of alleles on 2% agarose gel run at 7/cm for 60 minutes in indigenous chicken populations of Ethiopia. 1 kb ladder DNA was used as a reference.

Capillary electrophoresis and sequencing

The forward primer sequence was labeled with the ABI fluorescent dye PET. 1 µl PCR product was added to a mixture of 12 µl GeneScan 500 LIZ® Size Standard and 1,000 µl of HIDI formamide and denatured at 95℃ for 3 minutes and separated by capillary electrophoresis using an ABI3730 DNA genetic analyzer (Applied Biosystems, Foster City, CA) using GeneScan-500 Internal LIZ Size Standards based on size of amplicons. The fragment (allele) sizes generated were scored with Gene Mapper Software Ver 4.1 (Applied Biosystems, Foster City, CA, USA) and exported to Microsoft excel for preparation of input files for statistical analyses. To confirm polymorphisms from genotypes by capillary electrophoresis, homozygous and heterozygous, alleles were selected for sequencing. The same primer sequences used for genotyping by capillary

electrophoresis were employed except that they were now tailed with T7 (20 base pair) and SP6 (17 bp) tail sequences for the forward and reverse primers, respectively. Homozygote DNA fragments were purified using GeneJet PCR purification Kit (Thermo Fisher Scientific; cat. No. K0701) and heterozygote DNA fragments were purified using the Qiagen Gel Extraction Kit and sent for sequencing to BIONEER sequencing platform in Korea. Alleles were sequenced on an ABI 3730XL DNA Analyzer using T-7 and SP6 sequencing primers.

3.2.4. Data management and analysis

3.2.4.1. Population genetic diversity analysis

The genotypic data were subjected to various within and among populations genetic diversity analysis. These included: calculation of the total number of alleles, allelic frequency, and their distribution among the entire populations, polymorphic information content (PIC) for each population, Shannon's Information Index using GenAlEx software package version 6.5. The same package (Peakall and Smouse, 2012) was used to compute abundance of alleles (number of rare alleles and common alleles), partitioning of total genetic variation into within and among pre-grouped populations through Analysis of Molecular Variance (AMOVA) and Wright's F-statistics (within population inbreeding [F_{IS}], total inbreeding [F_{IT}], among population genetic differentiation [F_{ST}]). F_{IS} was calculated using the formula: $F = 1 - \frac{Ho}{He}$ while the pairwise Fst values are calculated from *Ho* and *He* (F_{ST} = (*He-Ho)*/*He*). Between populations comparison of the allele frequencies was performed by the chi-square test. Observed heterozygosity (*Ho*), expected (*He*) heterozygosity was estimated using the formula: $He = 1 - \sum (p^2_i + q^2_i)$ where p is

the allelic frequency of the allele one at a given locus and q is the frequency of the alternate allele at the same locus. The deviation of each population from Hardy-Weinberg Equilibrium (HWE) was also tested using GenAlEx software package. Correlation between sampling site geographic distances and genetic distances between indigenous chicken populations was also done using the Mantel test (XLSTAT, 2018). Number of homozygote and heterozygote genotypes were calculated using power marker analysis (Liu *et al*., 2002).

3.2.4.2. Population differentiation and statistical Analysis

Population differentiation and the genetic structure were examined by sampling sites and Major Agro-Ecological Zones (MAEZ) on the basis of available allelic frequency using principal component analysis (PCA) calculated with the XLSTAT software (XLSTAT, 2018). Pairwise *Fst* among all pairs of populations were computed using the Weir and Cockerham statistics (Peakall and Smouse, 2012). Analysis of the population structure was done using STRUCTURE software version 2.3.4 using an initial length of 50,000 burn-in periods followed by 150,000 MCMC (Markov Chain Monte Carlo). Individuals were grouped into a predefined number of population clusters (K) ranging from 2 to 10. For each value of K, 20 independent runs were performed using the admixture and allelic frequency correlated models. Pairwise comparisons of the 20 runs were carried using the algorithm implemented in CLUMPAK server (CLUstering Markov Packager Across K) (http://hpc.ilri.cgiar.org/beca/bioinfo/clc.html). The best K was calculated following the equation proposed by Evanno *et al*. (2005).

3.2.4.3. Sequence read data management and analysis

In addition, high-quality sequence reads with base call accuracy higher than 95% were assembled and resolved for conflicts using Qiagen's CLC work bench version 7. The resulting consensus sequences of chicken populations were aligned using the ClustalW program integrated into the MEGA (Molecular Evolutionary Genetics Analysis) software version 7 (Kumar *et al*., 2016). For this, a reference homologous sequences of the LEI0258 marker with SNP position was downloaded from the National Centre for Biotechnology Information (NCBI). The positioning of SNPs and Indels were done using the DnaSP 4.0 software package (Librado and Rozas, 2009). To determine the haplotype relationship of 13 new and 8 already NCBI described allele sequences, the median-joining network was done using Network 5.0.0.3. Based on the network only 10 haplotypes were identified and a tree was inferred by using the Maximum Likelihood method based on the Tamura-Nei model. Evolutionary analyses were conducted in MEGA7 (Kumar *et al*., 2016).

3.3. Results

3.3.1. LEI0258 locus diversity by sampling site and Major Agro-ecological Zones (MAEZ)

The microsatellite marker, LEI0258, has been used before as a proxy of the diversity of the MHC-B locus polymorphic in indigenous chickens. Here, we identified 29 LEI0258 alleles (100 genotypes; 64 heterozygotes and 36 homozygotes) from the studies of 24 populations. The effective number of alleles per population ranges from 4.0 (Hugub) to 11.76 (Arabo). Observed heterozygosity values range from 50% (Shubi Gemo) to 100% (Amesha Shinkuri, Meseret, Gesses, Arabo, Hadush Adi). Size and frequency of the alleles are presented in Table 7 and Table 8.

Across populations, the highest allele frequency and gene diversity are 16.31% and 91.9%, respectively, while it is 15.73% and 92.62% across MAEZ. Two private heterozygote alleles, size of 315 bp and 385 bp, were present in the Surta populations. Heterozygote private allele size of 185 bp, 411 bp, 277 bp, and 465 bp were found at Meseret, Ashuda, Loya and Hadush Adi populations at lower frequencies of 10%, 10%, 5%, 5%, respectively. The most frequent allele across population is alleles 315 bp (n = 77) followed by allele 197 bp (n = 57; Table S 39). An average of 2.06 Shannon index is obtained. The overall mean heterozygosity among the entire populations is 82.1%.

Allele 363 was present in all populations and in all agro-ecological zones examined except in A1 and M1 agro-ecologies. The percentage of polymorphic loci is 91.38% and 92.16% for populations across sampling sites and MAEZ. Another private allele size 185 bp was only possessed by

Meseret populations under SM2 (Tepid to cool sub-moist mid-highlands) agro-ecological zone. Other alleles were shared by some but not all populations. For instance, 209 bp and 460 bp was possessed by populations that prevail in Tepid to cool arid mid highlands (A1) and SA1 (Hot to warm semi-arid lowlands) for the former and Hot to warm moist lowlands (M1) for the later. Allele size 315 bp is only possessed by populations of all agro-ecologies.

Table 7. Allele frequencies (%) of LEI0258 in indigenous Ethiopian chicken population.

Allele/n	B	S	A	G	A	M	H	K	GE	KI	TT	AR	AS	DI	BG	SG	KU	LO	HA	MI	GI	MET	AL	NA	P
	8	9	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	9	10	10	10	10	
185	0	0	0	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
197	31	17	0	15	5	0	0	10	35	15	0	15	10	10	15	5	5	10	15	6	10	20	25	20	20
209	0	0	5	0	5	5	10	0	0	0	0	5	0	0	0	5	0	5	5	0	0	0	0	0	8
221	6	0	5	0	25	5	5	0	0	0	0	0	0	0	0	0	10	0	0	0	0	0	0	0	6
245	0	0	0	0	0	5	0	0	0	0	0	0	0	0	10	0	0	0	0	0	0	0	0	0	2
253	6	0	10	5	0	5	0	5	10	10	20	5	5	10	5	10	0	10	5	11	20	15	15	0	19
263	0	0	15	5	5	5	25	0	15	5	0	15	5	10	0	0	10	5	15	6	5	10	5	25	18
277	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0	0	0	1
289	6	0	5	10	0	0	0	0	10	25	5	5	15	15	0	0	5	10	5	6	10	5	10	0	16
300	0	0	5	0	0	0	0	10	5	0	10	5	0	0	15	35	0	5	10	6	0	0	0	0	10
302	0	0	0	0	0	0	0	5	0	0	0	0	0	0	5	0	10	0	0	0	0	0	0	0	3
312	0	17	0	10	15	15	0	5	5	0	25	5	10	15	10	15	0	0	0	17	15	5	5	10	17
315	31	17	20	30	15	25	10	10	5	10	20	5	25	20	15	5	20	15	15	11	25	15	25	5	24
325	0	0	0	0	0	0	0	5	0	0	0	5	0	0	0	0	0	0	0	6	0	0	0	0	3
327	0	6	0	0	0	0	0	0	0	10	5	0	0	15	0	0	0	10	0	6	10	0	0	0	7
340	0	0	0	0	25	0	5	20	0	5	0	5	0	0	0	0	0	0	5	0	0	0	0	35	7
351	0	0	0	0	0	0	40	10	5	5	0	0	0	0	5	0	0	0	0	11	0	0	0	0	6
363	6	22	25	5	0	15	0	20	5	10	10	10	5	5	5	10	20	10	10	11	0	5	5	0	20
375	13	0	10	20	0	0	0	0	0	0	0	5	0	0	10	0	15	5	5	0	0	10	10	5	11
385	0	0	0	0	0	5	0	0	0	0	0	5	10	0	0	5	0	10	0	6	0	0	0	0	6
397	0	0	0	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	5	0	0	3
411	0	0	0	0	0	0	0	0	0	0	0	0	10	0	0	0	0	0	0	0	0	0	0	0	1
426	0	11	0	0	0	0	0	0	5	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3
450	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0	0	0	5	0	0	2
460	0	0	0	0	5	0	5	0	0	0	0	5	0	0	0	0	5	0	0	0	0	5	0	0	5
465	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0	0	1
472	0	0	0	0	0	0	0	0	0	0	0	5	5	0	0	0	0	0	0	0	0	0	0	0	2
485	0	0	0	0	0	5	0	0	0	0	5	0	0	0	0	0	0	0	0	0	5	0	0	0	3
569	0	11	0	0	0	0	0	0	0	0	0	0	0	0	0	10	0	0	0	0	0	0	0	0	2

BA = Batambe; SU = Surta; AS = Amesha Shinkuri; GA = Gafera; AD = 025-Adane; ME = Meseret; HU = Hugub; KE = Kefis; GE = Gesses; KI = Kido; TT = Tsion Teguaz; AR = Arabo; AS = Ashuda; DI = Dikuli; BG = Bekele Girisa; SG = Shumbi Gemo; KU = Kumato; LO = Loya; HA = Hadushi Adi; MI = Mihiquan; GI = Gijet; MET = Metkilimat; AL = Alifa Midir; NA = Negasi Amba; P = No. of populations sharing the allele

Table 8. Allele frequencies (%) of LEI0258 in indigenous chicken grouped by MAEZ.

Allele/n	**A1**	**M1**	**M2**	**M3**	**SA2**	**SH1**	**SH2**	**SM2**	**P**
N	10	10	13	11	10	12	15	13	
185	0	0	0	0	0	0	0	4	1
197	0	5	15	23	5	13	3	12	7
209	10	5	0	0	5	0	0	0	3
221	5	25	0	0	0	0	0	0	2
245	0	0	0	0	0	0	3	4	2
253	0	0	4	14	10	8	0	12	5
263	25	5	4	9	0	8	3	8	7
289	0	0	8	9	0	13	7	4	5
300	0	0	4	0	35	0	7	0	3
302	0	0	0	0	0	0	3	0	1
312	0	15	0	9	15	0	7	8	5
315	10	15	12	23	5	17	20	8	8
325	0	0	4	0	0	0	0.	0	1
327	0	0	0	0	0	13	7	4	3
340	5	25	12	0	0	0	0	4	4
351	40	0	0	0	0	4	3	0	3
363	0	0	8	5	10	13	3	4	6
375	0	0	8	9	0	4	13	8	5
385	0	0	4	0	5	0	3	0	3
397	0	0	0	0	0	0	0	8	1
411	0	0	0	0	0	0	10	0	1
426	0	0	12	0	0	8	0	0	2
450	0	0	0	0	0	0	3	4	2
460	5	5	0	0	0	0	0	0	2
465	0	0	0	0	0	0	0	4	1
472	0	0	4	0	0	0	3	0	2
485	0	0	4	0	0	0	0	4	2
525	0	0	0	0	0	0	0	4	1
569	0	0	0	0	10	0	0	0	1

A1 = Tepid to cool arid mid highlands; M1 = Hot to warm moist lowlands; M2 = Tepid to cool moist mid highlands; M3 = Cold to very cold moist sub-afro alpine to afro-alpine; SA2 = Tepid to cool semi-arid mid highlands; SH1 = Hot to warm sub-humid lowlands; SH2 = Tepid to cool sub-humid mid highlands; SM2 = Tepid to cool sub-moist mid-highlands; P = N of population sharing the allele.

3.3.2. Population clustering by sampling site and MAEZ

The genetic structure of all populations were examined by sampling sites and MAEZ on the basis of all available allelic frequencies using principal component analysis (PCA)(XLSTAT, 2018; Figure 11). The first two components axes accounted for 21.54% and 17.53% of the variation, respectively, for sampling site and 35.66% and 23.60%, respectively for MAEZ. Accordingly, the PCA of allelic frequency covariates by sampling sites, shows two distinct groups of the indigenous Ethiopian chicken populations separated longitudinally (Figure 6). This grouping seems to follow the direction of the rift valley geographically. Within these two groups, the chicken populations did not cluster in relation to their geographic origins. The PCA by MAEZ does not show any distinct genetic cluster for the indigenous chicken populations of Ethiopia (Figure 7). According to Evanno *et al*.(2005), the best clustering of the 24 chicken populations was found at K = 2 (Figure 12) both at predetermined population and agro-ecological zone level (Figure 13).

The highest mean genetic distance (d = 0.94) was between Alfa Midir and Batambe followed by the former and Gafera (d = 0.90) populations (Table S 40; Table S 44). The average Fst for the entire population was 0.028. The pairwise *Fst* calculation shows the highest value (*Fst* = 0.12) between Hugub and Surta populations. In terms of analysis of genetic distance by MAEZ, the highest genetic distance is observed between Tepid to cool semi-arid mid highlands and hot to warm arid lowland plains (Table S 41). The Analysis of Molecular Variance shows the presence of 89% within individual variation across populations. The among-population variation and among individual variation was reported as 3% and 8%, respectively. Similarly, alleles, in tepid to cool sub-moist mid highlands are genetically distinct from alleles in Tepid to cool moist mid highlands

(M2), Cold to very cold moist sub-afro alpine to afro-alpine (M3), Hot to warm sub-humid lowlands (SH1), Hot to warm sub-humid lowlands (SH2) agro-ecologies. The fixation coefficient of the sub-population within the total population (F_{ST}), inbreeding/fixation/ coefficient of an individual in a subpopulation (F_{IS}) and total inbreeding /heterozygosity deficit/ coefficient of an individual within the total population (F_{IT}) in the locus are 0.03, 0.08 and 0.11, respectively. Pairwise population Fst are also indicated in Table S 42 with the highest value (0.12) for Hugub to Banja and Shubi Gemo to Hugub populations. The highest pairwise Fst (0.12) is also found between SA2 and A1 agro-ecologies (Table S 43). Structure analysis (K = 2) supports two different gene pools (Figure 12; Figure 13).

From the entire populations, only Kumato populations meet the assumption of Hardy Weinberg Equilibrium (HWE). Unrooted neighbor-joining tree topology indicated a clear IC subgrouping into two distinct clusters (Figure 8). Even though the reported rate of gene flow (Nm) was minimum (8.6), high rate of admixture was noted among the predetermined populations. The mantel correlation test across population genetic and geographic distance shows no correlation (Figure 11).

Table 9. Diversity indices of LEI0258 microsatellite locus in Ethiopian indigenous chicken populations across sampling sites.

Pop	N	Na	Ne	I	Ho	He	uHe	F	HWE (prob)	PAL
Batambe	8	7.000	4.414	1.680	0.750	0.773	0.825	0.030	0.21	
Surta	9	7.000	6.231	1.879	0.667	0.840	0.889	0.206	0.20	315, 385
Amesha_Shinkuri	10	9.000	6.452	2.013	1.000	0.845	0.889	-0.183	0.89	
Gafera	10	8.000	5.556	1.878	0.800	0.820	0.863	0.024	0.2	
025_Adane	10	8.000	5.556	1.861	0.700	0.820	0.863	0.146	0.08	
Meseret	10	12.000	7.692	2.264	1.000	0.870	0.916	-0.149	0.68	185
Hugub	10	7.000	4.000	1.623	0.700	0.750	0.789	0.067	0.09	
Kefis	10	10.000	7.692	2.164	0.700	0.870	0.916	0.195	0.32	
Gesses	10	10.000	5.556	2.011	1.000	0.820	0.863	-0.220	0.93	
Kido	10	10.000	7.407	2.151	0.800	0.865	0.911	0.075	0.15	
Tsion_Teguaz	10	8.000	5.882	1.900	0.800	0.830	0.874	0.036	0.35	
Arabo	10	15.000	11.765	2.597	1.000	0.915	0.963	-0.093	0.71	
Ashuda	10	10.000	7.407	2.151	0.800	0.865	0.911	0.075	0.42	
Dikuli	10	8.000	7.143	2.016	0.800	0.860	0.905	0.070	0.31	
Bekele_Girisa	10	11.000	9.091	2.293	0.900	0.890	0.937	-0.011	0.47	
Shubi_Gemo	10	9.000	5.405	1.942	0.500	0.815	0.858	0.387	0.24	
Kumato	10	9.000	7.143	2.068	0.800	0.860	0.905	0.070	0.02*	277
Loya	10	12.000	10.526	2.415	0.900	0.905	0.953	0.006	0.57	
Hadush_Adi	10	12.000	9.524	2.363	1.000	0.895	0.942	-0.117	0.49	263
Mihiquan	9	12.000	10.125	2.399	0.889	0.901	0.954	0.014	0.33	
Gijet	10	8.000	6.250	1.943	0.700	0.840	0.884	0.167	0.39	
Metkilimat	10	11.000	8.333	2.250	0.900	0.880	0.926	-0.023	0.37	
Alfa_Midir	10	8.000	5.714	1.888	0.800	0.825	0.868	0.030	0.23	
Negassi_Amba	10	6.000	4.167	1.566	0.800	0.760	0.800	-0.053	0.83	
Mean		9.458	7.043	2.055	0.821	0.846	0.892	0.031		
SE		0.438	0.416	0.053	0.026	0.009	0.009	0.027		

PAL = Private allele; He = Unbiased Expected Heterozygosity/ Nei's Gene diversity = (2N / (2N-1)) * He; I = Shannon's Information Index = -1* Sum (pi * Ln (pi)); *significantly deviate from HWE ($P < 0.05$)

Table 10. Diversity indices of LEI0258 microsatellite locus in indigenous Ethiopian chicken populations across MAEZ.

Pop	N	Na	Ne	I	Ho	He	uHe	F	HWE	PAL
A1	10	7.000	4.000	1.623	0.700	0.750	0.789	0.067	0.09	
M1	10	8.000	5.556	1.861	0.700	0.820	0.863	0.146	0.08	
M2	13	14.000	10.903	2.505	0.846	0.908	0.945	0.068	0.53	127,253,315
M3	11	8.000	6.368	1.958	0.818	0.843	0.883	0.029	0.24	
SA2	10	9.000	5.405	1.942	0.500	0.815	0.858	0.387	0.24	569
SH1	12	10.000	8.727	2.224	0.917	0.885	0.924	-0.035	0.22	
SH2	15	16.000	10.465	2.563	0.867	0.904	0.936	0.042	0.36	315
SM2	13	17.000	14.083	2.738	1.000	0.929	0.966	-0.076	0.32	375

PAL = Private allele; He = Unbiased Expected Heterozygosity/ Nei's Gene diversity = (2N / (2N-1)) * He; I = Shannon's Information Index = -1* Sum (pi * Ln (pi)); *significantly deviate from HWE ($P < 0.05$)

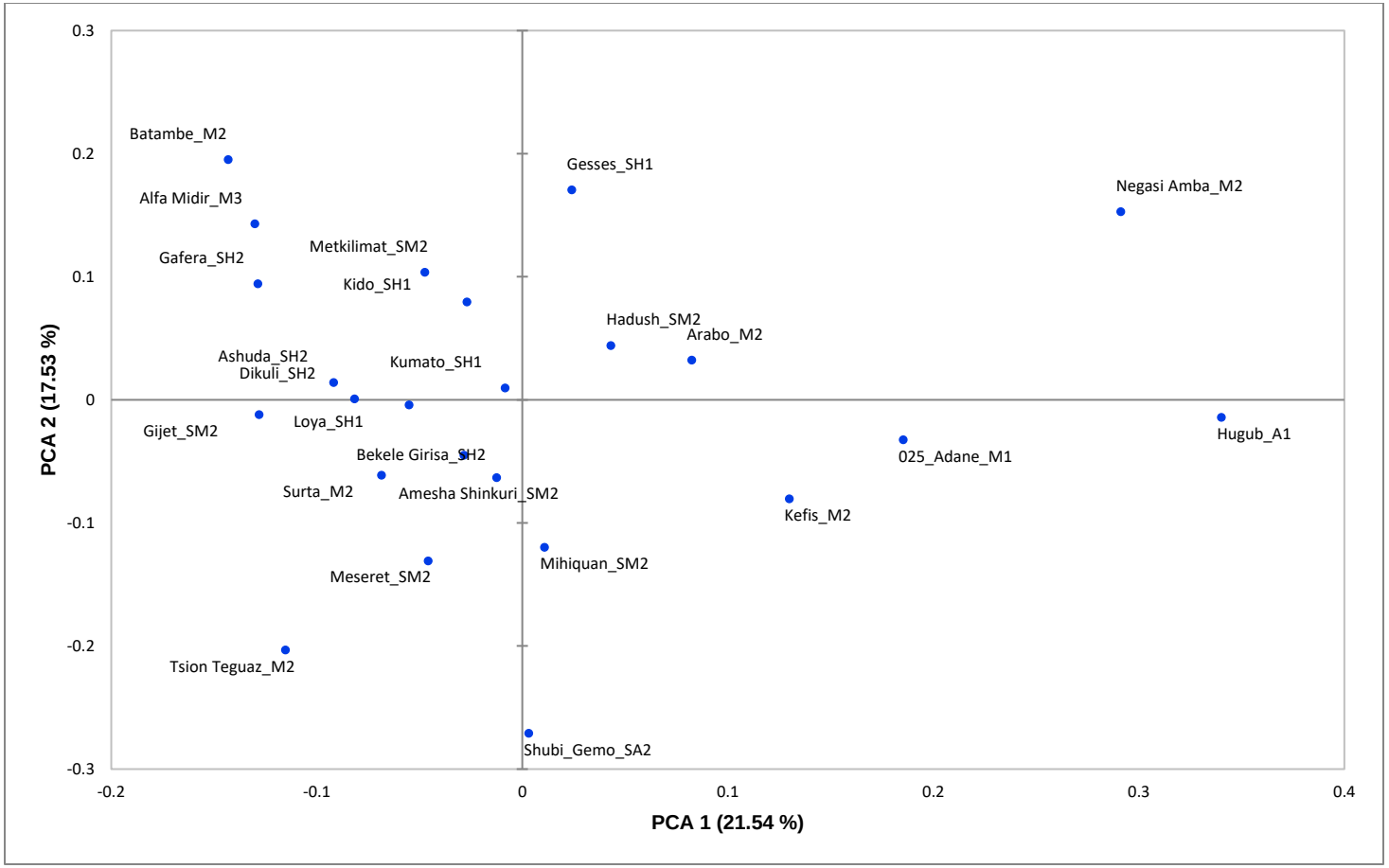


Figure 6. Principal component analysis of alleles frequencies by sampling site.

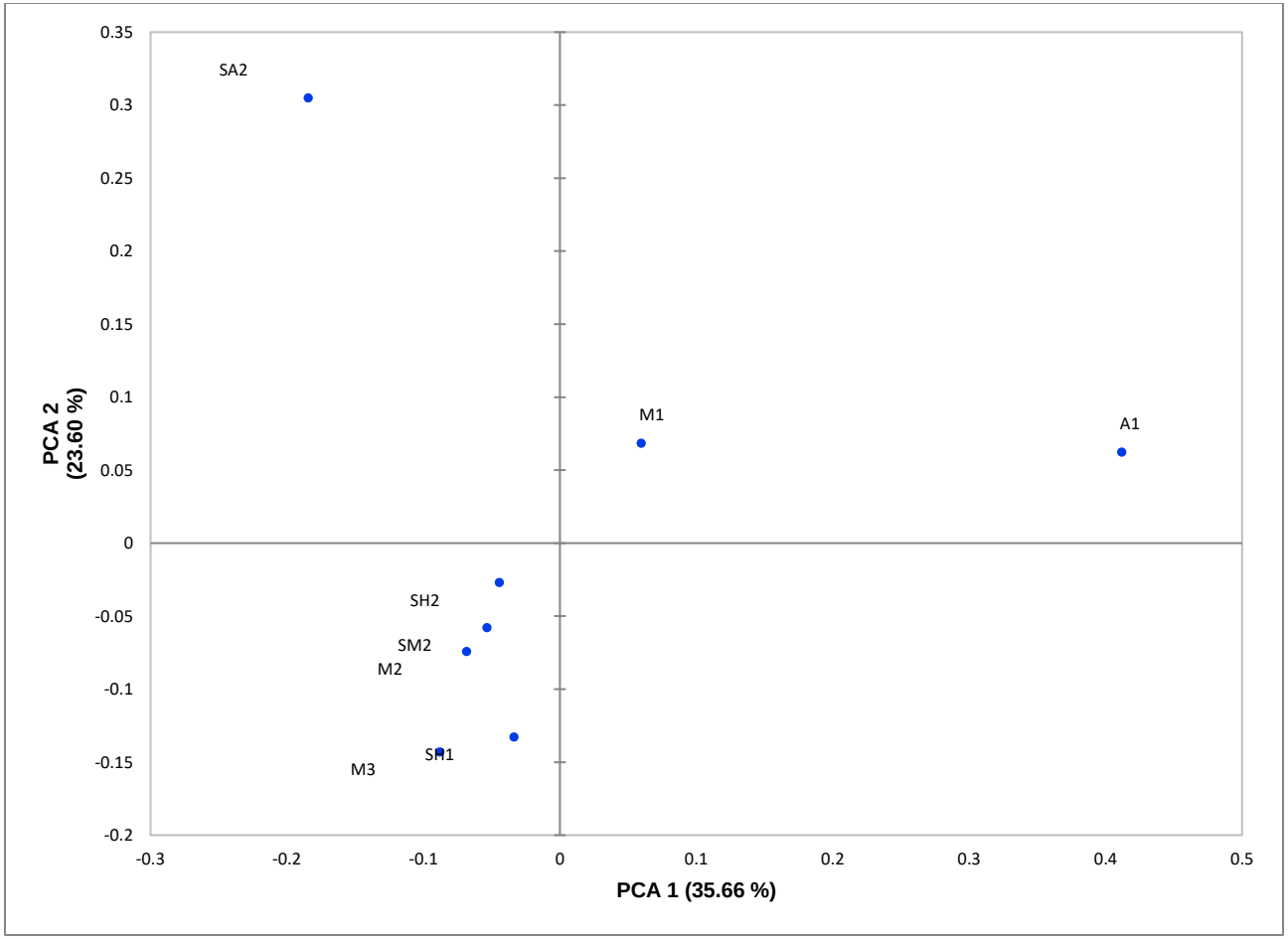


Figure 7. Principal Component Analysis of alleles frequencies across MAEZ.

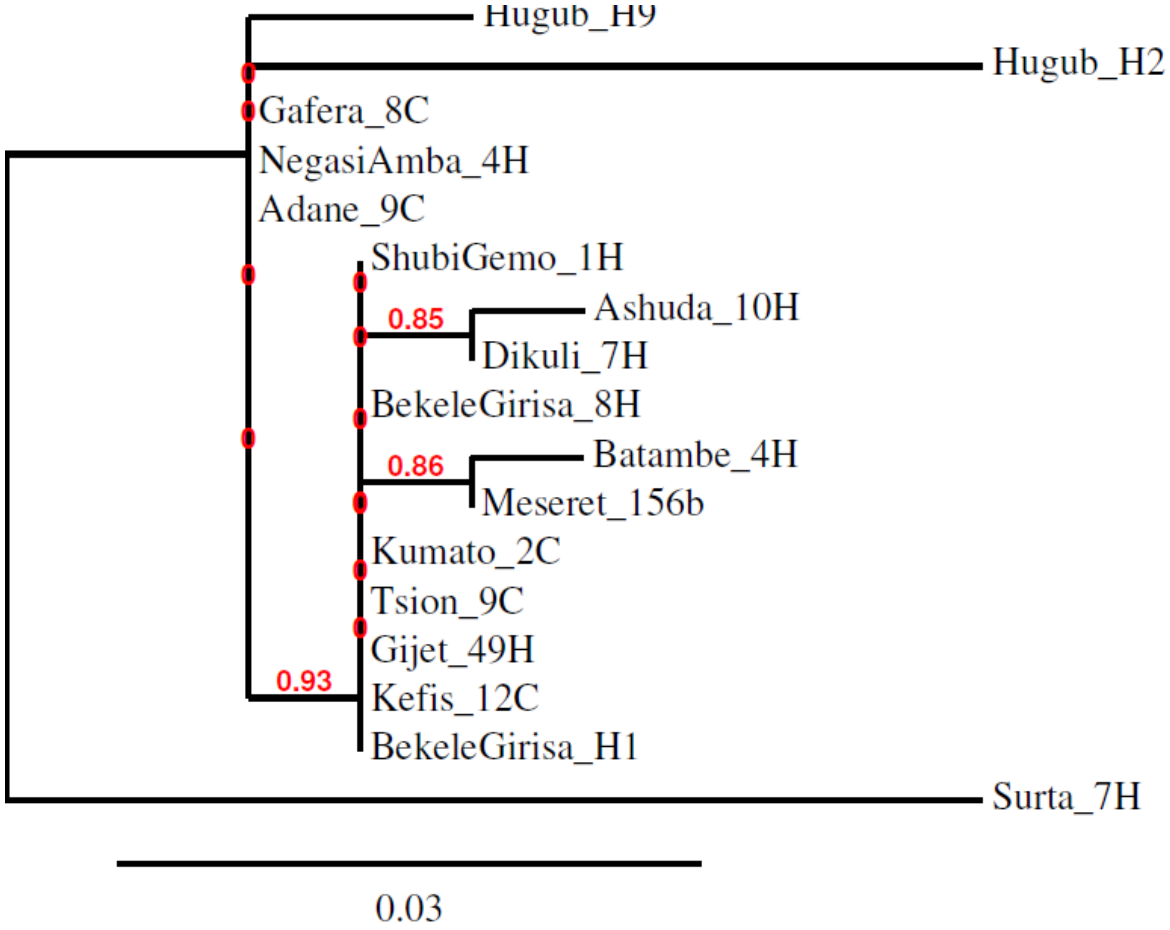


Figure 8. Relationships between populations for LEI0258 microsatellite polymorphism.

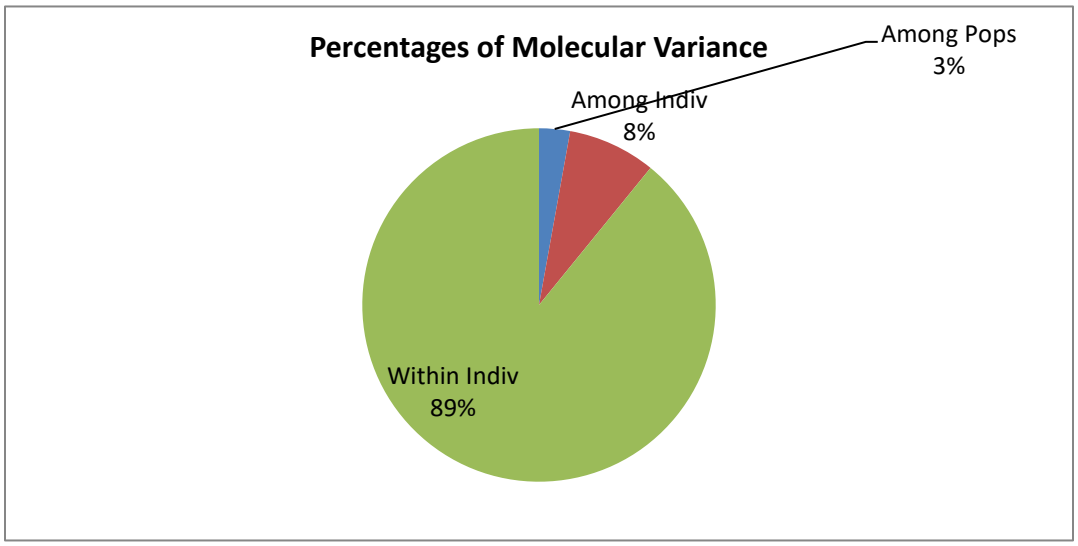


Figure 9. Results of Analysis of Molecular Variance across populations.

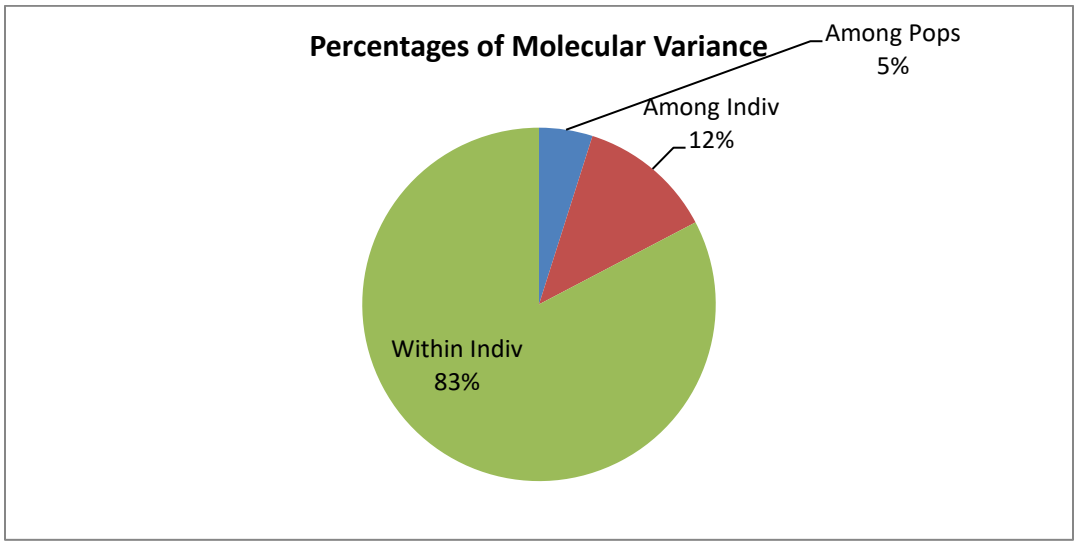


Figure 10. Results of Analysis of Molecular Variance across MAEZ.

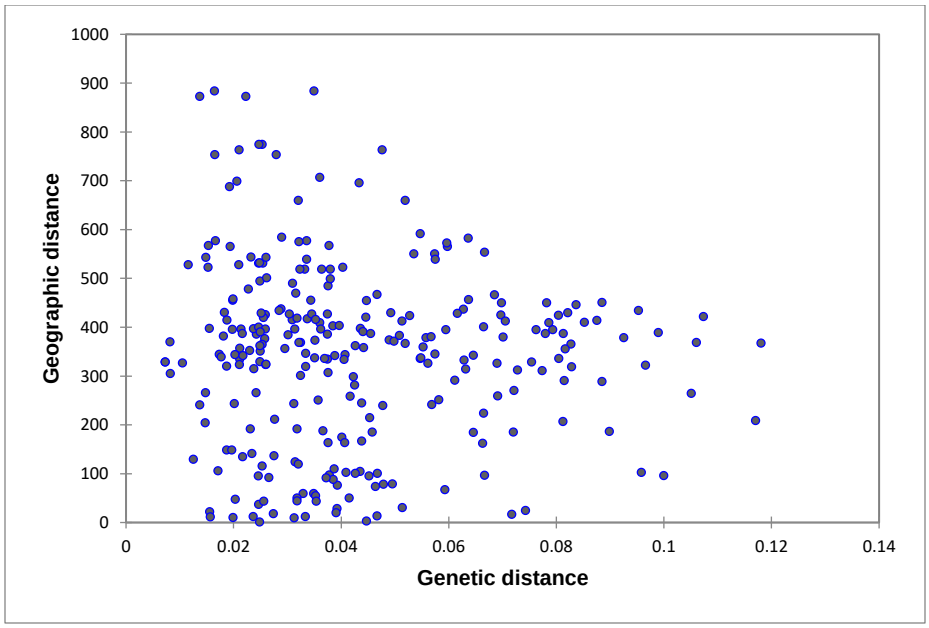


Figure 11. Relationship between geographic and genetic distances.

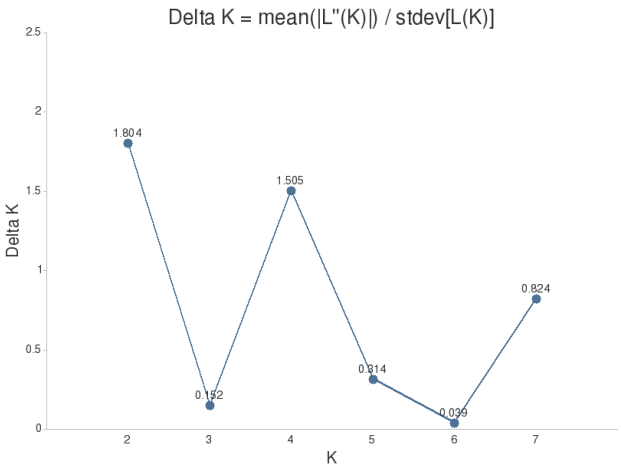


Figure 12. the optimum delta k according to Evanno *et al*., (2005).

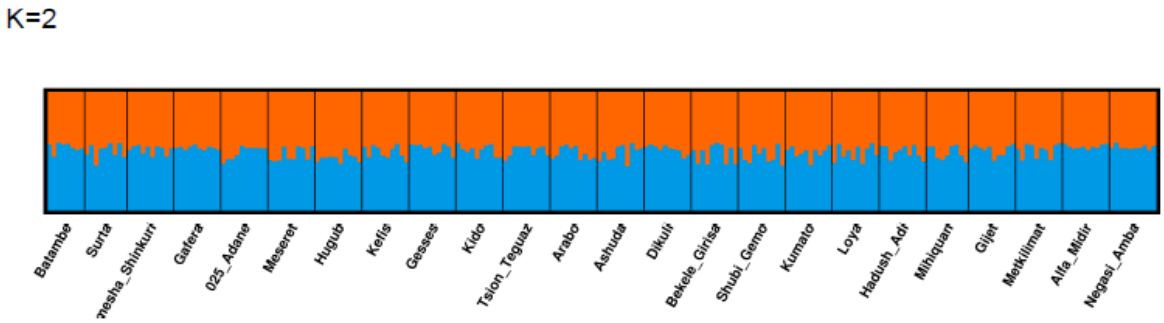


Figure 13. Structure bar plots showing the gene pool of the chicken populations.

3.3.3. Allelic sequence polymorphisms and relationships

Sequence information including repeat regions and flanking regions are presented at Table 1 for a subset of homozygote LEI0258 genotypes. Based on the blastn information from the National Center for Biotechnology Information (NCBI) confirmed the presence of 13 new alleles from the 21 alleles sequenced (submitted and given accession numbers; Appendix 1). Identical alleles are also indicated in Table 1. Variable Number of Tandem Repeats (VNTR) R12 was observed 2 to 17 times and for R13 (CTATGTCTTCTTT') we only observe one repeat.

The 23 to 30 position downstream of the repeat region was sequenced as "ATTTTGAG", whilst, 3 alleles sequences were found to have different repeats than respective reference sequences. 24 and 1 SNP substitutions were found at positions 39 and 46, respectively. 12 insertion SNPs and 2 deletions were noted on the upstream polymorphism positions of -30 to -29 positions. Besides, 2 nucleotide substitutions were reported at -61 upstream polymorphism, while, 3 substitution at -28 position. The consensus sequence size deviation from fragment size ranged from 1 to 115 bp. Further polymorphisms were also observed in different positions of the repeat structure other than the positions considered hereunder. B10, B11.1, B13, B72 haplotypes were obtained from the allelic sequence. The invariable (monomorphic sites) and variable (polymorphic) sites found were 412 and 35, respectively. A total of 26 singleton sites and 5 parsimony informative sites were observed from the package of DNA sequence polymorphism while the total number of mutation sites and indel events were 33 and 17, respectively. The number of indel haplotypes and indel diversity were 5 and 0.00465). Haplotype diversity (Hd) was 0.82. The haplotype-based phylogenic analysis using Neighbor-Joining (NJ) showed that indigenous chicken populations are mainly clustered into two gene pools comprising different subpopulations as obtained from the structure analysis of allele sizes from capillary electrophoresis.

Table 1. Overall polymorphisms identified within the LEI0258 alleles in indigenous chicken populations of Ethiopia.

[a]Chicken	NCBI Acc. No.	Fragment length (bp, by genotyping)	Consensus size (bp, by sequencing)	Upstream				R13	R12	Downstream					Acc. No.	Haplotype
				Δ	TT	G	TT			C	ATTTGAG	Δ	T	T		
				-61	-30 to -29	-28	-19-18			5	23-30	33	39	46		
Batambe_4H	MG495227	197	193	∘	∘	∘	∘	1	2	∘	Δ	∘	Δ	Δ	DQ239495	B11
Surta_7H*	MG495249	315/426	486	∘	Δ	Δ	∘	1	13	∘	∘	∘	Δ	∘	DQ239562	BW4
Hugub_H2*	MG495230	351/460	236	∘	Δ	∘	∘	1	4	∘	∘	∘	Δ	∘	KF535086	
Hugub_H9*	MG495244	351	345	∘	∘	∘	∘	1	15	∘	∘	∘	Δ	∘	DQ239508	B14
Gafera_8C*	MG495239	315	309	∘	∘	∘	∘	1	12	∘	∘	∘	Δ	∘	KF534941	
Tsion_9C*	MG495231	315/327	250	∘	∘	∘	∘	1	7	∘	∘	∘	Δ	∘	KF534930	
Adane_9C*	MG495245	312/340	357	∘	∘	∘	∘	1	16	∘	∘	∘	Δ	∘	DQ239506	B130
Ngasiamba_4H	MG495243	340	333	∘	∘	∘	∘	1	14	∘	∘	∘	Δ	∘	KF534946	
Ashuda_1C	MG495232	289	283	∘	Δ	Δ	Δ	1	10	∘	∘	∘	Δ	∘	KF535091	
Ashuda_9C*	MG495240	315	309	∘	∘	∘	∘	1	12	∘	∘	∘	Δ	∘	DQ239494	B10
Ashuda_10H*	MG495236	289	295	∘	Δ	∘	∘	1	11	∘	∘	∘	Δ	∘	DQ239550	B72
Dikuli_4H*	MG495237	315/411	307	∘	Δ	Δ	Δ	1	12	∘	∘	∘	Δ	∘	DQ239550	B72
Kefis_12C	MG495233	289	283	∘	Δ	Δ	Δ	1	10	∘	∘	∘	Δ	∘	KF535091	
Dikuli_7H	MG495241	321	321	∘	∘	∘	∘	1	13	∘	∘	∘	Δ	∘	KF534945	
Bekelegirisa_1H*	MG495246	300/302	379	∘	Δ	Δ	Δ	1	18	∘	∘	∘	Δ	∘	KF535100	
Bekelegirisa_8H*	MG495234	312/315	295	∘	Δ	Δ	Δ	1	11	∘	∘	∘	Δ	∘	KF534937	
Shubigemo_1H*	MG495235	300	295	∘	Δ	Δ	Δ	1	11	∘	∘	∘	Δ	∘	DQ239496	B11.1
Kumato_2C	MG495248	197/460	357	∘	Δ	Δ	Δ	1	16	∘	∘	∘	Δ	∘	KF535100	
Kumato_5H	MG495248	302	379	∘	Δ	Δ	Δ	1	18	∘	∘	∘	Δ	∘	KF535100	
Meseret_156b	MG495229	312/315	333	∘	∘	∘	∘	1	4	∘	Δ	∘	Δ	∘	KF534926	
Gijet_49H*	MG495238	253	295	∘	Δ	∘	Δ	1	12	∘	∘	∘	Δ	∘	DQ239550	B72

[a]The codes of chicken populations; [b]Δ Defined deletion compared with the reference sequence. ∘is consistent with the reference sequence; * unique alleles

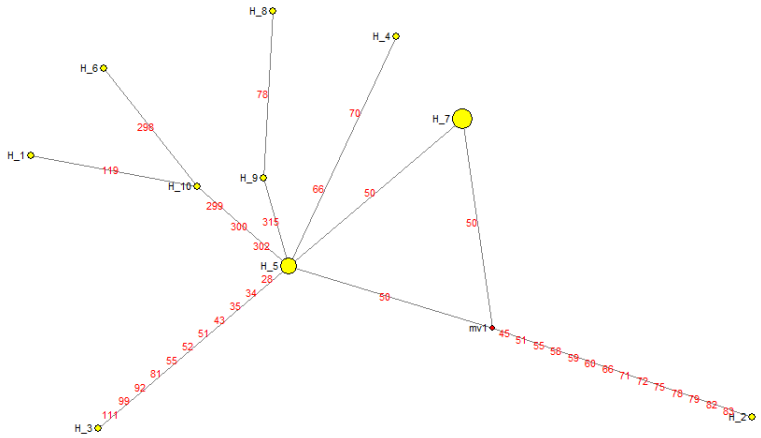


Figure 14. Network tree of allele sequences.

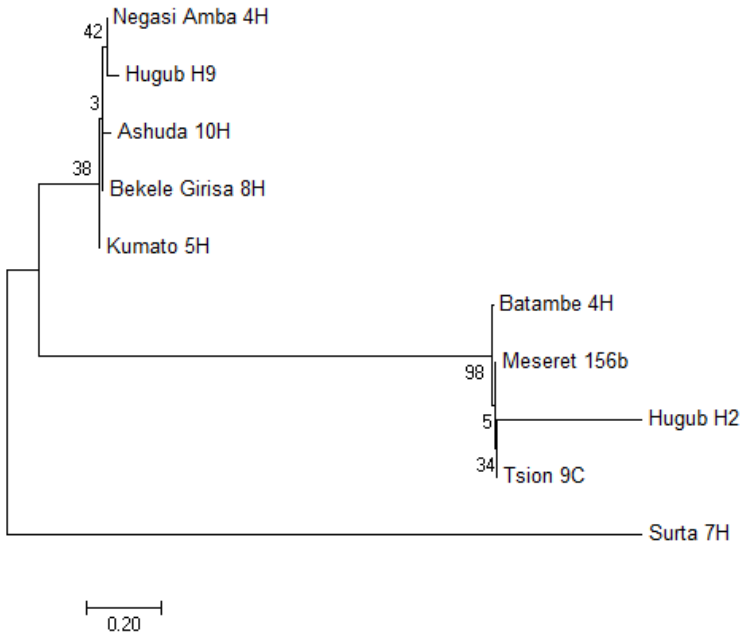


Figure 15. Haplotypes relationship tree of alleles by the Maximum Likelihood method.

The haplotype tree was inferred by using the Maximum Likelihood method based on the Tamura-Nei model. The tree with the highest log likelihood (-985.1747) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach and then selecting the topology with superior log-likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites (2 categories (+G, parameter = 0.0500)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 10 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. There were a total of 444 positions in the final dataset.

3.4. Discussion

3.4.1. Fragment length based genetic variation in the MHC region

In this study, we report polymorphism at the MHC-B microsatellite marker, LEI0258, in indigenous chicken village chicken populations from Ethiopia. From the 29 allele size reported here, 22 are novel alleles (Fulton *et al*., 2006; J. E. Fulton *et al*., 2016; Gupta *et al*., n.d.; Izadi *et al*., 2011; Keambou *et al*., 2014; Lwelamira *et al*., 2008; Ncube *et al*., 2014; Nikbakht *et al*., 2013).

The number of alleles reported was higher than the numbers reported by different authors in previous works on indigenous chicken populations (Han *et al*., 2013; Nikbakht *et al*., 2013). The allele size ranges from 185 and 569 bp with alleles frequencies ranging from 2.5% to 38 % across populations. The maximum allele size reported in this study is larger than the one characterized in other studies (e.g Han *et al*. 2013). Allele sizes of 197, 253, 263, 312, 315 and 340 bp were found in all 24 populations.

The high diversity at the marker may be a direct consequence of the diversity of disease challenges facing Ethiopian chicken within and across different agro-ecologies, with polymorphism at the locus maintained by balancing selection with high LEI0258 diversity increasing the diversity of antigens being presented to T-cells (Chazara *et al*., 2013).

Overall, 50% of the alleles in this study are only found in only two or three of the populations out of the 24 considered. With the exception of alleles, 197, 312, 315 and 351 bp, the remaining of the alleles occurred at a lower frequency (< 0.20). The low-frequency abundance of LEI0258

alleles might be attributed to a new mutation arising in a population and therefore available only in a few individuals. It might also be due to its susceptibility to disease and other selection pressures resulting unfit to survive the production challenge the chicken is facing in the variable environments where they were sampled. High frequency of allele 315 at Batambe population could imply a fitness or survival advantage to the individual carrying it resulting in it being selected for and occurring at higher frequencies (31%). This, however, needs to be further study in absence of any information regarding the possible association between disease resistance/susceptibility and the allele.

We did not identify here those alleles which previously have been shown to be a positive correlation with NDV (206 bp) and body weight (307 bp) ((Fulton *et al*., 2006; Fulton *et al*., 2016 and Lwelamira *et al*. 2008) For the later it may not be surprising considering the small size of Ethiopian village chicken compared to their commercial counterparts; while the former is suggest that allele (206 bp) may not be of relevance to NDV resistance/susceptibility in Ethiopian village chicken. Several LEI0258 alleles were shared among the predetermined populations implying that they have been subjected to either directional selection or due to recombination effect (Miller *et al*., 2004; Nikbakht *et al*., 2013; Salomonsen *et al*., 2014). Alleles 206 and 307 bp, reported in Tanzanian chicken to associate with Newcastle disease antibody response and body weight, respectively, were not reported in Ethiopian chicken in this study (Lwelamira *et al*., 2008).

The mean observed heterozygosity (82.1%) found in this study are far more than the expected level (50%) indicating a higher genetic variation in indigenous chicken populations of Ethiopia. In other words, a heterozygous population has a better degree of resisting/tolerating multiple disease infections that challenge chicken populations. The genetic differentiation/ fixation coefficient of

the subpopulation within the total population (F_{ST}), inbreeding/fixation coefficient of an individual in a subpopulation (F_{IS}) and total inbreeding coefficient/fixation coefficient of an individual within the total population /heterozygosity deficit/among chicken ecotypes (F_{IT}) of the overall populations in the locus are 0.08, 0.03 and 0.11, respectively. The Weir and Cockerham *Fst* (Fst < 0.05) value indicating low sub-structuring of Ethiopian indigenous chicken. Besides, the structure gene pool bar plot showed two different gene pools. From the entire populations, Kumato populations are found to be significantly different from the test of the Hardy Weinberg Equilibrium (HWE). The possible accountable factors that cause this deviation from HWE might be possible introgression with exotic chicken as they are very close to the exotic poultry multiplication centre. The other possible reasons might be due to a continuous exposure to disease and parasite challenges (viral/ bacterial infections) that indigenous chicken are exposed to the occurrence of natural selection at MHC locus to combat these challenges. Besides, our sampling might have target related birds.

The highest mean genetic distance (d = 0.94) was between Alfa Midir and Batambe followed by the former and Gafera (d = 0.90) populations. Overall, the genetic distances found in this study are small indicating that these populations are more related and have a common ancestor. Considering this result it looks that the genetic diversity pattern fragments these populations west to east from North to South geography line. This could be attributed to their proxy of entry history of chicken introduction to Ethiopia/ Africa. The average Fst for the entire population was 0.028 ascertaining that 2.8% of the total genetic variation corresponded to the differences among populations, whilst 97.2% was explained by differences among individuals. The smallest genetic differentiation

between some populations is justified by minimal selective breeding, uncontrolled mating and movement of a live chicken.

3.4.2. Allelic sequence polymorphisms and relationships

A subset of allele sequencing result ascertained the presence of single nucleotide polymorphisms (SNPs) in LEI0258. The two main VNTR were the R13 and R12. R13 with a 13 bp repeat unit, "CTATGTCTTCTTT' was found with a frequency of only once similar to Wang *et al*. (2014) and inconsistent with other studies with more frequencies (Chazara *et al*., 2013; Nikbakht *et al*., 2013). The 23 to 30 position downstream of the repeat region was sequenced as "ATTTTGAG". They agree with the sequences obtained by Fulton *et al*. (2016), Han *et al*. (2013), and Izad *et al*. (2011). Twenty-four and one SNP substitutions were found at positions 39 and 46, respectively. The number of R12 motifs (CTTTCCTTCTTT) in the individual sequences ranged from 2 to 18, whilst, only one R13 motif was found. 12 insertion SNPs and 2 deletions were noted on the upstream polymorphism positions of -30 to -29 positions. Besides, 2 nucleotide substitution were reported at -61 upstream polymorphism, while, 3 substitution at -28 position. 6 allele sequences were found to have different repeats than respective reference sequences (ATTTTGAG). Results of allele size from both fragment length and consensus sequences did not exactly much which might be because of the difference in environmental factors, technological approaches, and precisions. The size deviation ranged from 1 to 115 unlike what was reported by Han *et al*. (2013) who found size differences of 1 to 69 range. The comparison between the fragment sizes and consensus sizes (bp) across population consistently showed higher values for the later except for the Dara population. This result was not consistent with the works of Fulton (2016) and Han *et al*., (2013). Further

polymorphisms were also observed in different positions of the repeat structure other than the positions considered hereunder. Only a few haplotypes (B10, B11.1, B13, B72), were found when compared with the haplotypes reported by Fulton *et al*. (2016) and Chazara *et al* (2013). In contrast, none of these haplotypes were reported in the report of Wang *et al*. (2014) for Chines chicken and Ngeno *et al*. (2015) for Kenyan indigenous chicken.

The SNP based phylogenic analysis using Neighbor-Joining (NJ) showed that indigenous chicken populations are mainly clustered into two gene pools comprising different subpopulations as obtained from the structure analysis of allele sizes from capillary electrophoresis. From phylogenetic analysis, clear separation of ecotypes was not noted indicating genetic admixture between populations.

3.5. Conclusion

Very high diversity was found in Ethiopian indigenous chicken populations at LEI0258, this diversity is observed within all population. Our results support the importance of MHC diversity in response to the disease challenges faced by smallholder poultry production in Ethiopia. Breeding improvement programs will need to maximize this diversity through balancing selection that maintains polymorphisms and increases within-population diversity. This very high diversity report for Ethiopian indigenous chicken populations on LEI0258 locus will provide a framework for the existing and future chicken breed improvement interventions. Besides, we can infer that the genotyping of the tandem repeat microsatellite marker LEI0258 is a suitable method for MHC typing of indigenous Ethiopian chicken populations considering the high level of polymorphism observed at the locus within and across indigenous populations. Polymorphisms from the sequencing result, also support the genome diversity of indigenous Ethiopian village chicken populations. As a way forward, studying the relationship of these polymorphisms and the disease resistance/susceptibility haplotypes in Ethiopian chicken populations should be undertaken.

CHAPTER 4. WHOLE GENOME DIVERSITY OF INDIGENOUS CHICKEN POPULATIONS IN ETHIOPIA

Abstract

Selective breeding for genetic improvement is expected to leave distinctive selection signatures within genomes. The identification of selection signatures can help to elucidate the mechanisms of selection and accelerate genetic improvement. Ethiopia has several chicken breeds which have evolved in different agro-ecologies. Here, we assess the footprints of candidate signatures of positive selection from whole genome autosomal sequences comprising 14,857,039 SNPs genotyped in Improved Horro, Local Horro, Hugub, Arabo and Jarso chicken populations of Ethiopia. We identified selection signals in 20 kb windows, with sliding steps of 10 kb based on estimators of pooled heterozygosity (*Hp*) and F-statistics (*Fst*). Selective sweep analysis using *Hp* and *Fst* identified genomic regions associated with production and reproduction. A total of 595 candidate genes showed high evidence of positive selection in indigenous chicken populations, including genes were related to traits such as growth and egg production. Gene ontology analysis displayed several biological processes and KEGG pathways involved in oestrogen biosynthetic and nervous system developmentt processes and calcium signaling and biosynthesis of unsaturated fatty acids. The regions identified in this study are expected to provide genome landmarks to enhance the ongoing breed improvement operations in improved Horro and for the other four chicken populations.

Keywords: Indigenous, Chicken, Improved Horro, Signature of selection, SNP

4.1. Introduction

Indigenous chicken makes a profound contribution to the rural economies in Ethiopia by playing a major role for the rural poor and marginalized people as a subsidiary income and consumption. Genetic diversity represents the total genetic variation among populations and several measures of diversity have been developed over years (Barrandeguy and García, 2014). Sufficient genetic variation in livestock populations is necessary both for adaptation to future changes in climate and consumer demand and for continual genetic improvement of economically important traits (Aslam *et al*., 2012; Eggen, 2012; Schmid *et al*., 2015). To understand phenotypic variation in farm animals such as in poultry, it is essential to define all potential genomic variation within a genome (Schmid *et al*., 2015). Evolution of chickens and programs for their artificial selection rely on the availability of sufficient levels of genetic variation. In response to the global shift in environmental conditions and market demands for chicken products, the diversity of village chicken is needed for future improvements programs (Muchadeyi *et al*., 2008).

Different techniques are involved to study genetic variations., DNA variation known as SNPs, the most abundant sources of genome variation, have become increasingly markers of choice in genomics studies (Alderborn, 2000; Gheyas *et al*., 2015) with genome annotation, the link between biological or functional information and genome sequences an important gain in our understanding of how genomic variations influence phenotypes (Fulton, 2012). Previous studies on Ethiopian chicken failed to comprehensively characterize the chicken genomic diversity in Ethiopia. Only a few Ethiopian indigenous chicken populations have been characterized using molecular markers. These are Tillili (Alemayhu, 2003; Mogesse, 2007), Jarso, Horo, Chefie, Tepi (Tadelle *et al*., 2003), Gellila, Debre Ellias, Melo Hamusit, Farta (Mogesse, 2007), Sheka, Konso,

and Mandura ((Desta et al., 2014) chicken populations. With regard to the mapping of genes of interest in indigenous Ethiopian chickens, so far a single work has been published (Wragg *et al*., 2012). Wragg *et al.* (2012) studied randomly selected 15 birds from 5 Ethiopian chicken populations (in Gondar, Konso, Gumuz, sheka, and Guduro). Together with other breeds, the study mapped phenotypic traits (e.g. skin and egg color) using genome-wide association approaches. It illustrates for the first time the possibility and power to use indigenous outbreed chicken population for the fine genome mapping of Mendelian traits. Wragg and his colleagues also recommend including, a minimum of 90-110 kb SNPs for effective genome-wide associations study in village chickens.

The presence of genomic diversity in domestic chicken is of great importance and a prerequisite for rapid and accurate genetic improvement of selected breeds in various environments, as well as to facilitate rapid adaptation to potential changes in breeding goals (Nielsen, 2005). Hanotte *et al*. (2010), suggested that it is time to tap Africa's livestock genomes to better understand and exploit the genetic diversity of Africa's individual livestock breeds before they fade away. Understanding which factors shape levels of genetic diversity within genomes forms a central question in evolutionary genomics and is of importance for the possibility to infer episodes of adaptive evolution from signs of reduced diversity. There is an on-going debate on the relative role of mutation and selection in governing such diversity levels (Mugal *et al*., 2013). This study aims at characterizing genomic diversity through the discovery of genomic variants in 27 indigenous chicken populations of Ethiopia as a milestone for further works on management and conservation of chicken genetic resources, studying the genetic mechanism underlying local chicken adaptation.

4.2. Materials and methods

4.2.1. Whole blood sample collection

Blood samples were collected from 27 chicken populations in Ethiopia (Figure 16). Samples included 103 cocks and 157 hens. Except the improved Horro, Meseret, Tsion Teguaz, Jarso and local Horro populations, 10 chicken from each village were sampled. One or two chicken were sampled per household. Improved Horro was sampled from a breeding stock of 8^{th} generation under selection at Debre Zeit Agricultural Research Centre and used as a reference population. Unlike other populations, Jarso and Local Horro sequences were obtained and included from the previous studies. Photographs and weight of each bird were taken. The average weight of sampled chicken was 1.26 kg with age ranges of 5 to 36 months. Sampling considered different agro-ecological zones, altitudes ranging from 729-3500 meters, marketing points, and chicken phenotypic characteristics. From the wing vein of each chicken, 50 - 250 µl of whole blood were drawn with syringes using cryotubes filled with 1.5 ml absolute ethanol (100%) following the guidelines available at https://www.sheffield.ac.uk/nbaf-s/protocols_list.

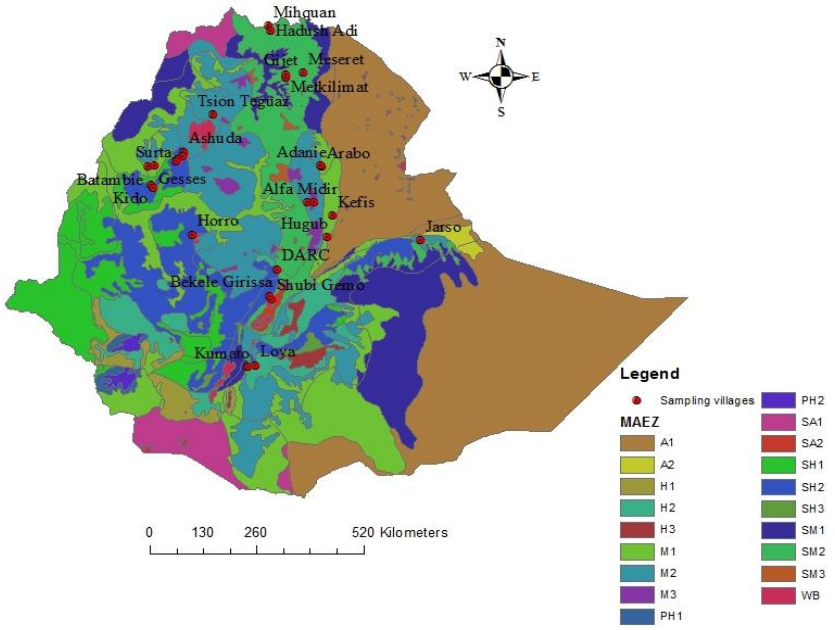


Figure 16. Agro-ecological map of Ethiopia with sampling sites (MOA, 2000).

WB = Water body; A1 = Tepid to cool arid mid highlands; Hot to warm semi-arid lowlands; H1 = Hot to warm humid lowlands; H2 = Tepid to cool humid mid highlands; H3 = Cold to very cold humid sub afro-alpine to afro-alpine; M1 = Hot to warm moist lowlands; M2 = Tepid to cool moist mid highlands; M3 = Cold to very cold moist sub-afro alpine to afro-alpine; SA1= Hot to warm semi-arid lowlands; SA2 = Tepid to cool semi-arid mid highlands; SH1 = Hot to warm sub-humid lowlands; SH2 = Tepid to cool sub-humid mid highlands; SH3 = Cold to very cold sub-humid sub-afro-alpine to afro-alpine; SM1 = Hot to warm sub-moist lowlands; SM2 = Tepid to cool sub-moist mid-highlands; SM3 = Cold to very cold sub moist sub afro-alpine to afro-alpine; PH1 = Hot to warm per humid lowlands; PH2 = Tepid to cool per-humid mid highlands.

4.2.2. DNA isolation

Total DNA was extracted from chicken whole blood at the BecA-ILRI Hub, Nairobi, Kenya facility (http://hub.africabiosciences.org/) using the Qiagen DNeasy blood and tissue kit protocol (Lwelamira *et al.*, 2008). To evaluate the DNA concentration a Thermo Scientific NanoDrop spectrophotometer 2000c was used. The integrity of DNA was confirmed by agarose gel electrophoresis whereby 20 ng/µl genomic DNA samples were loaded with 1 µl loading dye (6X)

on a 1% agarose gel containing 2.5 µl gel red at a voltage of 7/cm for 60 minutes, 3 µl of lambda DNA of size of 48,500 bp and a concentration of 20 ng/µl was used as size marker and the gel was then examined using UV light using GelDoc-It2 Imager to check the extracted DNA quality and quantity. The genomic DNA from (n = 284) was normalized to a final volume of 100 µl and final concentration of 50 ng/µl and sent to Edinburgh Genomics, UK, for whole genome sequencing.

4.2.3. DNA quality checking (QC) and library Preparation

The QC, library prep, and sequencing were performed at the Edinburgh Genomics facility. Genomic DNA (gDNA) samples were evaluated for quantity and quality using an AATI (Agilent Formerly Advanced Analytical) Fragment Analyzer and the DNF-487 Standard Sensitivity Genomic DNA Analysis Kit. The AATI ProSize 2.0 software was used to provide a quantification value and a quality (integrity) score for each individual gDNA sample. Genomic DNA samples having a quality score of > 7 and with high molecular weight were used. Based on the quantification results, gDNA samples were normalized to the concentration and volume required for the Illumina SeqLab TruSeq Nano library preparation method using the Hamilton MicroLab STAR. Next Generation sequencing libraries were prepared using Illumina SeqLab specific TruSeq Nano High Throughput library preparation kits in conjunction with the Hamilton MicroLab STAR and Clarity LIMS X Edition. The normalized gDNA samples were then sheared to a 450 bp mean insert size using a Covaris LE220 Focused-ultrasonicator. The inserts were ligated with blunt ended, Atailed, size selected, TruSeq adapters and enriched using 8 cycles of PCR amplification.

4.2.4. Library QC and sequencing

The libraries were evaluated for mean peak size and quantity using the Caliper GX Touch with a HT DNA 1k/12K/HI SENS LabChip and HT DNA HI SENS Reagent Kit. Those libraries were then normalized to 5 nM using the GX data and the actual concentration was established using a Roche LightCycler 480 and a Kapa Illumina Library Quantification kit and Standards. The normalized libraries were denatured and pooled in eights for clustering and sequencing using a Hamilton MicroLab STAR with Genologics Clarity LIMS X Edition. Libraries were clustered onto HiSeqX Flow cell v2.5 on cBot2s and the clustered flow cell is transferred to a HiSeqX for sequencing using a HiSeqX Ten Reagent kit v2.5. The samples were sequenced at a genome coverage of ~5-90X (mean = 36.1X). Demultiplexing is performed using bcl2fastq (2.17.1.14), allowing 1 mismatch when assigning reads to barcodes.

Adapters (Read1: AGATCGGAAGAGCACACGTCTGAACTCCAGTCA, Read2: AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGT) are trimmed during the demultiplexing process.

4.2.5. Mapping and variant calling

The pipelines for mapping and variant calling included: mapping reads against reference genome using BWA-mem, sorting BAM file, removing duplicated reads with PICARD, Base Quality Score Recalibration (BQSR) with GATK, calling variants using GATK, Variant Quality Score Recalibration (VQSR) for variant filtration with GATK, and finally selection of only bi-allelic SNPs which passed the VQSR step.

Mapping with BWA-mem

High quality paired-end reads (FASTAQ format) were aligned to the chicken (*Gallus gallus*) reference genome sequence (Gallus_gallus-5.0 or galGal5) (https://www.ncbi.nlm.nih.gov/genome/?term=Galus+galus+5), using Burrows-Wheeler Aligner software package (http://sourceforge.net/projects/bio-bwa/files/) with the command 'mem -t 8 -k 32 -M -R' (where –t = no. of threads; -k = min seed length; -M = Mark shorter split hits as secondary (for Picard compatibility) which permits high-quality queries for longer sequences as it is fast and accurate (Li and Durbin, 2010); and -R for defining read groups. The alignment output generated were stored in the SAM format and then converted to BAM formats using PICARD tools. Duplicated reads originating from a single fragment of DNA during sample preparation (such as library construction using PCR) were marked and removed using PICARD's MarkDuplicates command (https://broadinstitute.github.io/picard/command-line-overview.html#MarkDuplicates).

Base quality score recalibration

BQSR is a data pre-processing step that detects systematic errors made by sequencers in estimating the quality score of each base call. Base quality score is an important parameter for variant calling as it expresses confidence that the base has been called correctly. Unfortunately, the scores produced by the machines are subject to various sources of systematic technical errors, leading to over- or under-estimated scores. The BQSR step applies a machine learning algorithm to model these errors empirically and adjust the quality scores accordingly by considering a number of

covariates such as sequencing context of the base, position in read or sequencing cycle (https://gatkforums.broadinstitute.org/gatk/discussion/44/base-quality-score-recalibration-bqsr).

Variant calling

Variant calling from each sample was performed in the gVCF mode for cohort analysis using GATK's HaplotypeCaller (Figure 2). Joint genotyping of samples from each population were done using GATK's GenotypeGVCF tool for downstream analysis. Variant Quality Score Recalibration (VQSR) were also performed to increase sensitivity (identifying the real variants) and specificity (identifying false positives) using GATK followed by a selection of only bi-allelic SNPs that passed the VQSR step. For the VQSR step, we used 1M validated SNPs and 15 SNPs from dbSNP for recalibration purpose.

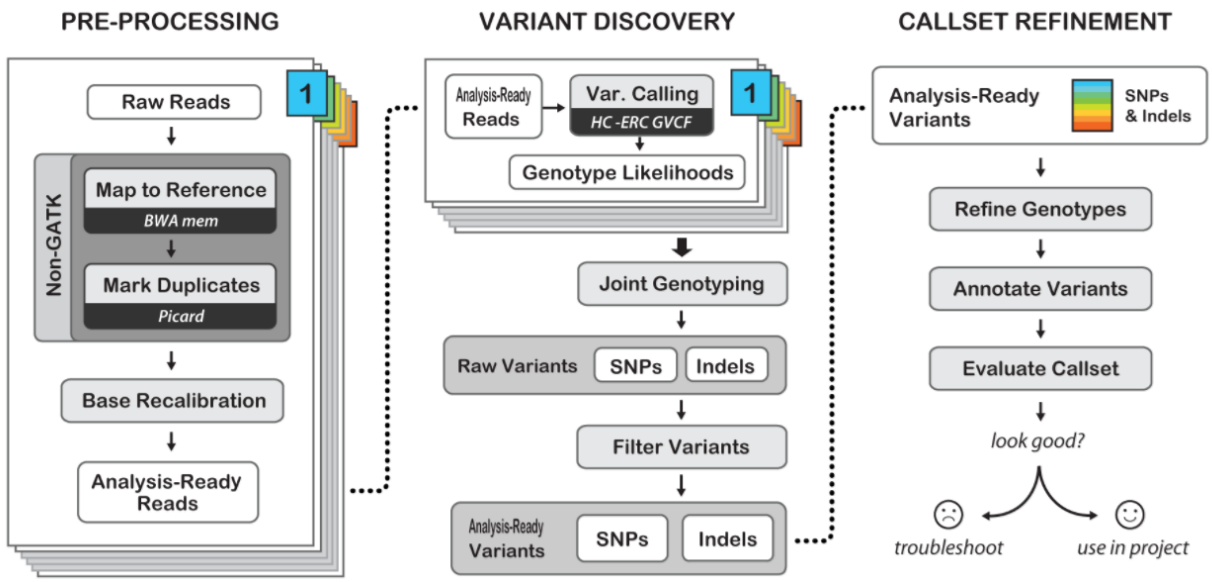


Figure 17. Overview of data analysis pipeline using BWA, PICARD, and GATK.

4.2.6. Population structure and genome-wide nucleotide diversity

Population structure and relationships between samples were established using Principal Component Analysis (PCA) using smartpca program in eigenstrat version 6.0 (Patterson *et al*., 2006; Price *et al*., 2006). PCA was performed using all SNPs from 27 populations (n = 20,867,451 SNPs). The top three principal components (PCs) provided the clearest separation of the data and were used to construct the PCA plot. Apart from the PCA, the genetic structure of each population was also assessed unsupervised, using ADMIXTURE version 1.3.0 (Alexander *et al*., 2009). Global admixture analyses were run for K = 2 to K = 10 assumed numbers of ancestors using 651,417 LD pruned SNPs. The optimal K value was determined based on the lowest cross-validation error. The following criteria was used for LD-pruning: "indep-pairwise 50 10 0.3", "bp-space 1000", "maf 0.1" and "geno 0.1". This command targets for removal each SNP that has an r^2 value of greater than 0.1 with any other SNP within a 50-SNP sliding window (advanced by 10 SNPs each time) and Minor allelic frequencies of 0.1. The average genome nucleotide diversity (π) for each population was determined using VCFtools version 0.1.13 in 20 kb windows over a 10 kb sliding step (Danecek *et al*., 2011). Structure and admixture plots where plotted using R-software package version 3.4.3.

4.2.7. Functional annotation and enrichment analysis of non-synonymous genes

To predict their functional consequence, SNPs were annotated against the Ensembl chicken gene database (release 92) using the software package ANNOVAR (Wang *et al*., 2010). The effects of non-synonymous SNPs on protein function were predicted based on evolutionary conservation using the Sorting Intolerant from Tolerant (SIFT) prediction algorithm which depends on the degree of conservation at individual amino acid (AA) positions (Sim *et al*., 2012). Using multiple

alignments of homologous but distantly related peptide sequences, SIFT calculates normalized probabilities (SIFT score) of observing all possible AA residues at a position (Gheyas *et al*., 2015; Ng, 2003). If the SIFT score is greater or equal to 0.05 the variant is considered evolutionary tolerant (TOL), whereas variants with a score less than 0.05 are regarded as intolerant (INTOL) and potentially deleterious (Choi and Chan, 2015; Kumar *et al*., 2009; Sim *et al*., 2012). The SNPs were further checked for their overlap with 1.1 million conserved elements (CE) obtained from the Roslin Institute (Eory *et al*., unpublished data; personal communication). These CEs were generated from multiple alignments of sequence data from 48 bird species and 1 anole lizard species using Genomic Evolutionary Rate Profiling (gerp++) (Davydov *et al*., 2010).

The proportion of homozygous SNPs were calculated using the "stat" option of the VCFtools version 0.1.113 (Danecek *et al*., 2011). To establish the biological significance of a list of genes carrying potential functional SNPs, the DAVID Bioinformatics Resources 6.8 (DAVID; Huang *et al*. 2009a, 2009b) was used. This allowed performing enrichment analysis of the Gene Ontology (GO) and the Kyoto Encyclopaedia of Genes and Genomes (KEGG) pathways (KOBAS version 3.0, http://kobas.cbi.pku.edu.cn/). For both analyses, the Fisher exact *P*-value < 0.05 default threshold were considered.

4.3. Results

4.3.1. Sequencing and variant calling

The average number of paired sequence reads generated from an individual sample in each population ranged between to about 202 million (Hadush Adi) and 475 million (Surta), resulting in average genome coverage of about 22X to 44X. On average 88% of the bases were covered by at least 5 reads and > 90% were covered with at least 10 reads (Table 11). More than 98% of read pairs in all samples were mapped to the Galgal 5.0 reference genome. The mean sequence depth of the entire chicken population sampled is about 39X (Figure 18).

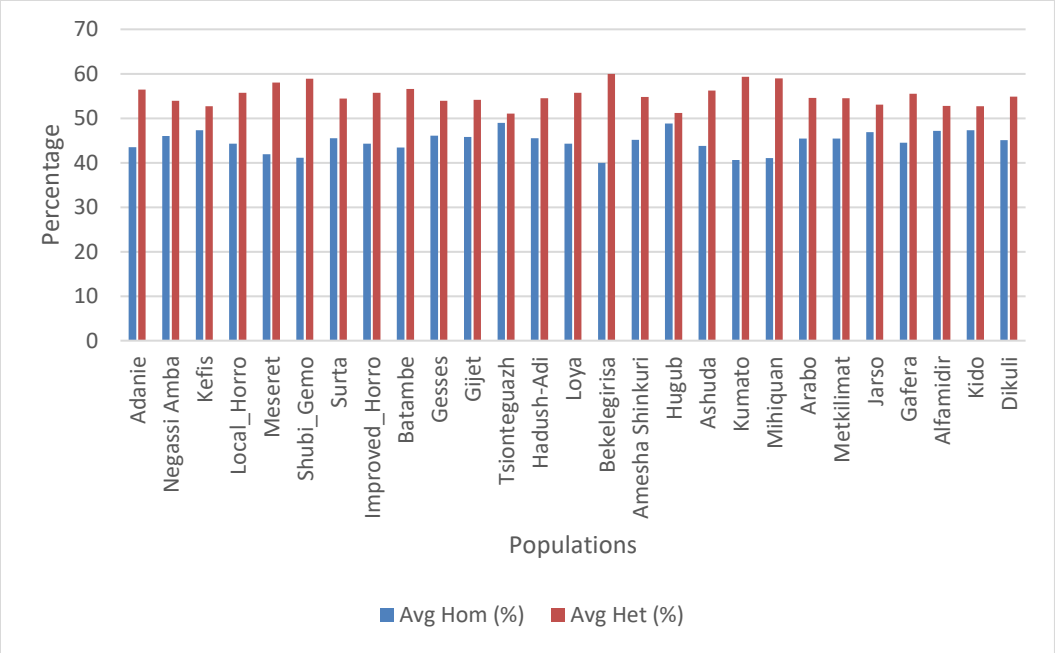
Variant calling and filtration resulted in the detection of about 21 million SNPs (n = 20,867,451) combining the 27 population. The number of SNPs detected within individual population ranges from 10 to 12 million. The mean SNP density reported is 21 SNPs ± 5 per kb or 1 SNP for every 48 bases. 28.12 % (n = 5,868,599) of the SNPs were already reported in dbSNP (build 147), which currently contains ~21 million SNPs (n = 20,867,451 SNPs) for chicken; while the rest of the SNPs (n = 14,998,852) are novel. Much lower SNP density is found in sex chromosomes than autosomes. The genome landscape plot for the genes for individual chromosome (1 kb window) is given in Figure S 2. The white ridges as evidenced by samtools view with no density coverage of SNPs are the gaps because of mapping issues in the reference genome (GC repeat regions) (Figure S 3). Widespread variations are noted in SNP density across chromosomes (Figure 20). The lowest SNP density was reported for chromosome W and the highest SNP density was reported for chromosome 26 followed by chromosome 6. Chromosome-wise SNP distribution plots across the Ethiopian indigenous chicken genome are depicted in Figure 19. The peak number of non-

synonymous SNPs were observed in chromosome 16. Except for Jarso, about 11% to 15% of the SNP are novel in each chicken population (**Table 12**). The private allele peak is owned by the Jarso chicken (n = 280448) and the lowest by the Batambe chicken (n = 34532). Alternate allele frequency ranges from 0.35 for Loya to 0.39 for Local Horro and Hugub chicken populations. About 18 - 19% of the SNPs overlap conserved elements. The population with a relatively highest putatively functional variant is Kumato followed by Local Horro chicken. The proportion of heterozygote SNPs is 55.21 % for the overall chicken population (n = 284). Bekele Girrisa chicken population has the highest average heterozygous SNPs (60%) followed by Kumato chicken (59%). The lowest average heterozygous SNPs is reported in Hugub chicken population (about 40%). The mean genome nucleotide diversity (π) for the entire chicken population is 0.02 ± 0.001. The average transition to transversion ratio is 2.35. The highest number of nucleotide substitutions was recorded for C > T and G > A (4×10^6; Figure 21).

Table 11. Summary results on sequencing and mapping of reads.

Sample	N	MR (%)	MD (X)	5_b (%)	10_b (%)	20_b (%)	40_b (%)
Batambie	436294418	99.06	40.33	87.04	78.69	73.73	60.20
Surta	475115042	98.72	41.51				
Amesha	427316335	99.21	39.02				
Hugub	360343162	99.48	35.67	90.11	88.02	81.85	40.17
Kefis	461097537	99.41	44.42	90.41	88.35	82.11	43.33
Gafera			43.45				
Tsion	244270731	99.29	22.04	75.64	64.63	47.75	9.31
Adanie	376903935	99.27	35.89	90.03	87.96	81.94	40.23
Arabo	309414324	99.02	31.30	89.54	85.79	72.33	24.10
Alfamidir	342600741	97.29	89.39	83.64	74.18	34.84	
Negasiamba	362919193	98.96	35.52				
Ashuda	436640467	99.07	39.76				
Dikuli	418411806	99.16	36.93				
Gesses	373183155	99.44	35.66	90.16	88.14	82.14	40.35
Kido	357193268	82.92	37.30				
Improved Horro	351003978	99.46	32.51				
Meseret	433954119	99.30	39.24				
Bekelegirisa	383898518	98.95	36.38				
Shubigemo	421492594	99.27	39.09				
Jarso	368646704	99.75	25.96	88.76	85.68	74.00	7.86
Local Horro	387105936	99.74	28.68	88.78	86.10	76.57	9.90
Kumato	404282348	99.45	38.13				
Loya	461026931	99.41	42.61				
Hadush Adi	201579979	98.29	39.68	87.47	79.22	57.72	41.98
Mihiquan	335214296	99.45	34.37				
Gijet	439628764	99.40	43.08	90.23	88.28	82.73	45.19
Metkilimat	339764180	99.36	33.99				

N = Average number of reads; MR: Total number of reads mapped to the Galgal 5.0 reference genome; MD: The mean sequence depth or the genome sequence coverage; 5_b: Percentage of the genome with bases covered by at least 5 reads; 10_b: Percentage of the genome with bases covered by at least 10 reads; 20_b: Percentage of the genome with bases covered by at least 20 reads; 40_b: Percentage of the genome with bases covered by at least 40 reads



Avg Hom = Average Homozygosity; Avg Het =Average Heterozygosity

Figure 18. The average percentage of homozygous and heterozygous SNPs (%) in Ethiopian indigenous chicken populations.

Table 12. Variant statistics within chicken populations from Ethiopia

Population	N	nSNPs	Known (%) *	Novel (%)	PA	µAAF	TS/TV	PI	CE (%)	PFV (%) **
Batambie	8	11278325	88	12	34532	0.384574	2.44	0.003646	2117632 (18.78)	8176 (0.07)
Surta	9	11769723	87	13	40052	0.371836	2.44	0.003757	2209322 (18.77)	8791(0.07)
Amesha Shinkuri	10	12037555	86	14	45467	0.366294	2.43	0.003718	2258138 (18.76)	9100(0.08)
Hugub	10	10873408	90	10	75551	0.390987	2.44	0.003442	2037719 (18.74)	7843(0.07)
Kefis	10	11606161	87	13	76463	0.374837	2.43	0.003609	2172148 (18.72)	8623(0.07)
Gafera	10	11938205	86	14	47192	0.36822	2.44	0.003663	2237236 (18.74)	9051(0.08)
Tsion	10	11646405	87	13	91269	0.377861	2.43	0.003488	2181362 (18.73)	8644(0.08)
Adanie	10	12254914	85	15	166779	0.363589	2.43	0.003662	2293708 (18.72)	9130(0.07)
Arabo	10	12025464	86	14	116991	0.36956	2.43	0.003491	2249348 (17.70)	9181(0.08)
Alfamidir	10	11302647	87	13	79002	0.382912	2.43	0.00326	2119442 (18.75)	8445(0.07)
Negasiamba	10	11366554	87	13	71076	0.381866	2.43	0.00336	2128289 (18.72)	8385(0.07)
Ashuda	10	11430789	87	13	49469	0.377795	2.43	0.003541	2140547 (18.73)	8637(0.08)
Dikuli	10	12009063	86	14	52605	0.360253	2.43	0.003695	2254716 (18.78)	9105(0.08)
Gesses	9	11313583	87	13	47730	0.383376	2.44	0.003444	2121533 (18.75)	8411(0.07)
Kido	9	11369167	86	14	146190	0.384662	2.42	0.003504	2116126 (18.61)	8502(0.07)
Improved Horro	30	11154784	88	12	48121	0.386675	2.44	0.003436	2092166 (18.76)	8043(0.07)
Meseret	10	12239534	86	14	121862	0.358991	2.43	0.003801	2292807 (18.73)	9405(0.08)
Bekelegirisa	10	12449396	86	14	96851	0.356569	2.43	0.003866	2334214 (18.75)	9637(0.08)
Shubigemo	10	11982320	87	13	91797	0.361542	2.44	0.003797	2253098 (18.80)	9027(0.08)
Jarso	14	12218592	100	0	280448	0.354585	2.45	0.003338	2296595 (18.80)	9442(0.08)
Local Horro	6	10602823	89	11	58140	0.392005	2.46	0.003577	1990141 (18.77)	7470(0.07)
Kumato	10	12595174	85	15	83208	0.353946	2.43	0.003949	2362678(18.76)	9843(0.08)
Loya	10	12300789	85	15	113533	0.351472	2.43	0.003882	2304034(18.73)	9593(0.08)
Hadush Adi	9	11542439	87	13	99497	0.375424	2.44	0.003741	2169976 (18.80)	8508(0.07)
Mihiquan	10	12442251	85	15	161855	0.354912	2.44	0.003865	2333135 (18.75)	9622(0.08)
Gijet	9	11751551	87	13	76662	0.368866	2.45	0.003745	2208579 (18.79)	8837(0.08)
Metkilimat	10	12203356	86	14	97841	0.361624	2.43	0.003782	2289221 (18.76)	9411(0.08)

N = Number of samples analyzed; **nSNPs** = total Number of SNPs obtained; *Check already reported SNPs in dbsnp; PI = Nucleotide diversity;**PFV = putatively functional variants (Del, stopgain/loss, splicing, and High Impact); PA = Private SNPs for each population; µAAF = Average Alternate allele frequency; CE = Conserved Element; %PFV is based on the total SNPs detected from each population.

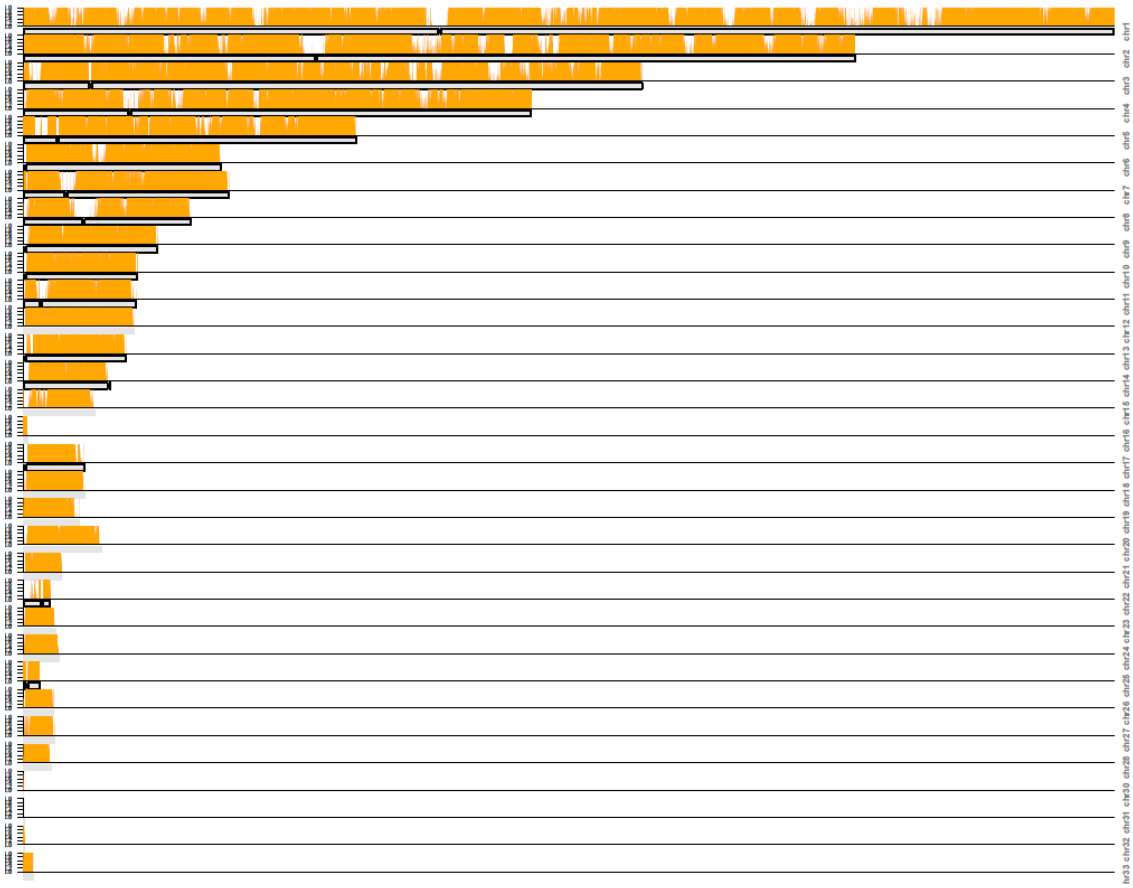
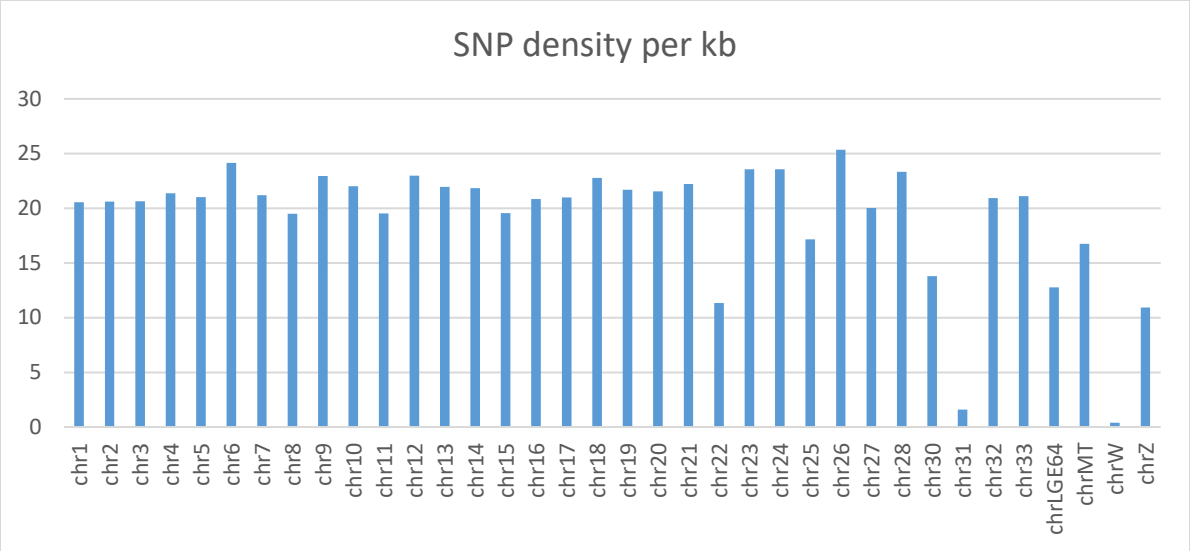


Figure 19. Chromosome-wise SNP distribution plot across the Ethiopian indigenous chicken genome.

The X-axis denotes the chromosome size, and the Y-axis indicates the chromosome number. If no SNPs are found in a block, we used a white color. Therefore, the deeper the color, the higher the number of SNPs. The window size used to count the SNPs was 1 kb.



Chromosomes	Mean ± SD SNP density
Macro (Chr1-5)	21 ± 4
Intermediate (Chr 6–10)	22 ± 4
Micro (Chr 11–28, Chr30-32, Chr MT, Chr LGE64)	19 ± 6
(Chr W)	0.4
Chr Z	11
All autosomes	20 ± 5

Figure 20. Mean SNPs density across 1 kb window for chicken chromosomes based on ~21million SNPs.

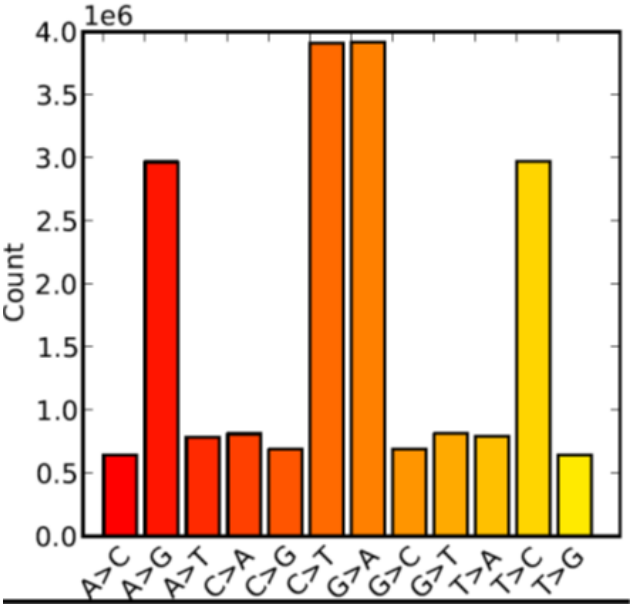


Figure 21. The rate of nucleotide substitution across Ethiopian indigenous chicken population genome.

4.3.2. Population structure and genomic diversity

PCA plots show the presence of six potential clusters of populations, with PC1 and PC2 jointly explaining 41.4% of the total genetic variance (Figure 22). PC1 (25.95%) separates Improved Horro from the rest of non-improved chicken populations. Jarso and Hugub populations were separated from Improved Horro and other populations by PC2 (15.45%). The remaining of the populations are placed quite close to each other in the PCA plot, although they could be separated into three more clusters. Admixture analysis suggested four gene pool groupings as the lowest cross-validation error was observed for K = 4 (Figure 23). LD pruned principal component analysis (left) and optimum admixture $2 < K < 4$ plot (right) for Ethiopian indigenous chicken population are indicated in Figure S 1. Admixture analysis after pruning also clustered Improved Horro, Jarso, hugub populations in gene pool one with a certain level of admixture from gene pool two (Figure 24). Both PC and Admixture plots illustrate clustering of Improved Horro, Arabo, Jarso, and Hugub populations independently, leaving the rest of the populations altogether. In other words, the majority of the population share quite a lot of SNPs and are closely clustered. PCA analysis plots prior to LD pruning are also presented in Figure 22.

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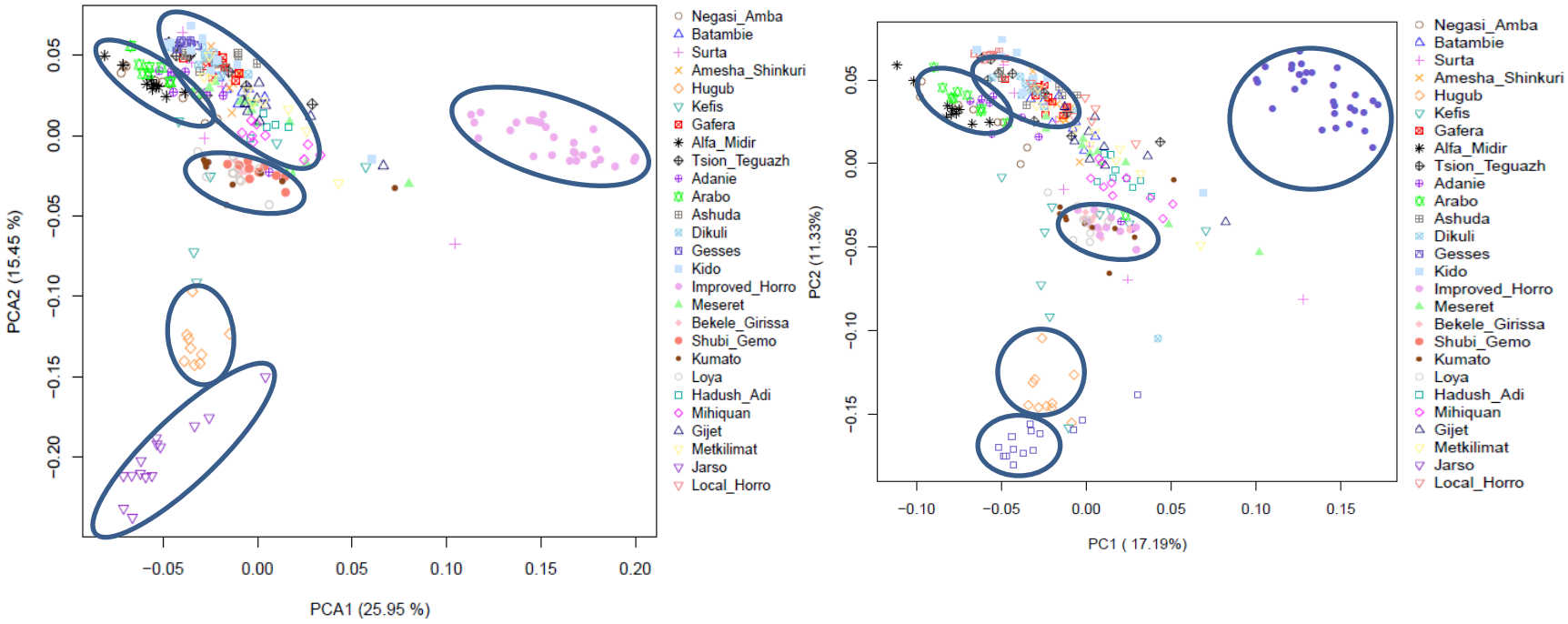


Figure 22. Principal component analysis plot of non-filtered (n = 20,867,451 SNPs) (left) and LD pruned SNPs (n = 651,417) (right).

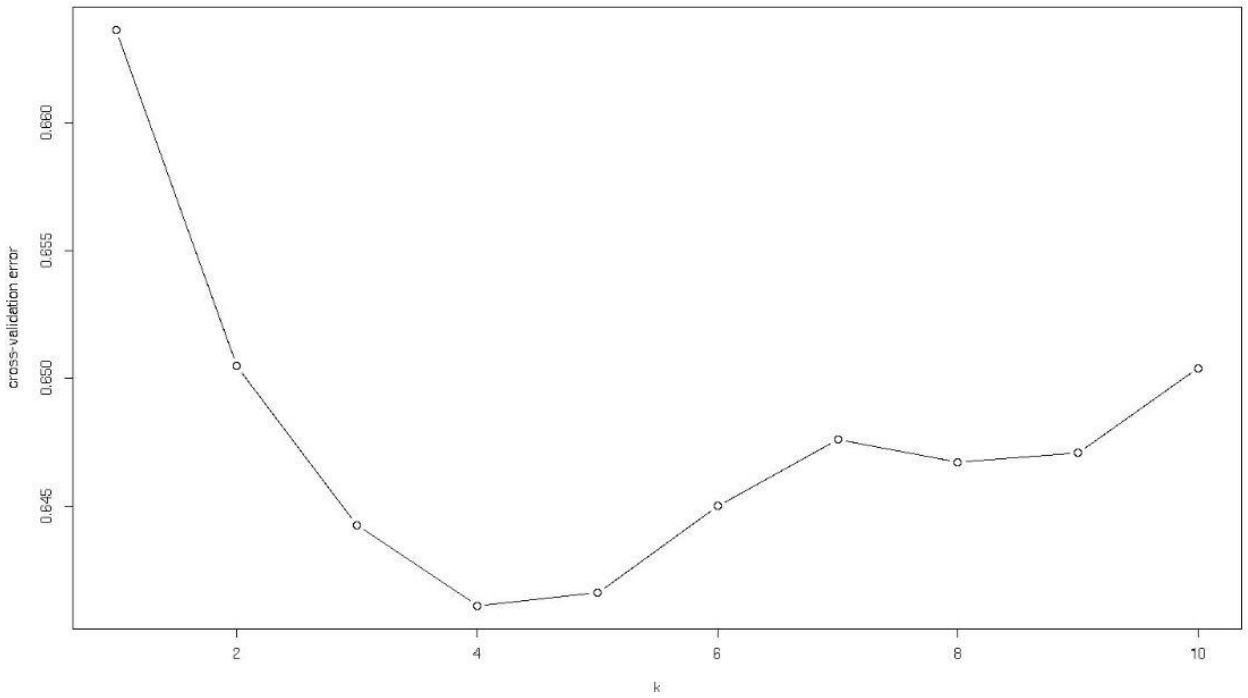


Figure 23. Cross-validation errors of different k values used for admixture analysis

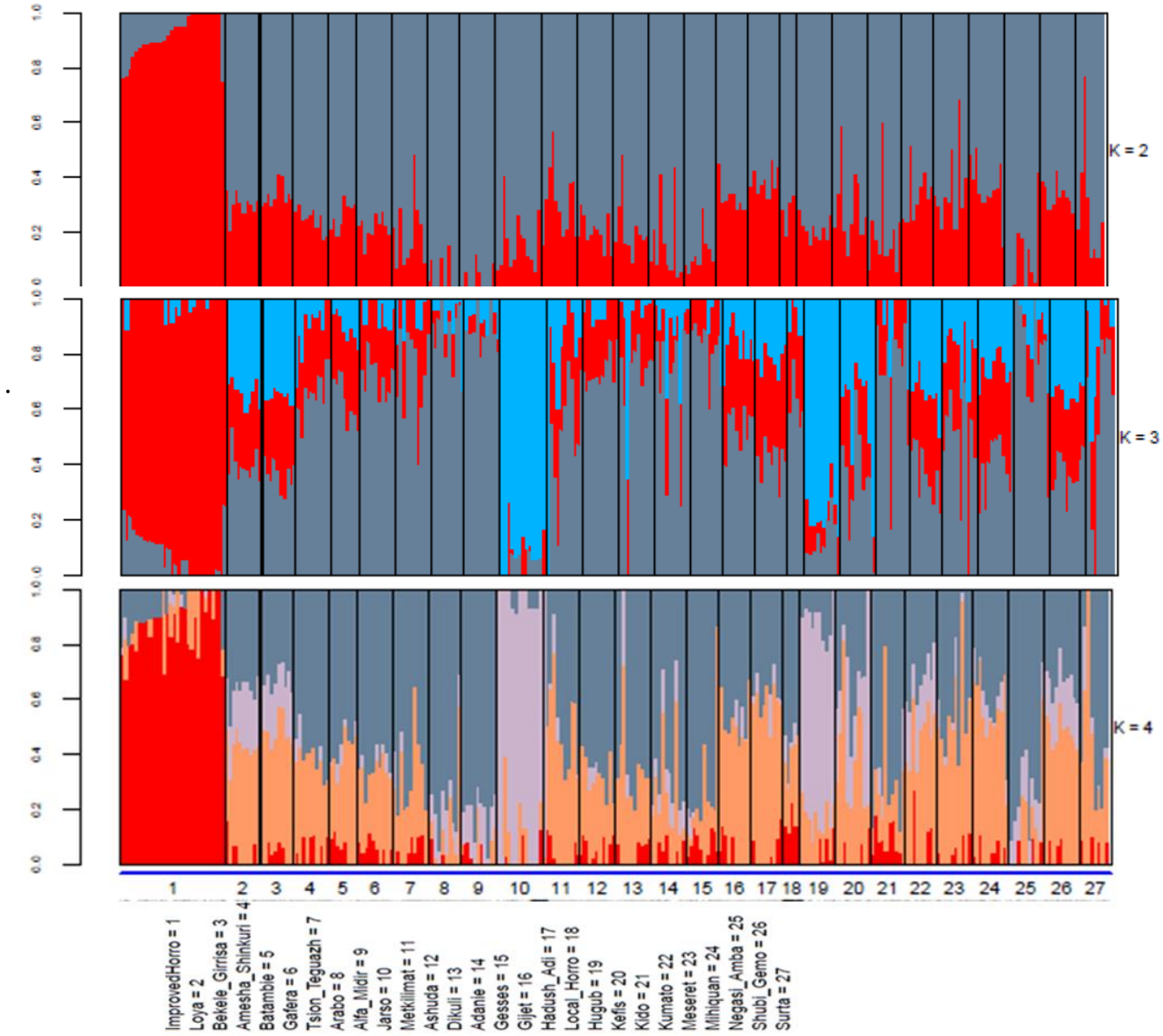


Figure 24. The admixture plots for Ethiopian indigenous chicken populations (K = 4).

4.3.3. Coding and non-coding variants

Annotation of 21 million SNPs against ENSEMBL gene annotation database shows that 46.36% of SNPs are located within genes (intronic + exonic + UTRs + splicing) and the rest are found outside genes (intergenic and up/downstream). However, only 1.6% (n = 331,968) of the SNPs are in protein-coding regions (i.e. exon) (Table 13). SNPs in exonic regions were further classified into synonymous (65.14%; variants which do not alter the amino-acid sequence in proteins), non-synonymous (34.38%; variants that change amino-acid sequence in a protein) and stop gain or loss (0.98%; variants that leads to gain or loss of stop codon) polymorphisms (Figure 26). The synonymous and non-synonymous (AA-altering) number of SNPs are 190,041(0.48%) and 100,293 (0.98%), respectively. Whereas, the other AA altering variant, number of stop gain/loss accounts for about 0.36% (n = 1,209). Even though non-synonymous SNPs change amino acid sequence within a protein, the effects are not always harmful or radical on protein function. Using SIFT, 21.9% of the non-synonymous variants (n = 44, 553) were predicted as 'intolerant' (INTOL) having a radical effect, 64.94% (135,917) were predicted 'tolerant' (TOL), whereas the prediction for other variants had low confidence level (Figure 27). The average percentage of homozygous and heterozygous SNPs (%) in Ethiopian indigenous chicken populations.

Table **12** shows the number and percentage of putatively functional SNPs that are present in high frequency and were detected from 27 populations.

Apart from the amino-acid altering variants, other potentially functional categories reported in this study are splicing variants (0.006%), variants in 3′ and 5′ UTR regions with possible roles of regulating protein translation (0.82%); those within 1 kb up- or downstream of transcription start or end sites (3.06%) with possible roles on transcriptional regulation; and finally, the SNPs belonging to the non-coding RNA (ncRNAs) (2.61%) (Table 13). Nonsynonymous number of SNPs/Kb across chromosomes are presented in Figure 25.

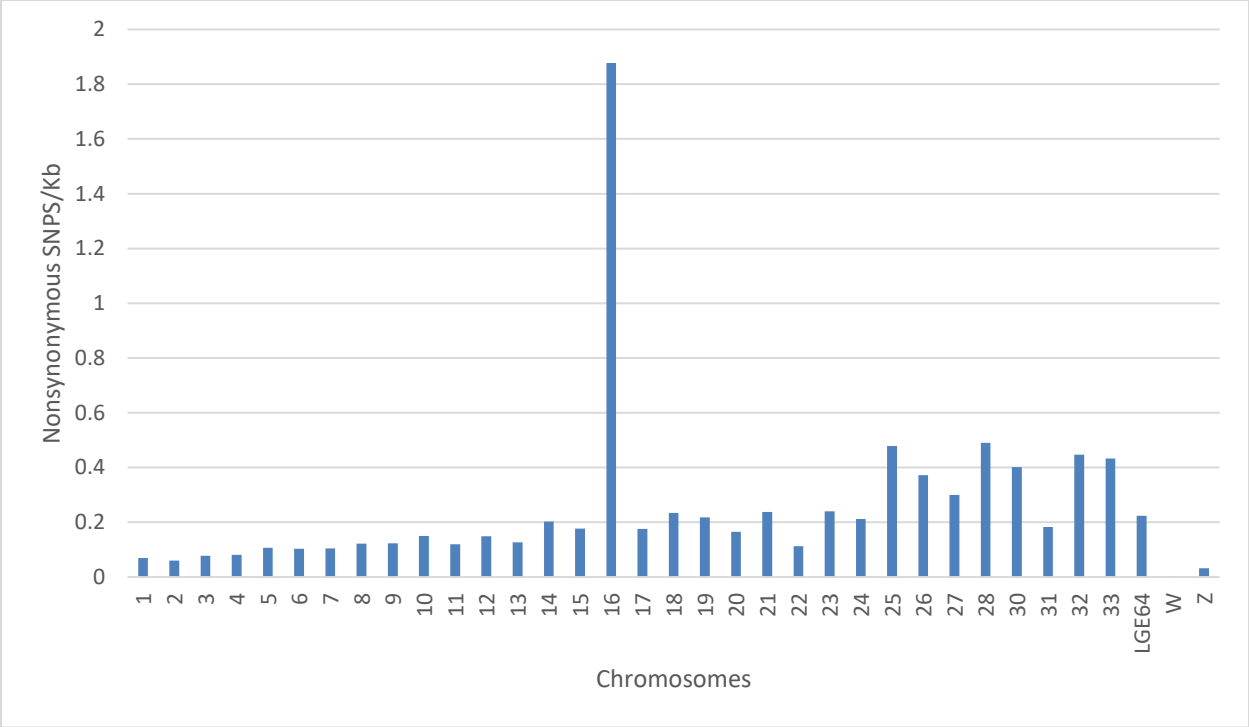


Figure 25. Non-synonymous number of SNPs/Kb across chromosomes.

Table 13. Summary of annotation of SNPs and their alternative allele frequency (AAF) in Ethiopian chicken populations.

Annotation category	Number (%)	Mean AAF(SD)	No. detected from >10 populations with mean AAF > 0.9 (%)	No. detected from > 27 populations with mean AAF > 0.9 (%)	No. of private SNPs with AAF > 0.9 (%)
Intergenic	10,556,684 (50.59)	0.26 (0.26)	435444 (2.087)	282933 (0.014)	9883 (0.0005)
Intronic	9,169,275 (43.94)	0.26 (0.26)	366476 (1.76)	234965 (0.011)	5377 (0.0003)
Upstream/downstream	638532 (3.06)	0.25 (0.26)	24616 (0.12)	14257 (0.0007)	505 (0.00002)
Exonic	331968 (1.59)	0.24 (0.26)	14954 (0.07)	9606 (0.0005)	482 (0.00002)
-Nonsynonymous	100293 (0.48)	0.21(0.25)	4015 (0.02)	2580 (0.0001)	154 (0.000007)
-Nonsynonymous deleterious	24728 (0.11)	0.14 (0.18)	329 (0.002)	152 (0.000007)	25 (0.000001)
-Nonsyonymous tolerated	75565 (0.36)	0.23 (0.27)	2428 (0.012)	2428 (0.0001)	129 (0.000006)
-Stop-gain/loss	1269 (0.006)	0.18 (0.22)	22 (0.0001)	11 (0.0000005	1 (0.00000005)
Synonymous	190041(0.91)	0.26 (0.27)	9417 (0.045)	6055 (0.0003)	278 (0.00001)
UTR3'/UTR5'	171,175 (0.82	0.24 (0.25)	6550 (0.031)	4067 (0.0002)	89 (0.000004)
ncRNA	544429 (2.61)	0.25 (0.25)	19187 (0.092)	12357 (0.0003)	584 (0.00003)
Splicing	1269 (0.006)	0.24 (0.26)	48 (0.0002)	22 (0.000001)	2 (0.0000001)
Conserved elements	3859925 (18.5)	0.26 (0.00)	158053 (0.76)	102316 (0.005)	2252 (0.00011)

Upstream: a variant that is located in the 1-kb region upstream of the gene start site; stop gain: a non-synonymous (ns) SNP that leads to the creation of a stop codon at the variant site; stop loss: a non-synonymous SNP that leads to the elimination of a stop codon at the variant site; splicing: a variant within 2 bp of a splice junction; downstream: a variant that is located in the 1-kb region downstream of the gene end site.

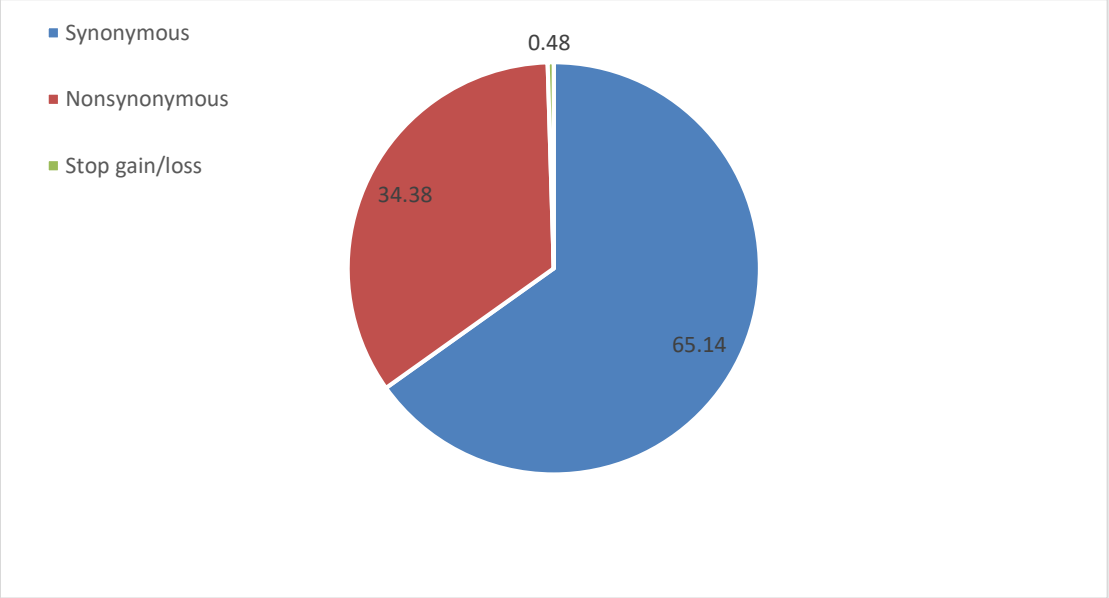


Figure 26. Exonic variant summary in each annotation category based on ANOVAR (%)

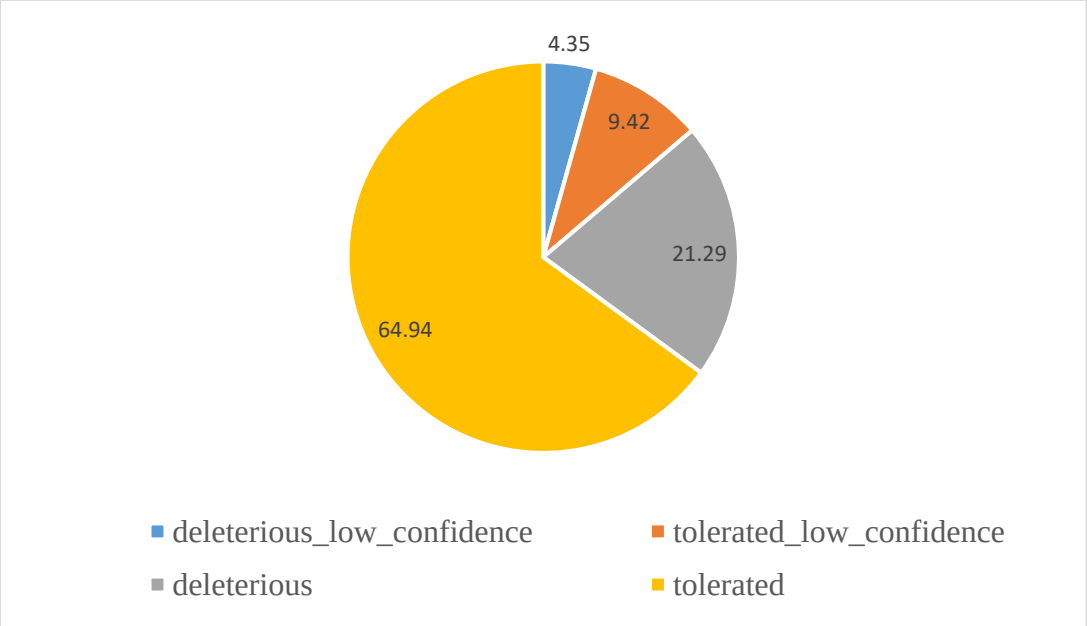


Figure 27. VEP based SIFT analysis for Amino acid altering (non-synonymous and stop gain/loss) SNPs (%).

4.3.4. SNPs within evolutionarily conserved elements

The 21 million SNPs were annotated against 1.1 million conserved elements (CEs) across 48 birds plus lizard sequences (Eory *et al*., unpublished data; personal communication). These CEs covers about 2.1% of the chicken genome (total length of CEs is 186,488,363 bases). The total number of SNPs that overlapped with CEs are 3,859,925 (18% of the 21 million SNPs), of which 2,619,665 are reported in dbsnp, while the remaining are novel.

4.3.5. Allele frequency spectrum of SNPs in different annotation categories

The frequency spectrum of non-reference or alternative alleles (AAF) of variants from different annotation categories were compared (Figure 28; Figure 29). The allele frequency distribution of different annotation categories showed that the largest proportion of variants fell within the AAF frequency bin of ≤ 10%. However, the proportion of low-frequency variants was higher for potentially harmful variants like deleterious missense and stop gain/loss (> 60%) compared to variant belonging to the neutral categories (e.g. intergenic, intronic, and synonymous; < 40%). Polymorphisms that are potentially functional or deleterious but are present at high frequency (e.g. AAF > 0.9) may be under selection. Table 4 shows the number and percentage of putatively functional SNPs present in high frequency and were detected from 27 populations.

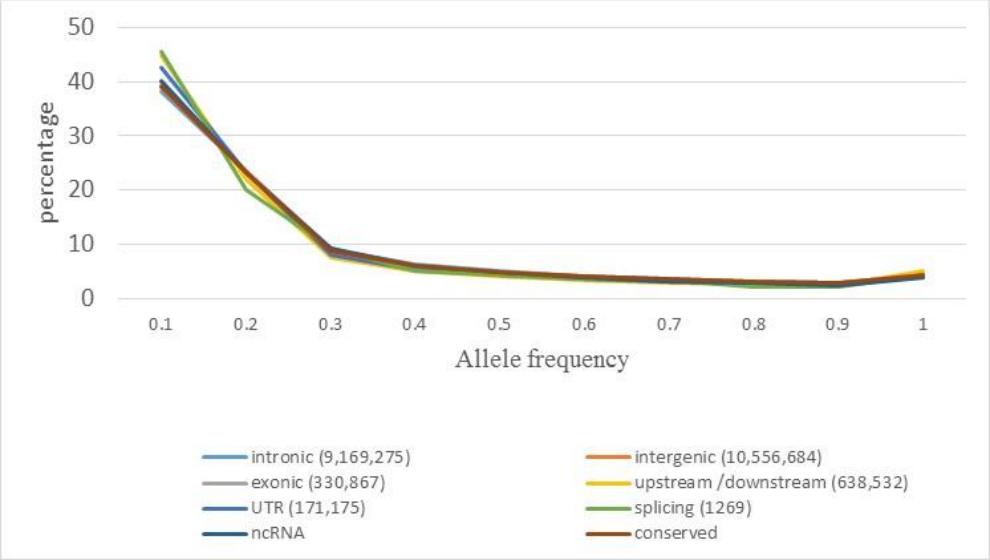


Figure 28. AAF spectrum different variants (left); AAF spectrum of synonymous, nonsynonymous and stop gain/loss SNPs.

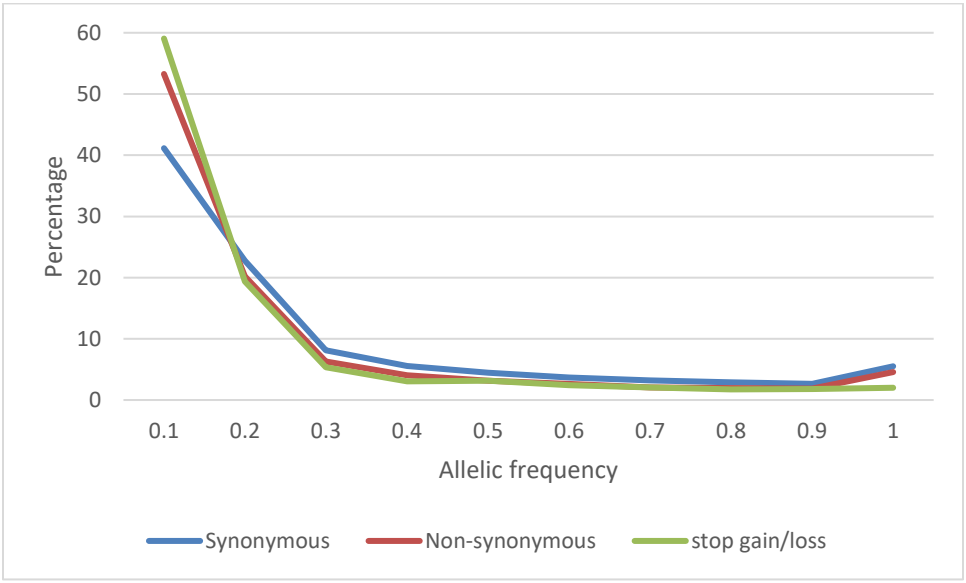


Figure 29. AAF spectrum of synonymous, non-synonymous and stop gain/loss SNPs.

4.3.6. Functional annotation and enrichment Analyses

One thousand four hundred twenty-five functionally annotated SNPs identified in the entire dataset (27 populations) were checked for their functions and biological pathways (Table S 45). GO term enrichment analysis shows significant ($P \leq 0.05$). GO terms related to innate antibacterial and antifungal immunity response (IPR000157; Toll/interleukin-1 receptor homology (TIR) domain, IPR007110); Immunoglobulin-like fold and energy biosynthetic ((GO: 0016887; ATPase) activity, (GO: 0006183; GTP biosynthetic process), (GO: 0006228; UTP biosynthetic process), GO: 0006241; CTP biosynthetic process)). Similarly, 385 non-synonymous deleterious genes (352 reported) detected in 10 populations (Table S 46) where functionally annotated and GO term enrichment analysis gave genes responsible mainly for DNA repair and binding (GO:0042162, GO:0006281), ATP binding (GO:0005524) and WD40 repeat domains (IPR017986, IPR015943, IPR001680) (Table 15). Annotation of non-synonymous deleterious SNPs with AAF > 0.9 from 27 populations (Table S 47) and their functional characterization has confirmed genes attributed to methyltransferase, protein autophosphorylation, a class of nuclear body called promyelocytic leukemia (PML) (Table 16).

Table 14. GO terms enriched for non-synonymous deleterious variants in 27 chicken populations based on SIFT prediction.

Category	Term	Pathway ID	Count	P-value
GO term biological function	Microtubule-based movement	GO:0007018	6	0.004910801
	cytoskeleton-dependent intracellular transport	GO:0030705	3	0.026430039
	GTP biosynthetic process	GO:0006183	3	0.017017792
	UTP biosynthetic process	GO:0006228	3	0.017017792
	CTP biosynthetic process	GO:0006241	3	0.017017792
	Cilium morphogenesis	GO:0060271	4	0.035292561
	Homophilic cell adhesion via plasma membrane adhesion molecules	GO:0007156	7	0.020793417
GO term molecular function	ATPase activity	GO:0016887	9	9.95E-04
	Microtubule motor activity	GO:0003777	6	0.002723165
	Serine-type endopeptidase inhibitor activity	GO:0004867	5	0.02212991
	4 iron, 4 sulfur cluster binding	GO:0051539	4	0.02383427
INTERPRO	Toll/interleukin-1 receptor homology (TIR) domain	IPR000157	6	2.09E-04
	Interleukin-1 receptor family	IPR015621	3	0.012953862
	Immunoglobulin-like fold	IPR013783	22	0.001598181
	Immunoglobulin-like domain	IPR007110	17	0.002214937
	Immunoglobulin subtype	IPR003599	13	0.012352987
	Kinesin, motor region, conserved site	IPR019821	4	0.04201322
	Serpin domain (SERine Proteinase Inhibitors)	IPR023796	4	0.018536739
	Serpin family	IPR000215	4	0.020916244
	Nucleoside diphosphate kinase	IPR001564	3	0.016977895
	C-type lectin fold	IPR016187	7	0.006188548
	Sushi/SCR/CCP	IPR000436	4	0.045649524
SMART	TIR	SM00255	5	0.001657044
	IG	SM00409	13	0.020118713
	SERPIN	SM00093	4	0.022489789
	NDK	SM00562	3	0.019548392
	CCP	SM00032	4	0.054729557

Summary of Go functions, pathways and processes showing functions related to health involved in innate antibacterial and antifungal immunity response and biosynthetic activity. ID = identifier, GO = gene ontology; SMART = Simple Molecular Architecture Research tools.

Table 15. GO terms enriched for non-synonymous deleterious variants in 10 chicken populations based on SIFT prediction.

Category	Term	Pathway ID	Count	PValue
INTERPRO	WD40-repeat-containing domain	IPR017986	9	0.016272
GOTERM molecular function	Telomeric DNA binding	GO:0042162	3	0.021679
INTERPRO	WD40 repeat	IPR001680	8	0.02589
GOTERM molecular function	oxidoreductase activity	GO:0016491	5	0.025893
GOTERM cellular component	lysosome	GO:0005764	5	0.02709
INTERPRO	WD40/YVTN repeat-like-containing domain	IPR015943	9	0.028383
GOTERM Biological function	DNA recombination	GO:0006310	3	0.028499
GOTERM cellular component	lamellipodium	GO:0030027	5	0.030521
GOTERM_BP_DIRECT	peptidyl-serine phosphorylation	GO:0018105	5	0.031163
GOTERM cellular component	external side of plasma membrane	GO:0009897	5	0.034197
GOTERM cellular component	centriole	GO:0005814	4	0.035157
GOTERM cellular component	neuronal cell body	GO:0043025	5	0.03812
GOTERM Biological function	DNA repair	GO:0006281	5	0.038616
GOTERM Biological function	positive regulation of cholesterol homeostasis	GO:2000189	2	0.041447
GOTERM molecular function	alpha-1,3-mannosyltransferase activity	GO:0000033	2	0.042633
INTERPRO	Sialidases	IPR011040	2	0.044212
GOTERM molecular function	ATP binding	GO:0005524	21	0.045558

Table 16. Go terms enriched for non-synonymous deleterious variants with allele frequency greater than 0.9 in 27 chicken populations based on SIFT prediction.

Category	Term	Pathway ID	Count	**P-value**
GOTERM Molecular Function	Methyltransferase activity	GO:0008168	3	0.008812026
GOTERM Biological Process	Protein Autophosphorylation	GO:0046777	4	0.018881257
GOTERM Cellular Component	PML body	GO:0016605	3	0.036055331
GOTERM Biological Process	Replicative senescence	GO:0090399	2	0.036791597
GOTERM Biological Process	Positive regulation of DNA damage response, signal transduction by p53 class mediator	GO:0043517	2	0.048757466

Summary of Go functions, pathways and processes showing functions related to health involved in innate antibacterial and antifungal immunity response and biosynthetic activity. ID = identifier, GO = gene ontology

4.4. Discussion

4.4.1. Genomic diversity of indigenous chicken populations

Single nucleotide polymorphisms (SNPs) and other mutations may disrupt the RNA structure by interfering with the molecular function and hence cause a phenotypic effect (Sabarinathan *et al*., 2013). In this study, we performed whole-genome sequencing for SNPs and used the identified SNPs to characterize genetic diversity in indigenous chicken populations of Ethiopia. About 21 million (n = 20,867,451) high quality SNPs were discovered in 27 populations (n = 284 birds). The 21 million SNPs discovered in this study were higher than the number of SNPs discovered in a previous study by Gheyas (2015) who reported 15 million SNPs. The number of SNPs detected in individual populations ranges from 10 to 12 million, which is higher than what was reported by Lawal (2018) who reported 5.8 million to 6.7 million SNPs for domestic chicken including two (Local horro and Jarso) Ethiopian populations. Widespread variations have been noted in chicken SNP density across chromosomes due to the variation in the nature of each chromosome and assembly. The mean SNP density reported in this study is 21 SNPs per kb (± 5) or 1 SNP per every 48 bases is higher than the figure reported by Gheyas *et al* (2015) who reported 15 SNPs/kb. From the total SNPs, about 28.12% (5,868,599) of the SNPs are already reported in dbSNP (build 147) which currently contains ~21 million SNPs (n=21,303,759) for chicken; while the rest of the SNPs (n=14,998,852) are novel. In terms of the mean density per Kb discovered and the novel SNPs, this study reported comparatively in concordance with the previous study by Gheya *et al*., (2015) who reported 16 ± 10.01 SNPs/Kb. In contrast to the findings of Gheyas *et al*. (2015), macro chromosomes where found to have a higher number of SNP density despite high recombination rate and in turn high SNP polymorphism in micro chromosomes (Burt, 2005). Even though the

high gene-density of the smaller chromosomes would make them susceptible to hitchhiking effects that could erode genetic variation, these effects appear to be offset by the far higher recombination rate of the microchromosomes (Aslam *et al*., 2012).

Much lower SNP density is found in sex chromosomes than autosomes as the high number of repetitive sequences mainly in W chromosome, whereas, the highest SNP density was reported for Chromosome 26 followed by chromosome 6 in spite of their lowest chromosomes size unlike what is reported by Gheyas *et al*. (2015). The high density of SNPs were obtained for chromosome Z in the current reference genome (11 SNPs/kb) compared to an average of ~3 SNPs/kb reported by Kranis *et al*. (2013). This specific finding is in line with the statement of Wong *et al*. (2004) who stated that SNP density is independent of chromosome size. The second lowest SNPs/Kb detected from Chr31 could be mainly because of the partial representation of this chromosome in the current reference genome (Kranis *et al*., 2013). Our result, also is not in line with the findings of previous studies which reported reduced genetic variations (much lower number of SNPs) on ChrZ than on autosomes for a multitude of potential reasons like low male effective population size due to skewed reproductive success among males leading to male effective population size, selective sweep due to selection on sex-linked characters combined with lower recombination rates (Sundstrom, 2004). Despite, lower chromosome length, chromosome 16 was also found to have a higher number of SNPs (21 ± 5) though this chromosome is an exception to the characteristic of high recombination polymorphism rates in micro-chromosomes. This may be due to the presence of highly variable MHC genes Whereas, the W chromosome is the sex-limiting chromosome in chicken and its reduced genetic variability is the result of selection and the complete lack of

recombination outside the pseudo autosomal region (Berlin and Ellegren, 2004; Moghadam *et al*., 2012; Wright *et al*., 2016; Xu *et al*., 2018).

The peak number of non-synonymous SNPs were observed in chromosome 16. Even though non-synonymous SNPs change amino acid sequence within a protein, the effects are not always harmful or radical on protein function. Much higher SNP density in Chr16 (probably because it contains highly variable MHC regions) and also in smaller chromosomes (chr25-33). A smaller chromosome may be gene rich and hence you see greater SNP density. About 18 to 19% of the SNPs overlapped the conserved elements. The population with a relatively highest putatively functional variant is Kumato followed by local Horro chicken population. The proportion of SNPs that were found heterozygous 55.21% for the overall chicken population (n = 284) is higher than the average heterozygous SNPs recommended (50%). The mean genome nucleotide diversity (π) of the entire chicken population is 0.02 ± 0.001 reported in this study lies in the range reported by Lawal (2018). The lowest average heterozygous SNPs is reported for Hugub chicken populations (about 40%). The local habitat of this specific population is Hot to warm semi-arid lowlands. The lowest heterozygous SNPs could be attributed to the fact that as the area is extremely hot and low density of the chicken population (narrow breeding base). The average transition to transversion ratio of detected SNPs is 2.35 (Aslam *et al*., 2012). The expected Ti/Tv ratio of true novel variants can vary across the genome attributed to a variability in the CpG and GC content of the genome. For instance, in the case of exomes, an increased presence of methylated cytosine in CpG dinucleotides in exonic regions leads to an increased Ti/Tv ratio due to an easy deamination and transition of a methylated cytosine to a thymine. It is also observed that GC content is higher in birds and mammals than in invertebrates. Observed Ti/Tv ratio in this study is lower than the

findings from Alsam *et al*. (2012) (2.45). This finding is in contrast to the fact that birds have higher TS/TV ratio for owning smaller genome size and a higher GC percentage in bird genomes.

Principal component and admixture analyses suggest the presence of four ancestral gene pools across the populations. The close proximity of majority of the populations often reflected their geographic proximity. The clustering of these population follows the geographical pattern where they are sampled from.

4.4.2. Functional annotation of genes in indigenous chicken populations

The functional information of these variants can help in the prediction of phenotypes or genetic merit with higher accuracy and selection of individuals can be done accordingly. Annotation of 21M SNPs against ENSEMBL gene annotation database shows that 46.36% of SNPs are located within genes (intronic + exonic + UTRs + splicing) and the rest are available outside genes (intergenic and up/downstream), while, only 1.6% (n=331,968) of the SNPs are in protein-coding regions (i.e. exonic). However, the study by Wong *et al*. (2014) showed that only ~37% of the variants fell within genes with only 1.2% fell within the coding regions. Non-coding RNAs are an important class of genes, responsible for the regulation of many key cellular functions (Cao, 2014; Frías-Lasserre and Villagra, 2017; Gardner *et al*., 2015). The highest number and percentage of putatively functional SNPs that are present in high frequency and were detected from 27 populations shows that these genes are adaptive.

SNPs in a coding region can be synonymous (do not result in a change in amino acid; selectively neutral) and non-synonymous. The synonymous and non-synonymous (AA-altering) number of

SNPs are 190,041(0.48%) and 100293 (0.98%), respectively. Whereas, the other AA altering variant, number of stop gain/loss accounts for about 0.36% (n=1,209). Even though non-synonymous SNPs change amino acid sequence within a protein, the effects are not always harmful or radical on protein function. Using SIFT, 21.9% of the non-synonymous variants (n = 44, 553) were predicted as 'intolerant' (INTOL) having a radical effect, 64.94% (135,917) were predicted 'tolerant' (TOL), whereas the prediction for other variants had low confidence level (Figure 11). Much higher SNP density in Chr16 (probably because it contains highly variable MHC regions) and also in smaller chromosomes (chr25-33). A smaller chromosome may be gene rich and hence may have greater SNP density. Apart from the amino-acid altering variants, other potentially functional categories are also reported in this study, such as splicing variants (0.006%); variants in 3′and 5′ UTR with possible roles of regulating protein translation (0.82%); those within 1 kb up- or downstream of transcription start or end sites (3.06%) with possible roles on transcriptional regulation; and finally, the SNPs belonging to ncRNAs (2.61%).

Genomic regions conserved across distantly related species are assumed to be under purifying selection, and hence variants within these regions are likely to be harmful (Gheyas *et al.*, 2015). Hence, SNPs overlapping evolutionarily conserved elements were checked as these may have potential functional effects. The 21 million SNPs were annotated against 1.1 million conserved elements (CEs) across 48 birds plus a lizard. These CEs covers about 2.1% of the chicken genome (total length of CEs is 186,488,363 bases).

The allele frequency distribution of different annotation categories showed that the largest proportion of variants fell within the AAF bin of ≤ 10%. However, the proportion was higher for

potentially harmful variants like deleterious missense and stopgain/loss (> 60%) compared to neutral categories like intergenic, intronic, and synonymous (< 40%). This is expected as potentially detrimental SNPs are expected to be mostly low frequency. However, contrary to our expectation, we did not find any variation in the AAF pattern of SNPs within the CE category with potentially neutral variants. SNPs that are potentially function or deleterious but are present in high frequency (e.g. AAF > 0.9) is expected to have greater impact and may be under selection.

Seven hundred ninety-five reported functionally annotated genes found from the entire 27 population were extracted and checked for their functions and biological pathways with the highest stringency. GO terms related to innate antibacterial and antifungal immunity response (IPR000157; Toll/interleukin-1 receptor homology (TIR) domain, IPR007110); Immunoglobulin-like fold and energy biosynthetic ((GO: 0016887; ATPase) activity, (GO: 0006183; GTP biosynthetic process), (GO: 0006228; UTP biosynthetic process), GO: 0006241; CTP biosynthetic process)). Toll proteins or Toll-like receptors (TLRs) and the Interleukin-1 receptor (IL-1R) superfamily are both involved in innate antibacterial antifungal, anti-Protozoan and anti-viral immunity in chicken, insects and in mammals (Blasius and Beutler, 2010; Cohen, 2014; Liao *et al*., 2010; Liu and Zhao, 2007; Ma *et al*., 2007). Interleukin-1 receptor family participates in the regulation of immune responses, inflammatory reactions, and hematopoiesis (Armant, 2002; Beutler, 2004; Mukherjee *et al*., 2016; Takeda and Akira, 2001; Vasselon, 2002). Protein protease inhibitors constitute a very important mechanism for regulating proteolytic activity. Annotation of non-synonymous deleterious SNPs with AAF > 0.9 and their functional characterization has confirmed genes attributed to Methyltransferase, Protein auto-phosphorylation, a class of nuclear body called promyelocytic leukemia (PML) which react against SP100 auto-antibodies during

viral infections; and a cell aging process associated with the dismantling of a cell as a response to telomere shortening and/or cellular aging and genes that controls positive regulation of DNA damage response, signal transduction by p53 class mediator. The VPS36 gene which is also known to have a plausible function in comb characters have been discovered as non-synonymous variant in the 27 indigenous chicken populations of Ethiopia (Shen *et al*., 2016b). Similarly, the MX1 gene responsible for morbidity, early mortality, viral shedding, and cytokine responses have been found in nonsynonymous variants of the 27 population. It is an interferon-induced gene which inhibits the proliferation of single-stranded RNA viruses (Fulton *et al*., 2014; Mishra *et al*., 2011; Schusser *et al*., 2011; Selvaramesh *et al*., 2018; Wang *et al*., 2012). The gene Chicken Aggrecan Core Protein (ACAN) which has an association with Tibia Dyschondroplasia is also found harboring non-synonymous deleterious variants in 10 populations (Fan *et al*., 2013; Stattin, 2009).

4.5. Conclusions

This study confirms the existence of significant genomic diversity in indigenous chicken populations of Ethiopia, with most of the variants previously undescribed in commercial breeds. On top of this, a sizable number of novel SNPs has been found in this study which was not reported in previous similar works.

CHAPTER 5. EFFECT OF SIGNATURE OF SELECTION ON THE GENOME LANDSCAPE OF IMPROVED HORRO AND INDIGENOUS CHICKEN IN ETHIOPIA

Abstract

Selective breeding for genetic improvement is expected to leave distinctive selection signatures within genomes. The identification of selection signatures can help to elucidate the mechanisms of selection and accelerate genetic improvement. Ethiopia has several chicken ecotypes which have evolved in different agro-ecologies. Here, we assess the footprints of candidate signatures of positive selection from whole genome autosomal sequences comprising 14,857,039 SNPs genotyped in Improved Horro, Local Horro, Hugub, Arabo and Jarso chicken populations of Ethiopia. We identified selection signals in 20 kb windows, with sliding steps of 10 kb based on estimators of pooled heterozygosity (*Hp*) and F-statistics (*Fst*). Selective sweep analysis using *Hp* and *Fst* identified genomic regions associated with production and reproduction. A total of 595 candidate genes showed high evidence of positive selection in indigenous chicken populations, including genes were related to traits such as growth and egg production. Gene ontology analysis displayed several biological processes and KEGG pathways involved in oestrogen biosynthetic and nervous system development processes and calcium signaling and biosynthesis of unsaturated fatty acids. The regions identified in this study are expected to provide genome landmarks to enhance the ongoing breed improvement operations in improved Horro and for the other four chicken populations.

Keywords: Indigenous, Chicken, Improved Horro, Signature of selection, SNP

5.1. Introduction

The genetic make-up of populations is the result of a long-term process of adaptation to specific environments, ecosystems and of artificial selection. Selective breeding for genetic improvement is expected to leave distinctive selection signatures within genomes. The identification of a signature of selection can help to elucidate the mechanisms of selection and accelerate genetic improvement by well understanding molecular pathways underlying phenotypic traits and breeding goals (Elferink *et al*., 2012). Selection leads to specific changes in the patterns of variation among selected loci and in neutral loci linked to them (Guo *et al*., 2016). These genomic footprints of selection are termed as signatures of selection and usually used as to identify loci that have been subjected to selection. Various statistical approaches, either the allelic frequency spectrum or the properties of haplotype segregation in populations are being used for detecting selection signatures at genome-wide scale (Qanbari *et al*., 2015). Among others, pooled heterozygosity (*Hp*) statistic is a variability indicator based on allele counts across sliding windows. The other commonly used statistic is the fixation index (Fst), which measures the genetic differentiation based on variations in allelic frequencies among populations (Qanbari and Simianer, 2014). The loci in the tails of the empirical distribution of *Fst* are the candidate targets of selection (Akey, 2002). The evolution of new functions and adaptation to new environments occurs by positive selection, whereby beneficial mutations increase in frequency and eventually become fixed in a population (Tang *et al*., 2007). Local environmental adaptation and artificial selection can change the allele frequencies at specific loci, leading to a higher level of population differentiation (*Fst*) (Yang *et al*., 2014). Adaptation or positive natural selection leaves an imprint on the pattern of genetic variation found in a population near the site of selection (Xue *et al*., 2009).

Local breeds make up most of the world's poultry genetic diversity and are still very important in developing countries where they represent up to 95 percent of the total poultry population. These local breeds, which are well-adapted to extensive husbandry systems and suitable for resource-poor poultry farmers endowed with very limited means, should be thoroughly studied as a basis for enhancing their use and conservation (Besbes *et al*., n.d.). To understand phenotypic variation in farm animals and in poultry, in particular, it is essential to define all potential genomic variation within a genome (Schmid *et al*., 2015). Discovery of genes with large effects on economically important traits has for many years been of interest to breeders (Wolc *et al*., 2014). In this study, we used *Hp* and *Fst* statistics to detect the signature of selection in improved and other indigenous chicken populations.

Recent advances in sequencing technologies have helped in the detection of candidate genome regions playing crucial roles in the evolution of production and reproduction traits in chicken. In this regard, various genes responsible for growth and egg production has been found. This study aims to elucidate the effect of on-station improvement on the signature of positive selection in an indigenous chicken, the Improved Horro, compared to non-improved indigenous chicken (Local Horro, Hugub, Arabo, and Jarso).

5.2. Materials and methods

5.2.1. Experimental population description and breeding scheme for Improved Horro

A breeding program has been established in 2008 to improve the productivity of Horro chicken, an indigenous population in the western highlands of Ethiopia. The breed improvement was established with the aim of making Horro chickens more productive in terms of egg number and body weight through selective breeding while maintaining genetic diversity. Breeding objectives are growth rate and egg production with a target of gaining 1500 gm and 200 eggs/hen/year, respectively. The population was established from 3000 eggs purchased from two village market sheds in Horro. The pedigree descended from 26 cocks and 260 hens were hatched and raised at the poultry research farm of Debre Zeit Agricultural Research Centre (DZARC) (Dana, 2011). The base population had a wide range of morphological and genetic diversity.

At each generation, 50 males and 300 females were selected to produce the next generation, representing selected proportions of approximately 10-20% in the males and 50-60% in the females. Collected eggs were artificially incubated. All hatched chicks were checked for deformity, vaccinated (against Marek's disease at the hatchery, Newcastle diseases at Day 1 and 21, Gumboro at day 7, Fowl pox in week 10 and Fowl Typhoid in week 14) , wing tagged, weighed and randomly assigned to pens of concrete floor filled with bedding material. Birds in all age classes were provided *ad libitum* access to feed in the form of starter, pullet and layer ration and water. More specifically, the chicks were feed *ad libitum* with a standard chick (0-8 weeks: 20% CP and 2950 Kcal/kg of ME), grower (8-20 weeks: 18% CP and 2750 Kcal/kg of ME) and layer (21-onwards: 16% CP and 2750 Kcal/kg of ME) diet formulated at the centre. The chickens were

reared in a single deep litter house until 18 weeks of age under a standard housing space, with natural lighting after 8 weeks of age. Body weight and cumulative egg production were recorded on weekly basis. Males and females were selected on their body weight at 16 weeks (BW16) as well as for the later on their cumulative egg production 24 weeks after the start of laying (EN24). From week 18 onwards, the selected males and all females were transferred to the layer house and kept in floor pens with 1 cock and 10 hens per pen. Pens were fitted with trap nests to facilitate full pedigree recording. Eggs were collected from selected hens for 10-12 days and incubated in three hatches to produce the next generation (Woldegiorgiss, 2015).

5.2.2. Sampling strategy, DNA extraction, and sequencing

Blood samples were collected from 27 chicken populations in Ethiopia (Figure 16). Samples included 103 cocks and 157 hens. Except the improved Horro, Meseret, Tsion Teguaz, Jarso and local Horro populations, 10 chicken from each village were sampled. One or two chicken were sampled per household. Improved Horro was sampled from a breeding stock of 8th generation under selection at Debre Zeit Agricultural Research Centre and used as a reference population. Unlike other populations, Jarso and Local Horro sequences were obtained and included from the previous studies. Photographs and weight of each bird were taken. The average weight of sampled chicken was 1.26 kg with age ranges of 5 to 36 months. Sampling considered different agro-ecological zones, altitudes ranging from 729-3500 meters, marketing points, and chicken phenotypic characteristics. From the wing vein of each chicken, 50 - 250 µl of whole blood were drawn with syringes using cryotubes filled with 1.5 ml absolute ethanol (100%) following the guidelines available at https://www.sheffield.ac.uk/nbaf-s/protocols_list.

Total DNA was extracted from chicken whole blood at the BecA-ILRI Hub, Nairobi, Kenya facility (http://hub.africabiosciences.org/) using the Qiagen DNeasy blood and tissue kit protocol (Lwelamira *et al.*, 2008). To evaluate the DNA concentration a Thermo Scientific NanoDrop spectrophotometer 2000c was used. The integrity of DNA was confirmed by agarose gel electrophoresis whereby 20 ng/µl genomic DNA samples were loaded with 1 µl loading dye (6X) on a 1% agarose gel containing 2.5 µl gel red at a voltage of 7/cm for 60 minutes, 3 µl of lambda DNA of size of 48,500 bp and a concentration of 20 ng/µl was used as size marker and the gel was then examined using UV light using GelDoc-It2 Imager to check the extracted DNA quality and quantity. The genomic DNA from (n = 284) was normalized to a final volume of 100 µl and final concentration of 50 ng/µl and sent to Edinburgh Genomics, UK, for whole genome sequencing.

5.2.3. Library QC and sequencing

The libraries were evaluated for mean peak size and quantity using the Caliper GX Touch with a HT DNA 1k/12K/HI SENS LabChip and HT DNA HI SENS Reagent Kit. Those libraries were then normalized to 5 nM using the GX data and the actual concentration was established using a Roche LightCycler 480 and a Kapa Illumina Library Quantification kit and Standards. The normalized libraries were denatured and pooled in eights for clustering and sequencing using a Hamilton MicroLab STAR with Genologics Clarity LIMS X Edition. Libraries were clustered onto HiSeqX Flow cell v2.5 on cBot2s and the clustered flow cell is transferred to a HiSeqX for sequencing using a HiSeqX Ten Reagent kit v2.5. The samples were sequenced at a genome coverage of ~5-90X (mean = 36.1X). Demultiplexing is performed using bcl2fastq (2.17.1.14), allowing 1 mismatch when assigning reads to barcodes.

Adapters (Read1: AGATCGGAAGAGCACACGTCTGAACTCCAGTCA, Read2:

AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGT) are trimmed during the demultiplexing process.

5.2.4. Mapping and variant calling

The pipelines for mapping and variant calling included: mapping reads against reference genome using BWA-mem, sorting BAM file, removing duplicated reads with PICARD, Base Quality Score Recalibration (BQSR) with GATK, calling variants using GATK, Variant Quality Score Recalibration (VQSR) for variant filtration with GATK, and finally selection of only bi-allelic SNPs which passed the VQSR step.

Mapping with BWA-mem

High quality paired-end reads (FASTAQ format) were aligned to the chicken (*Gallus gallus*) reference genome sequence (Gallus_gallus-5.0 or galGal5) (https://www.ncbi.nlm.nih.gov/genome/?term=Galus+galus+5), using Burrows-Wheeler Aligner software package (http://sourceforge.net/projects/bio-bwa/files/) with the command 'mem -t 8 -k 32 -M -R' (where –t = no. of threads; -k = min seed length; -M = Mark shorter split hits as secondary (for Picard compatibility) which permits high-quality queries for longer sequences as it is fast and accurate (Li and Durbin, 2010); and -R for defining read groups. The alignment output generated were stored in the SAM format and then converted to BAM formats using PICARD tools. Duplicated reads originating from a single fragment of DNA during sample preparation (such as library construction using PCR) were marked and removed using PICARD's MarkDuplicates command (https://broadinstitute.github.io/picard/command-line-overview.html#MarkDuplicates).

Base quality score recalibration (BQSR)

BQSR is a data pre-processing step that detects systematic errors made by sequencers in estimating the quality score of each base call. Base quality score is an important parameter for variant calling as it expresses confidence that the base has been called correctly. Unfortunately, the scores produced by the machines are subject to various sources of systematic technical errors, leading to over- or under-estimated scores. The BQSR step applies a machine learning algorithm to model these errors empirically and adjust the quality scores accordingly by considering a number of covariates such as sequencing context of the base, position in read or sequencing cycle (https://gatkforums.broadinstitute.org/gatk/discussion/44/base-quality-score-recalibration-bqsr).

Variant calling

Variant calling from each sample was performed in the gVCF mode for cohort analysis using GATK's HaplotypeCaller (Figure 2). Joint genotyping of samples from each population were done using GATK's GenotypeGVCF tool for downstream analysis. Variant Quality Score Recalibration (VQSR) were also performed to increase sensitivity (identifying the real variants) and specificity (identifying false positives) using GATK followed by a selection of only bi-allelic SNPs that passed the VQSR step. For the VQSR step, we used 1M validated SNPs and 15 SNPs from dbSNP for recalibration purpose.

5.2.5. Selective sweep detection

A total of 14, 857, 039 recalibrated autosomal SNPs were generated from 70 chicken samples (5 populations) and used for downstream analysis of signatures of selection. For each indigenous population we also produce environmental suitability maps for indigenous chicken populations based on the following environmental variables: Minimum temperature of the coldest month, precipitation seasonality, precipitation of the wettest quarter, precipitation of the driest quarter, % of cultivated land, % of grass/scrub/woodland, proportion of crop rainfed or irrigated and carbon content (g/kg).

Selection sweep detection was carried out using *Hp* and *Fst* statistics using VCFtools version 0.1.13 in an overlapping window bin size of 20 kb and a step size of 10 kb. These statistics involves comparing the average number of nucleotide differences from pair wise DNA sequences and the number of segregating sites. Using the pool heterozygosity (*Hp*) method (Rubin *et al*., 2010), the levels of heterozygosity were measured for the autosomal genome (chromosomes 1-28 and 30-33) at a window of 20 kb and 10 kb step size.

The pooled heterozygosity (*Hp*) values were calculated using the following equation:

$$\mathrm{Hp} = \frac{2 \sum \mathrm{n_{MAJ}} \sum \mathrm{n_{MIN}}}{(\sum \mathrm{n_{MAJ}} + \sum \mathrm{n_{MIN}})} \quad \mathrm{Equ}(1)$$

Where $\sum \mathrm{n_{MAJ}}$ and $\sum \mathrm{n_{MIN}}$) are the sums of major and minor allele frequencies respectively for all the SNPs within each the 20-kb window. At each detected SNP position, we counted the number

of reads corresponding to the most and least frequently observed allele (nMAJ and nMIN, respectively) for each population. The values of *Hp* calculated for each window size were then subsequently Z-transformed using the equation:

$$\mathrm{ZHp} = \frac{\mathrm{Hp} - \bar{\mathrm{x}}(\mathrm{Hp})}{\sigma(\mathrm{Hp})} = \mathrm{Equ}(2)$$

Where $\bar{X}$ the mean and σ is is the standard deviation of the Hp value. Windows with a large number of heterozygote SNPs show values above zero, they may reflect balancing selection signature. Only windows with at least 20 SNPs were extracted and set for analysis. Following this criterion, 1117, 1152, 1029, 1444 and 911 windows with SNPs < 20 were excluded for Improved Horro, Local Horro, Arabo, Hugub and Jarso populations. Respectively. From the remaining windows, a genome-wide significant threshold score of Z (*Hp*) ≤ - 4.0 was considered (Rubin *et al*., 2010).

Population differentiation values (*Fst*) which compare differences in allele frequencies between population were calculated for each SNP as described in Akey *et al*. (2002). *Fst* was calculated from the allele frequencies (not the allele counts) using the standard equation:

$$\mathrm{Fst} = \mathrm{P_{i\,total}} - \mathrm{P_i\ within}\quad \mathrm{Equ\ (3)}$$

Where, $\mathrm{P_i\ within} = \frac{\mathrm{P(i)\ population\ 1 + P(i)\ population\ 2}}{2}$ and $\mathrm{P_i} = 1 - \mathrm{fA2} - \mathrm{fT2} - \mathrm{fC2} - \mathrm{fG2}$ with fN being the frequency of nucleotide N (A, T, C or G), $\mathrm{P_{i\,total}}$ is the total $\mathrm{P_i}$ for which allele frequencies in both populations are averaged. The *Fst* values were Z-transformed as follows:

$$\mathrm{ZFst} = \frac{\mathrm{Fst} - \mu\mathrm{Fst}}{\sigma\mathrm{Fst}}$$

Where, μ is the mean and σ is the standard deviation of the Fst.

Putatively selected regions were selected based on windows within the 1% level low and high ZFst values.

5.2.6. Gene ontology and pathway analyses

To establish the biological significance of the genes found within each candidate selected region, the genes putatively under selection were submitted to DAVID Bioinformatics Resources 6.8 (https://david.ncifcrf.gov/) for enrichment analysis of the Gene Ontology (GO) and the Kyoto Encyclopaedia of Genes and Genomes (KEGG) pathways (KOBAS version 3.0, http://kobas.cbi.pku.edu.cn/). All chicken genes annotated in Ensembl were included. The two analyses restricted over-represented genes to the Fisher exact *P*-value < 0.05 default threshold.

5.3. Results

5.3.1. Principal component analysis

The genetic structure of the populations was examined on the basis of all SNPs using principal component analysis (PCA) (Figure 30). The first two components account for 19.27% and 7.1% of the variation respectively. They separate clearly the five populations.

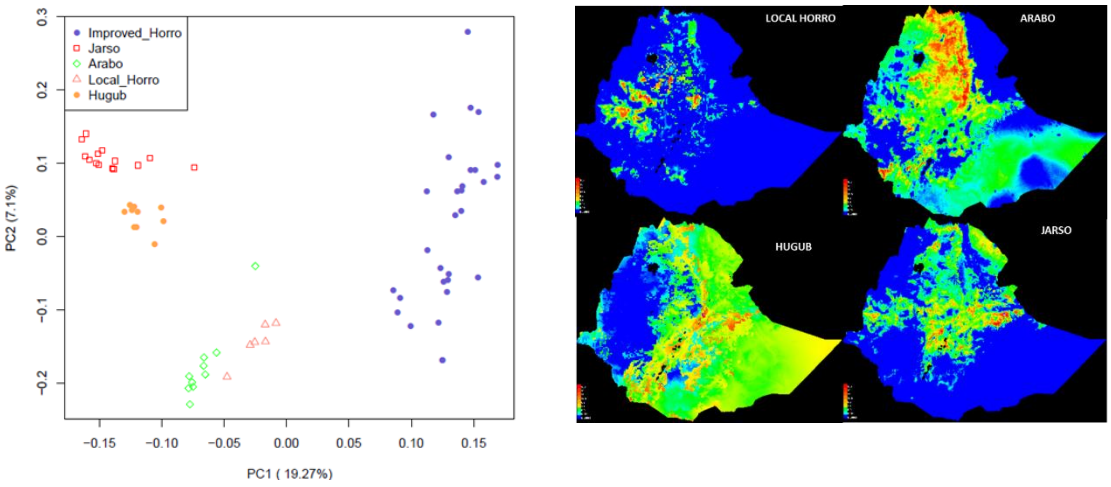
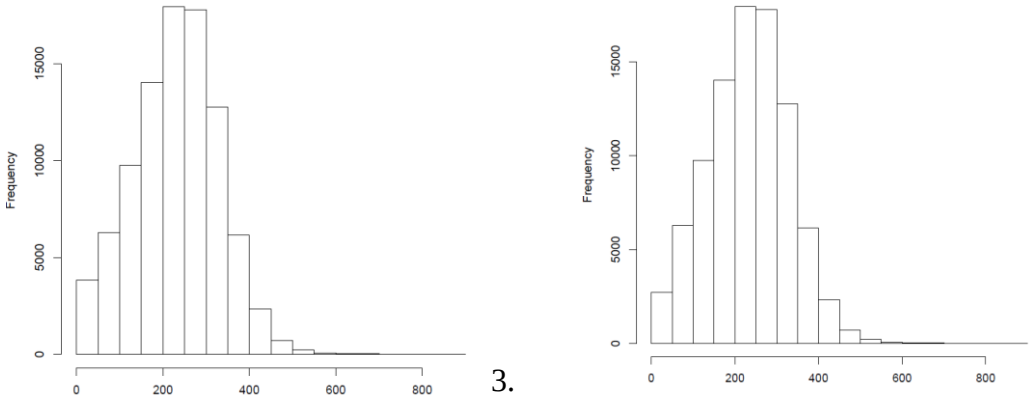


Figure 30. PCA plot of Improved Horro (left) and other indigenous chicken populations and suitability maps for the four indigenous chicken populations (right).

5.3.2. Genome-wide selective sweep detection using Hp

In Improved Horro chicken population, from the total number of 91,996 windows 90,877 windows with 20 and above SNPs were analyzed (Table S 48). The mean *Hp* value is 0.33 ± 0.058, while the minimum and maximum ZHp is -5.71 and 2.88, respectively, with 417 windows below the genome-wide threshold of $\leq$ - 4 (Table S 48). The proportion of windows with significant ZHp in

Improved Horro is 0.46% (417*100)/90878). These windows define 417 candidate sweep regions including 125 annotated genes (Table S 49). Chromosomes 1 to 15, chromosome 17, chromosome 20 and Chromosome 24 show significant window ≤ -4 (Figure 32). Across the genome, the strongest peak is located on chromosome 1 and 12 (Chr1: 189490000 to 189510000 bp; Chr12: 190890000-190930000 bp regions) with a ZHp score of -5.71 for the chromosome 1, including the Thyroid Hormone Stimulating Receptor (THSR) gene (Table 20).



3.

Figure 31. SNP count of Improved Horro (n = 30) before and after filtering.

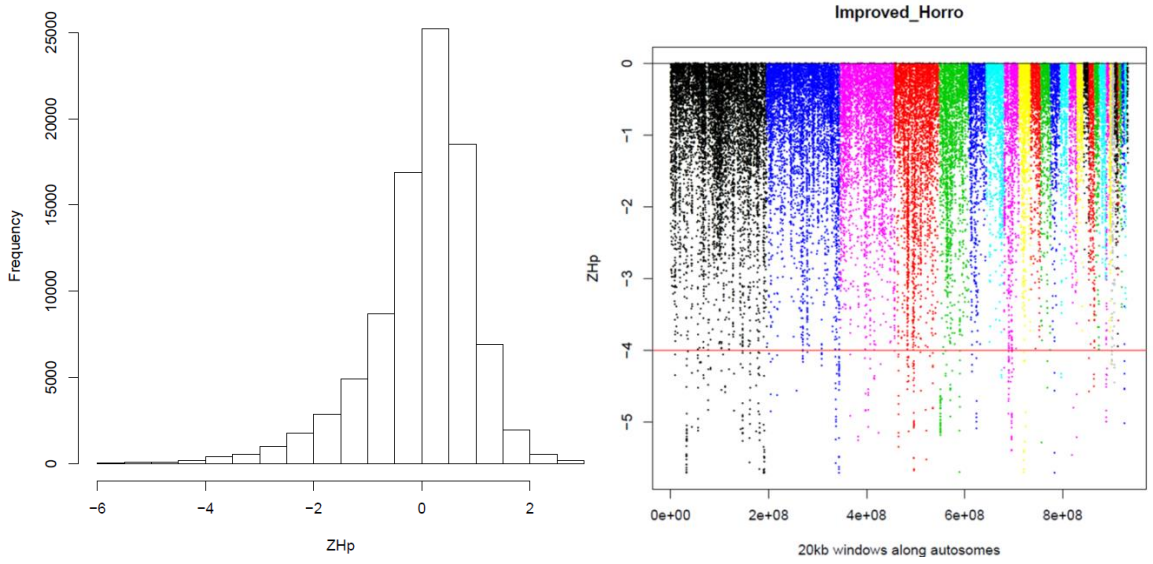


Figure 32. The frequency of ZHp values and Manhattan plot in Improved Horro (n = 30).

In Local Horro chicken population, from a total of 91905 windows, 90753 windows with 20 and above the number of SNPs were analyzed of which 311 windows (0.34%) passed the genome-wide significant threshold of ≤ -4 (ZHp) (Table S 50). These define 311 candidate sweep regions including 83 genes (Table S 51). Chromosomes 1 to 15, chromosome 17, chromosome 20 and chromosome 24 show significant peaks (Figure 34). Across the genome, the strongest peaks are located on chromosome 2, 3 and 5 (11 sweep regions) with a Z (Hp) score of -5.8. Similarly to the Improved Horro the TSHR (Chromosome 5: 40858950- 40811286) and Angiotensin II Receptor Type 1 (AGTR1) (Chromosome 5: 12430615 to 12398415) genes are found with significant windows regions (Table S 50).

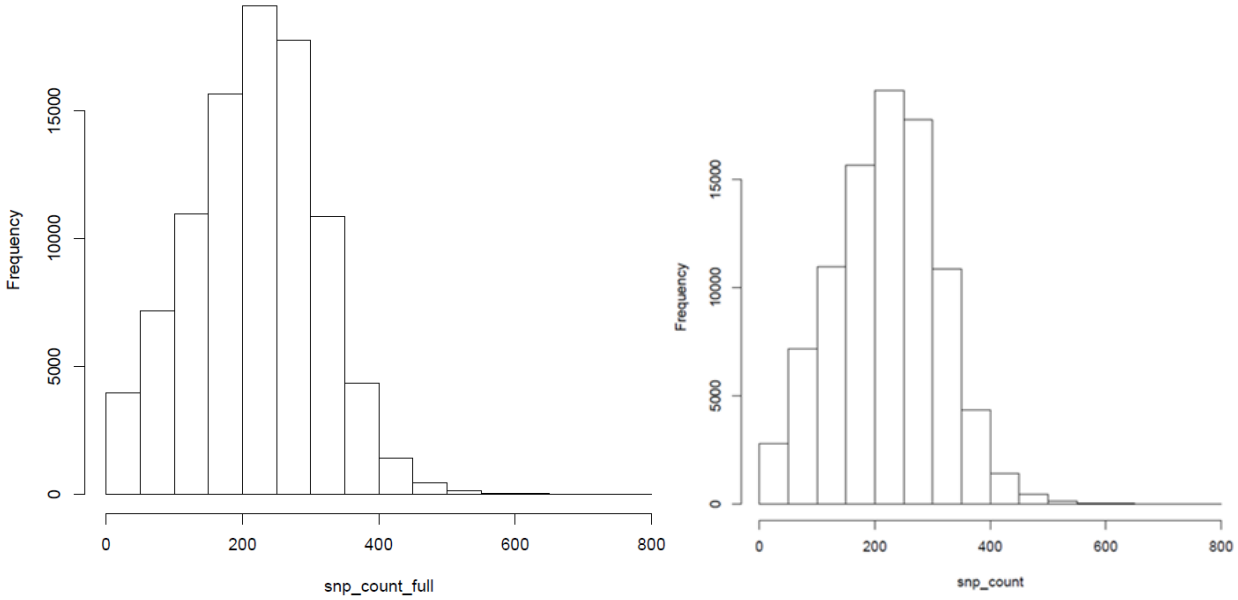


Figure 33. SNP count of Local Horro chicken (n = 6) before and after filtering.

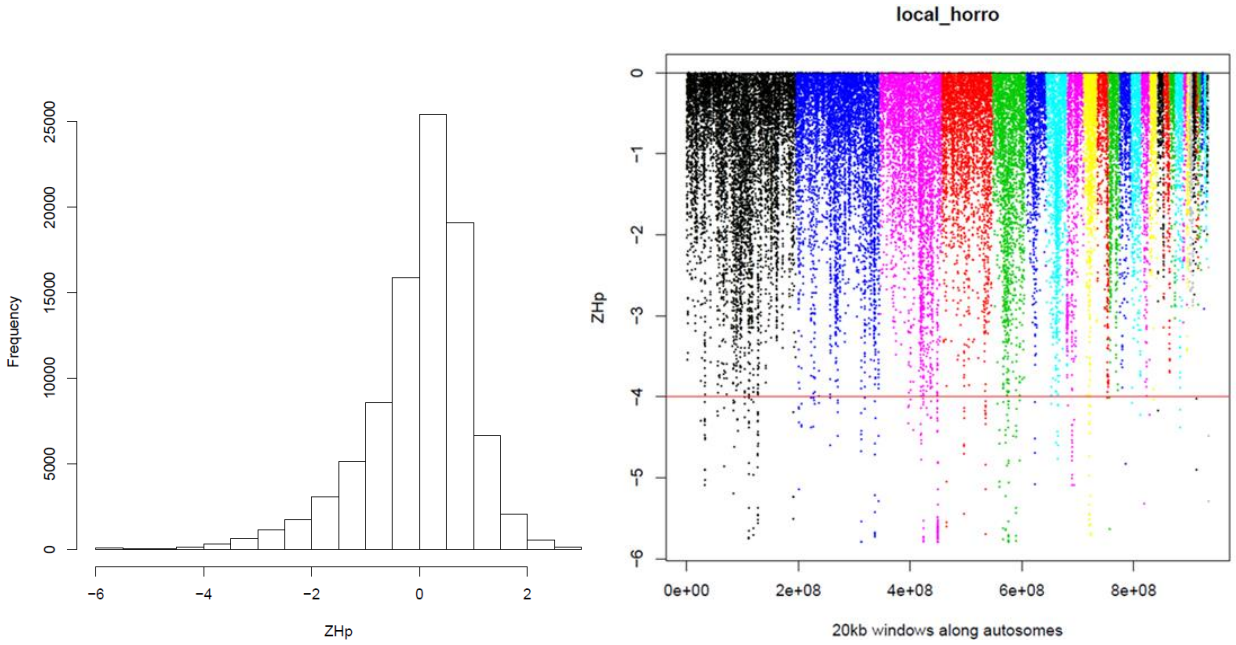


Figure 34. The frequency of ZHp values for and Manhattan plot in Local Horro chicken (n = 6).

In Jarso chicken population, from a total number of 91966 windows, 91055 windows with 20 and above the number of SNPs were analyzed (Table S 52) of which, 31 windows (0.034%) passed the genome-wide significant threshold of < - 4 windows (ZHp). Chromosomes 1 to 9 and chromosome 13 have significant peaks. Thirteen annotated genes are found in these windows (Table S 53). Across the Jarso genome, the strongest peak is located on chromosome 13 (position 520,000 to 550000 bp) with a ZHp score of -4.68 (Figure 36).

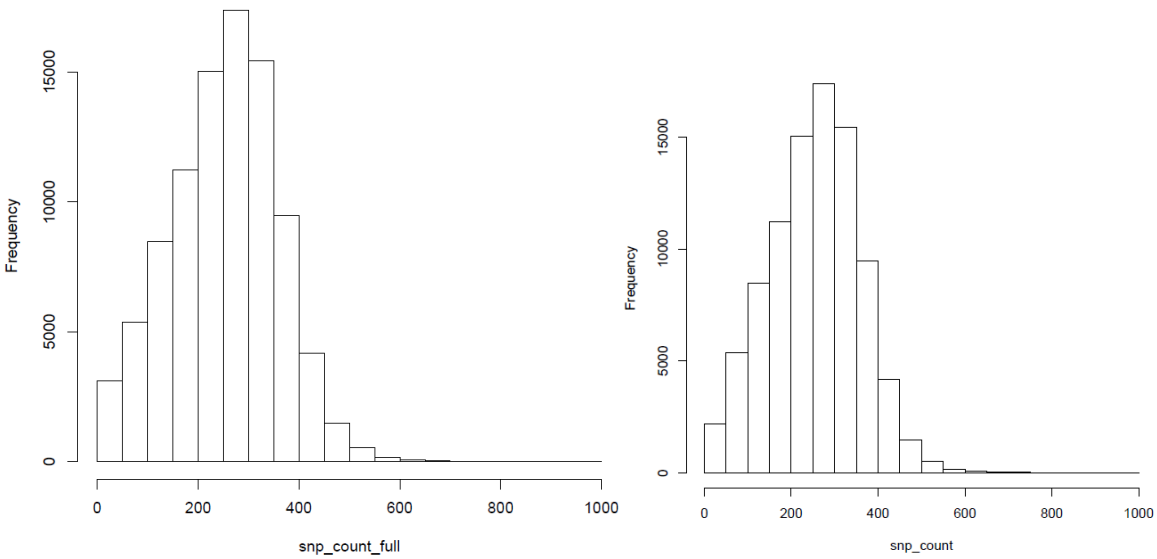


Figure 35. Average SNP count of Jarso (n = 14) before and after filtering

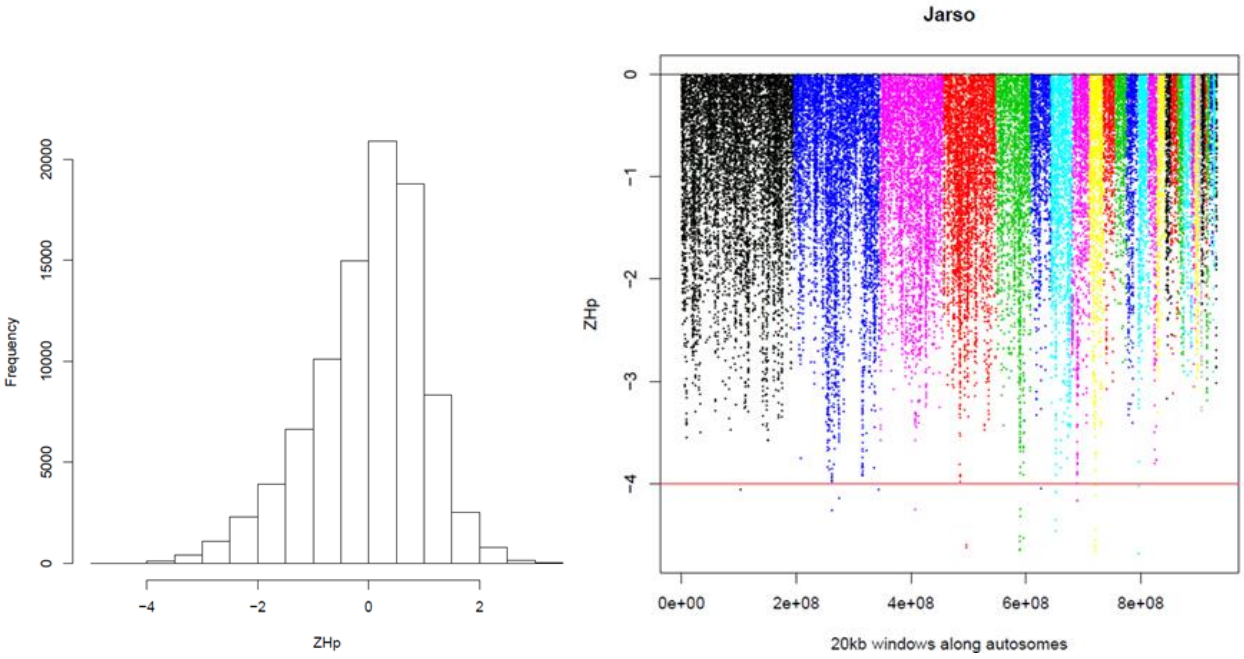


Figure 36. The frequency of ZHp values for and Manhattan plot in Jarso chicken (n = 14).

In Hugub chicken population, from the total number of 92006 windows, 90560 windows with 20 and above number or SNPs were analyzed (Table S 54) of which, 242 windows (0.12%) passed the genome-wide significant threshold of ≤ -4 (ZHp) (Table S 55). The mean *Hp* value for the

window across the genome is 0.33 ± 0.063. Whereas the minimum and maximum Z-transformed pooled heterozygosity value are -5.12 and 2.72, respectively. These significant regions include 78 annotated genes (Table S 56). Chromosomes 1 to 9 and chromosome 13 show significant peaks ≤ - 4 (Figure 38). Across the genome, the strongest peaks are observed on chromosome 3 (50630000-50650000; 7020000-7040000; 7930000 - 7960000; 18930000-18950000 bp) with a ZHp score of -5.12. A gene of particular biological interest on chromosome 3 (position: 26395277 to 26573746) is the Protein Kinase C Epsilon (PRKCE).

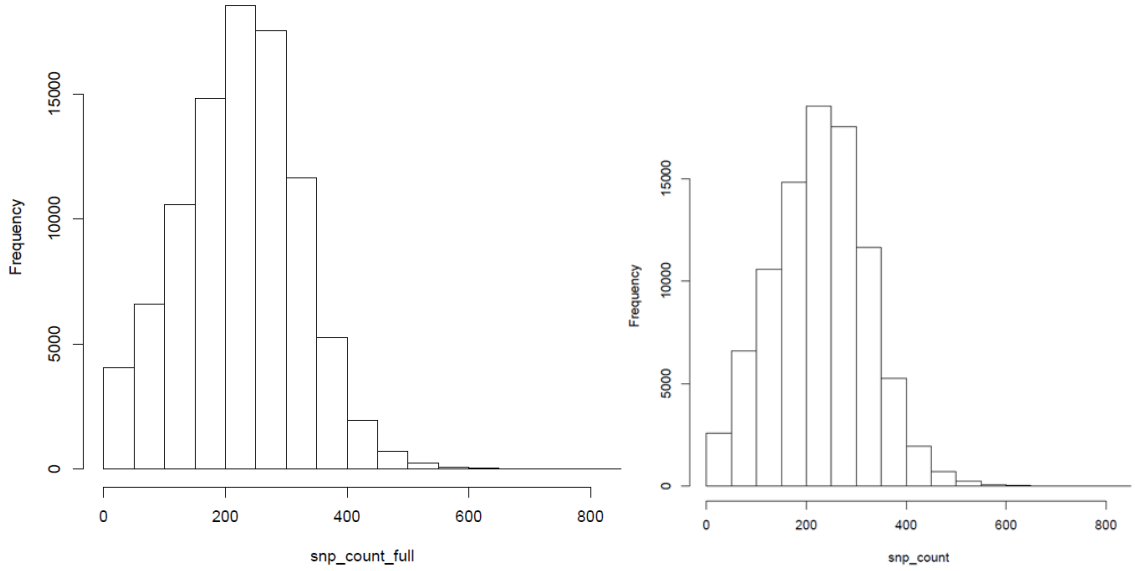


Figure 37. Average SNP count of Hugub (n = 10) before and after filtering.

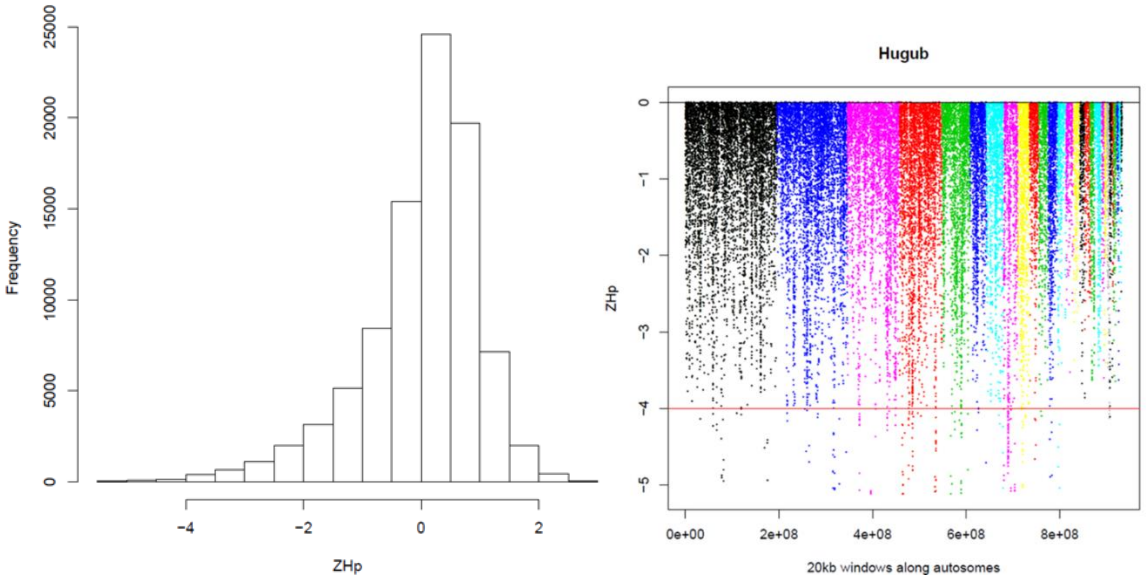


Figure 38. The frequency of ZHp values for and Manhattan plot in Hugub chicken (n = 10).

In Arabo chicken population, from the total number of 92250 windows, 91221 windows with 20 and above number SNPs were analyzed (Table S 57). The mean *Hp* value is 0.30 ± 0.061, while the Z transformed minimum and maximum *Hp* value are - 4.896 and 3.02, respectively. Fifty windows (0.055%) passed the genome-wide significant threshold of ≤ - 4 (ZHp) (Table S 57). These windows defined 50 candidate sweep regions with 14 annotated genes (Table S 58). Chromosomes 1 to 9 and Chromosome 13 show significant peaks. Across the Arabo chicken genome, the strongest peak is located on chromosome 3 (82480000-82500000bp) (Figure 40) with a ZHp score of - 4.896 and 14 genes Tudor domain containing (TDRD), Diaphanous-Related Formin 3 (DIAPH3), Ankyrin Repeat And KH Domain Containing 1 (ANKHD1), Steroid Receptor RNA Activator 1 (SRA1), Phosphodiesterase 1C (PDE1C), Echinoderm microtubule-associated protein like 4 (EML4), Regulating synaptic membrane exocytosis 1 (RIMS1), Deleted in Liver Cancer 1 (DLC1), Thyroid stimulating Receptor (TSHR) and Bone morphogenetic protein receptor type 2 (BMPR2). GO enrichment analysis in Arabo chicken indicates enrichment in Caveola cellular component functions (Table 20).

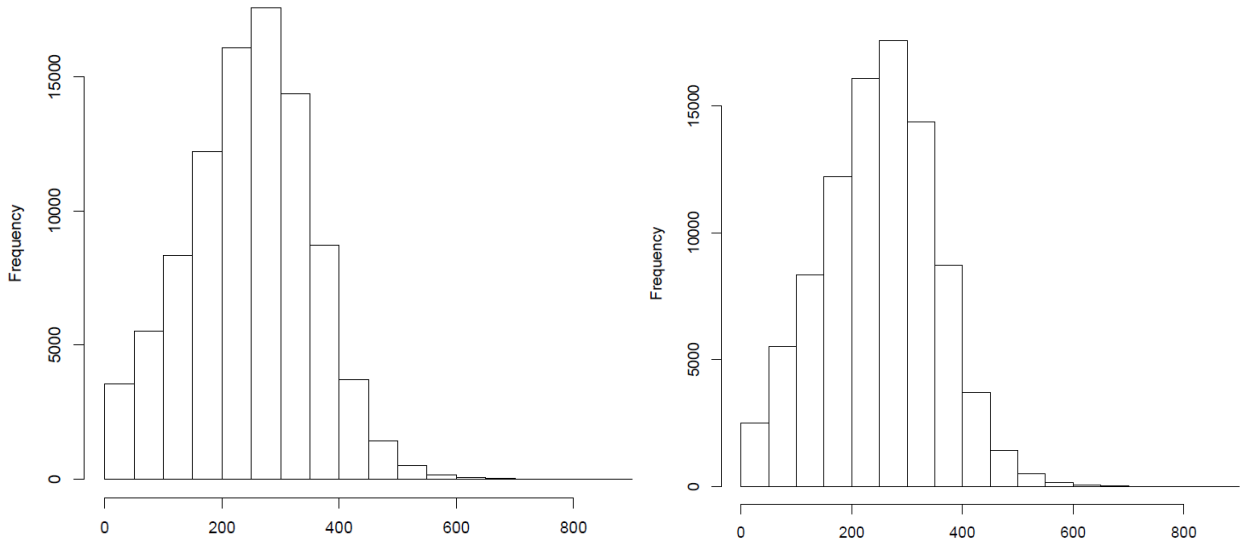


Figure 39. Average SNP count of Arabo chicken (n = 10) before and after filtering.

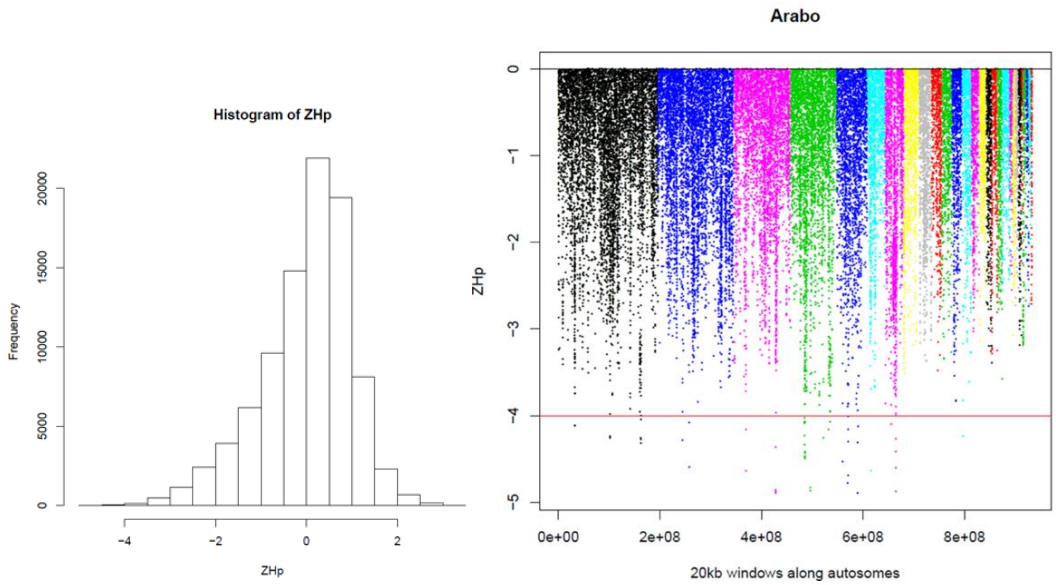


Figure 40. The frequency of ZHp values for and Manhattan plot in Arabo chicken (n = 10).

5.3.3. Consequences of pooled heterozygosity (Hp) variants detected

The different variant consequences are reported in Table 17. From the ZHp variants (ZHp < -4), the highest Hp variant is reported for Improved Horro compared to the other indigenous chicken population of Ethiopia Table 18. The number of novel variants ranges from 4.6% (Jarso) to 7.4% (Improved Horro). The lowest mean Hp is reported for Jarso (0.29 ± 0.062) chicken population. A difference was not noted in terms of missense variants between Improved and Local Horro chicken population using Hp method, while with no difference in mean and max Hp (Table 18). The minimum missense variant is reported for Jarso population. SIFT prediction of Hp variants also shows the tolerated and non-tolerated deleterious Hp variants in the candidates of selection signature regions (Table 19).

Table 17. Summary of variant and Hp statistics in Improved Horro and other Ethiopian indigenous chicken populations.

Population	Improved Horro (n/%)	Local Horro	Arabo	Hugub	Jarso
Sample size	30	6	10	10	14
Single nucleotide variant	33677	26322	4358	20,281	2637
Novel variants	2482 (7.4)	1323 (5.0)	255 (5.9)	1202 (5.9)	121 (4.6)
Existing variants	31195 (92.6)	24999 (95.0)	4103 (94.1)	19,079 (94.1)	2516 (95.4)
Overlapped genes	345	235	36	235	45
Overlapped transcripts	871	569	104	462	96
Windows number	91,994	91,905	92250	92004	91966
Windows with more than 20 SNPs	90,877	90,753	91221	90560	91055
μHp	0.33 ± 0.06	0.33 ± 0.06	0.30 ± 0.07	0.33 ± 0.06	0.29 ± 0.06
minZHp	-5.71	-5.8	-4.9	-5.12	-4.68
Max ZHp	2.88	2.88	3.02	2.72	3.34

Table 18. Summary of all Hp consequences.

Population	Improved Horro	Local Horro	Arabo	Hugub	Jarso
Missense	304	304	24	213	20
Splice region variant	328	244	9	95	35
Synonymous	1077	1000	64	513	108
5UTR	162	177	2	105	2
3UTR	1801	737	5	309	314
Non-coding transcript exon	1034	556	33	299	109
Intron Variant	121102	77,505	21,622	40,194	8,386
Non-coding transcript	10696	7,846	2,165	5,536	1,499
Upstream	8882	5,736	185	4,654	559
Downstream	11127	5,637	93	5,482	1,738
Intergenic	12671	11,567	2,105	9,788	1,169
Splice donor/acceptor	1(1)	0(3)			
Stop gain/lost	0(2)	4(1)		2(0)	
Micro RNA	1				

Upstream: a variant that is located in the 1-kb region upstream of the gene start site; stop gain: a non-synonymous (ns) SNP that leads to the creation of a stop codon at the variant site; stop loss: a non-synonymous SNP that leads to the elimination of a stop codon at the variant site; splicing: a variant within 2 bp of a splice junction; downstream: a variant that is located in the 1-kb region downstream of the gene end site; upstream/downstream: a variant that is located in the downstream and upstream regions of two genes.

Table 19. Sift prediction of Hp variants.

Population	Deleterious low confidence	Deleterious	Tolerated low confidence	Tolerated
Improved Horro (n = 30)	2	31	17	82
Local Horro (n = 6)	1	23	6	176
Arabo (n = 10)		7	2	14
Hugub (n = 10)	4	14	19	97
Jarso (n = 14)		12	6	

5.3.4. Common selected Hp sweep regions and functional annotation of genes across populations

The genome of the considered chicken populations was checked for overlapping sweep regions. Sixty-four windows were merged and checked for duplicate/overlapped regions (Table S 67). 145 duplicate values were obtained from the regions across populations. Finally, 64 regions were found in overlapping regions between chicken populations. From these regions, 31 genes were obtained for further functional annotation (Table S 68). Enriched functions for commonly selected regions include calcium signaling and other biological processes (Table 20).

Table 20. Functional annotation of genes in Improved Horro and other indigenous chicken populations of Ethiopia.

Improved Horro (n = 30)				
Category	Term	ID	N	$P < 0.05$
GOTERM cellular component	Voltage-gated calcium channel complex	GO:0005891	3	0.004713343
KEGG_PATHWAY	MAPK signaling pathway	gga04010	6	0.005301658
KEGG_PATHWAY	Calcium signaling pathway	gga04020	5	0.010739355
GOTERM Molecular function	Low voltage-gated calcium channel activity	GO:0008332	2	0.017132492
INTERPRO	C2 calcium-dependent membrane targeting	IPR000008	4	0.02099244
INTERPRO	Laminin G domain	IPR001791	3	0.023680002
GOTERM cellular component	Cytoplasmic, membrane-bounded vesicle	GO:0016023	3	0.027615941
GOTERM Biological Process	Regulation of nucleic acid-templated transcription	GO:1903506	2	0.034513351
GOTERM Molecular function	Methylated histone binding	GO:0035064	2	0.045049799
GOTERM Biological Process	Calcium ion import	GO:0070509	2	0.048945698
Local Horro (n = 6)				
GOTERM Biological Process	Nervous system development	GO0007399	3	0.028538
Hugub (n = 10)				
Go term molecular function direct	Heparin-binding	GO:0008201	3	0.040196
Jarso (n = 14)				
GOTERM Biological Process	Adult locomotory behavior	GO:0008344	2	0.019311
GOTERM Molecular function	DNA binding	GO:0003677	3	0.032634
GOTERM Biological Process	Nervous system development	GO:0007399	2	0.038322
Arabo (n = 10)				
Go term cellular component	Caveola	GO:0005901	2	0.017181377

5.3.5. Fst variants detected

For ZHp candidate signature of selection regions, the highest genetic differentiation is observed between the Improved Horro and Hugub chicken populations (0.55 ± 0.06; Table S 63) and the lowest is between Improved Horro and Local Horro (0.08 ± 0.02; Table S 59). Interestingly, the highest number of missense *Fst* variant is found between Improved Horro and Local Horro implying that the ongoing selection process in Improved Horro may be fixing in the later is mainly targeting amino acid-altering putatively functional variants involving non-tolerable deleterious variants (Table 23).

5.3.6. Genome-wide selective sweep detection using Fst

Pair wise Fst results between Improved Horro and other indigenous chicken populations of Ethiopia namely Local Horro, Jarso, Hugub, and Arabo chicken populations are given below.

From the total pair wise Fst windows (91,989) between Improved and Local Horro 90,572 windows with greater than 20 SNPs, the top 1% windows (906) were considered as significant windows for downstream analysis (Table S 59). The minimum and maximum Fst values were 0.04 and 0.15, respectively. The significant genetic differentiation based on Fst values was mainly concentrated in the majority of the chromosomes Table 24). Detection of selection at the genome level using the Fst outlier method yield 311 candidate genes showing high evidence of positive selection from these significant regions (Table S 60). Between the highly differentiated regions of these populations, an interesting gene called Ral GTPase activating protein catalytic alpha subunit 1 (RALGAPA1) has been found.

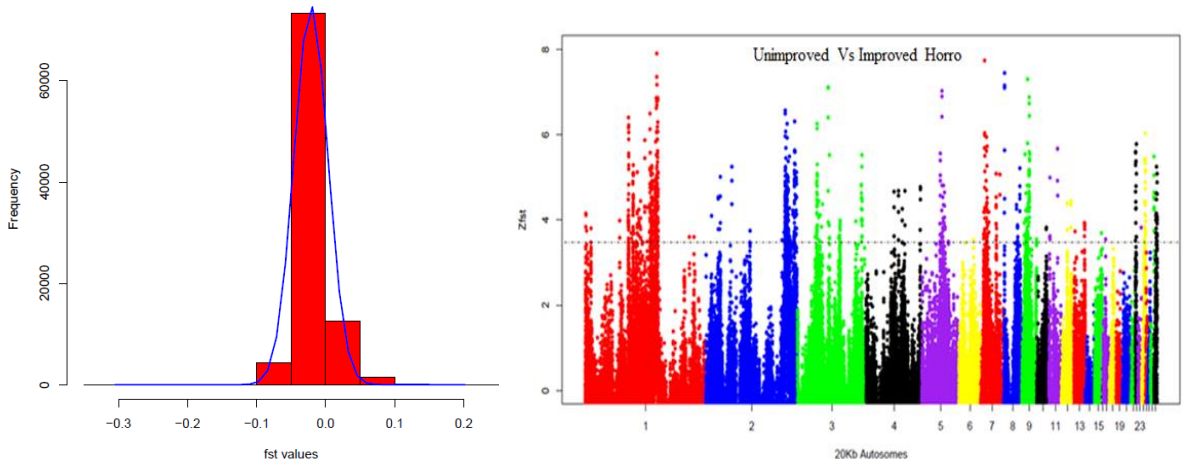


Figure 41. Histogram and Manhattan plot showing the distribution of Fst values for Improved Horro Vs Local Horro chicken populations.

The number of windows in Improved Horro and Jarso population is 92,123 windows. Windows with greater than 20 SNPs is 91, 395. The top 1% significant windows where 914 windows (Table S 61) and from these windows 272 genes (Table S 62) were extracted for further functional annotation using Database for Annotation, Visualization and Integrated Discovery (DAVID).

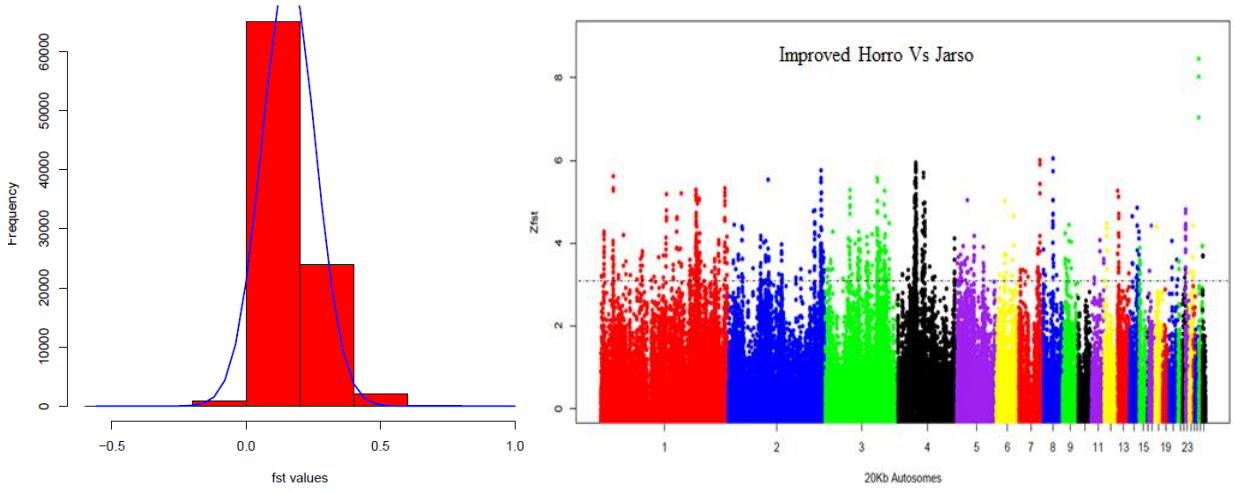


Figure 42. Histogram and Manhattan plot showing the distribution of Fst values for Improved Horro Vs Jarso chicken populations.

The total number of Windows Fst for Improved Horro and Hugub populations is 92, 017. From this windows, 91,167 number of windows have greater than 20 SNPs. 1% these windows yield 911 windows (Table S 63), which encompasses 26 candidate genes under the regions of selection pressure (Table S 64).

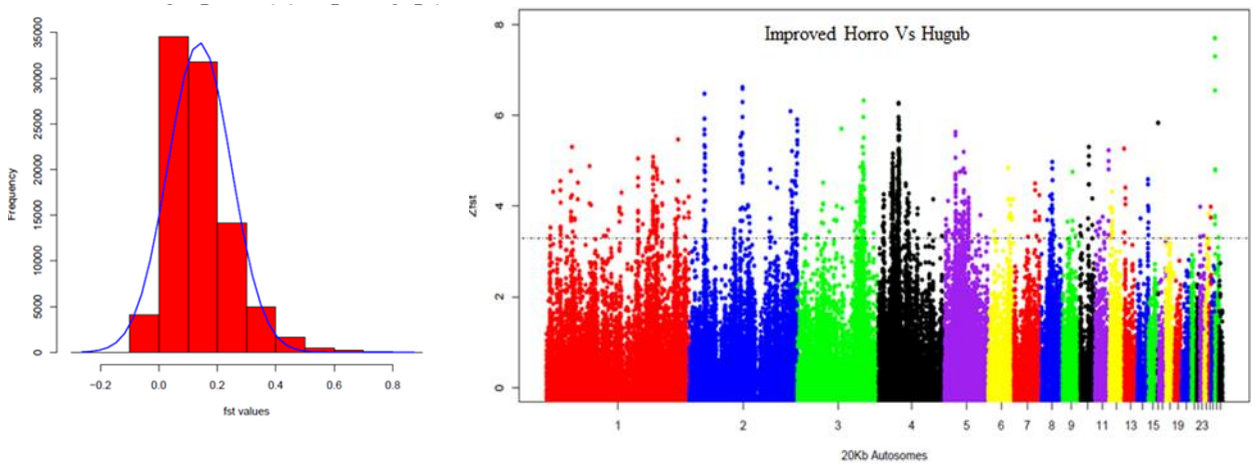


Figure 43. Histogram and Manhattan plot showing the distribution of Fst values for Improved Horro Vs Hugub chicken populations.

The total number of windows for Improved Horro and Arabo population is 92,118. 91300 windows have greater than 20 SNPs. From these windows a total of 913 windows (Table S 65) have 1% significant windows and 26 genes were fetched from these regions (Table S 66).

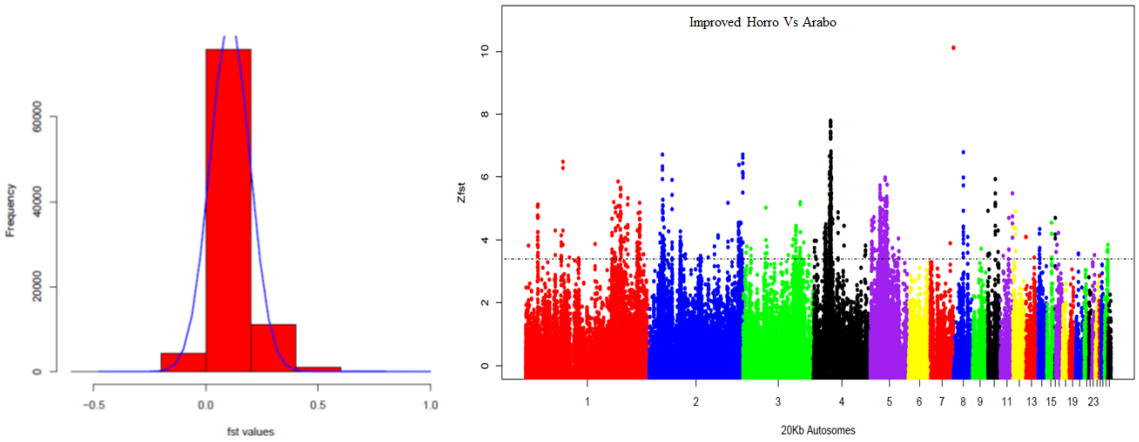


Figure 44. Histogram and Manhattan plot for Ethiopian Improved Horro and Arabo chicken showing the pairwise comparison of selection pressure.

5.3.7. Consequences of Fst variants detected

The highest Fst variant statistic were obtained (n = 157,323) between Improved Horro and Local Horro followed by Improved Horro and Jarso (n = 135,913) (Table 21. The highest proportion of novel Fst variants are between Improved Horro and Jarso (14.6%) followed by Improved Horro and Arabo (13.2%). The highest mean Fst (0.09 ± 0.02) is between IH and LH but the maximum genetic differentiation was between IH and HUG (Fst = 0.82). In terms of Fst variant consequences, the highest missense variant is obtained between IH and LH followed by IH VS HU (Table 22). The number of Fst variants based on SIFT prediction is indicated in Table 23. The highest deleterious variants are found between IH and LH (n = 180) followed by IH and AR (n = 127).

Table 21. Fst variant Statistics.

Population	IH VS LH (n/%)	IH VS AR (n / %)	IH VS JAR (n / %)	IH VS HU (n / %)
SNV	157,323	124,268	135913	108,541
Novel variants	19,232 (12.2)	16,450 (13.2)	19,855 (14.6)	13,850 (12.8)
Exiting variants	138,091 (87.8)	107,818 (86.8)	116,058 (85.4)	94,691 (87.2)
Overlapped genes	907	716	777	582
Overlapped transcripts	1,956	1,482	1,746	1,406
Fst windows > 20 SNPs	90572	91300	91395	91167
Significant windows (P < 0.01)	906	913	914	912
Min Fst	0.06	0.40	0.46	0.48
Mean Fst	0.09 ± 0.02	0.48 ± 0.08	0.53 ± 0.06	0.55 ± 0.06
Max	0.18	0.8	0.76	0.82

SNV = Single nucleotide variant; IH = Improved Horro; AR = Arabo; JAR = Jarso; HU = Hugub; n = number

Table 22. Fst all consequences.

Population	IH VS LH	IH VS AR	IH VS JAR	IH VS HUG
Missense	3,185	1,473	1,797	2,375
Splice region	1,592	881	776	640
Synonymous	7,115	4,454	4,281	3,429
5UTR	1,478	1,719	1,788	666
3UTR	8,859	6,999	8,084	4,638
Noncoding Transcript Exon	4,802	4,617	5,652	4,135
Intron	43,352	41,695	50,499	36,617
Non-coding transcript	59,335	38,960	46,593	56,160
Upstream gene	66,220	44,935	44,749	29,015
Downstream gene	59,689	42,489	45,497	27,076
Intergenic	43,352	41,695	50,499	36,617
Splice donor/acceptor	10(9)	21(4)	20(19)	10(5)
Stop gain/lost	10(2)	5(4)	12(7)	5(1)
Micro RNA		3	1	1
Start lost / regained	5(4)			4

IH = Improved Horro; LH = local Horro; JR = Jarso; Hu = Hugub; 5UTR = 5 prime untranslated region; 3UTR = 3 prime untranslated region

Upstream: a variant that is located in the 1-kb region upstream of the gene start site; stop gain: a non-synonymous (ns) SNP that leads to the creation of a stop codon at the variant site; stop loss: a non-synonymous SNP that leads to the elimination of a stop codon at the variant site; splicing: a variant within 2 bp of a splice junction; downstream: a variant that is located in the 1-kb region downstream of the gene end site; upstream/downstream: a variant that is located in the downstream and upstream regions of two genes.

Table 23. Number of F_{ST} variants based on SIFT prediction.

Population	Deleterious Low confidence	Deleterious	Tolerated Low confidence	Tolerated
Improved Horro VS Local Horro	33	180	82	646
Improved Horro VS Arabo	23	124	43	390
Improved Horro VS Jarso	29	127	89	532
Improved Horro VS Hugub	13	85	36	354

5.3.8. Commonly selected Fst sweep regions and annotation of genes across populations

The genome of the considered chicken populations was checked overlapping sweep regions. 3644 regions were merged and checked for duplicate/overlapped regions.1652 duplicate values were obtained from the regions across populations. Finally, 667 windows (Table S 69) were found overlapping. From these regions, 190 genes were obtained for further functional (Table S 70). It was evident that these selection signals mainly concentrated in macro and microchromosome such as chromosomes 1 to 10.

Table 24. Functional annotation of genes in Improved versus other indigenous chicken populations.

Category	Term	ID	N	P < 0.05
Improved versus Local Horro				
GOTERM Biological Process	Late endosome to vacuole transport	GO:0045324	2	0.023434
INTERPRO	Ankyrin repeat-containing domain	IPR020683	6	0.025137
GOTERM Biological process	Cell-cell adhesion	GO:0098609	3	0.04263
GOTERM Cellular component	postsynaptic membrane	GO:0045211	4	0.04394
GOTERM Biological process	Cellular response to fatty acid	GO:0071398	2	0.046323
GOTERM Biological Process	Positive regulation of CREB transcription factor activity	GO:0032793	2	0.046323
GOTERM Biological process	Protein transport	GO:0015031	4	0.047637
Improved Horro versus Jarso				
GOTERM Cellular component	Cell cortex	GO:0005938	4	0.016022
GOTERM Cellular component	Cleavage furrow	GO:0032154	3	0.016867
GOTERM Cellular component	Ruffle membrane	GO:0032587	3	0.036196
INTERPRO	Haemoglobin, beta	IPR002337	2	0.037098
INTERPRO	Ion transport domain	IPR005821	4	0.038218
GOTERM Molecular function	GTPase activator activity	GO:0005096	5	0.040684
INTERPRO	Potentiating neddylation domain	IPR005176	2	0.046158
INTERPRO	Defective-in-cullin neddylation protein	IPR014764	2	0.046158
INTERPRO	Cullin, conserved site	IPR016157	2	0.046158
GOTERM molecular function	Protein kinase activity	GO:0004672	4	0.046783
GOTERM molecular function	Ubiquitin-like protein binding	GO:0032182	2	0.04715
Improved Horro Versus Hugub				
GOTERM Biological process	hematopoietic progenitor cell differentiation	GO:0002244	4	0.004749
INTERPRO	Cadherin-like	IPR015919	4	0.016567
GOTERM cellular component	ciliary rootlet	GO:0035253	2	0.032998
GOTERM Biological process	Homophilic cell adhesion via plasma membrane adhesion molecules	GO:0007156	4	0.036298
GOTERM Biological process	Apoptotic process	GO:0006915	4	0.040854

Category	Term	ID	N	P < 0.05
GOTERM cellular component	Extracellular space	GO:0005615	10	0.055477
KEGG_PATHWAY	Gap junction	gga04540	3	0.079866
INTERPRO	Pleckstrin homology-like domain	IPR011993	6	0.084988
GOTERM cellular component	Interstitial matrix	GO:0005614	2	0.0958
Improved Horro and Arabo				
INTERPRO	Armadillo-type fold	IPR016024	8	0.017504
PIR_SUPERFAMILY	fatty acid desaturase/sphingolipid desaturase	PIRSF015921	2	0.019163
KEGG_PATHWAY	Biosynthesis of unsaturated fatty acids	gga01040	3	0.020228
INTERPRO	Zinc finger, FYVE/PHD-type	IPR011011	5	0.020317
INTERPRO	Fatty acid/sphingolipid desaturase	IPR012171	2	0.02156
INTERPRO	FAM122	IPR026716	2	0.02156
INTERPRO	Tetraspanin, EC2 domain	IPR008952	3	0.023362
GOTERM_BP_DIRECT	Estrogen biosynthetic process	GO:0006703	2	0.031684
GOTERM_BP_DIRECT	Positive regulation of axon regeneration	GO:0048680	2	0.042023
INTERPRO	Diaphanous autoregulatory	IPR014767	2	0.04266
INTERPRO	Zinc finger, N-recognin	IPR003126	2	0.04266
SMART	ZnF_UBR1	SM00396	2	0.04589

Table 25. Functional annotation of commonly selected genes based on Fst

Category	Term	ID	N	P<0.01
INTERPRO	Fatty acid/sphingolipid desaturase	IPR012171	2	0.014103
KEGG_PATHWAY	Fatty acid metabolism	gga01212	3	0.031962
INTERPRO	Cullin protein, neddylation domain, conserved site	IPR019559	2	0.041723
GOTERM Biological process	Positive regulation of G1/S transition of the mitotic cell cycle	GO:1900087	2	0.045811
INTERPRO	Cullin homology	IPR016158	2	0.048508
INTERPRO	Fatty acid desaturase, type 1	IPR005804	2	0.048508

5.4. Discussion

5.4.1. Candidate of signals of selection using Hp method

The selective sweep can have a dramatic impact on the level of population subdivision, particularly when the sweep has not yet spread to all populations within a species (Nielsen *et al*., 2011). The size of a selective sweep may depend on factors such as the local recombination rate, whether the selected variant ever reached complete fixation, the number of generations it took before fixation and any population admixture at a time point after the sweep initially occurred (Rubin *et al*., 2010). Across the Improved Horro genome, the strongest peak is located on chromosome 1 and 12 (189490000 to 189510000 bp) with a Z Hp score of -5.71 including Thyroid Stimulating Hormone Receptor (TSHR) and other variable genes. The TSHR gene (Chromosome 5: 40811286-40858950 bp) which is a previously reported locus with a pivotal role in metabolic regulation and reproduction process (Rubin *et al*., 2010), is reported in Improved Horro chicken population. It is regarded as one of the most striking selective sweeps found in all domestic chicken. The established selective sweeps around the TSHR gene in domestic chicken is identified in the five chicken populations and this was considered as a proof of principle demonstrated that the identification of selection signals using Hp methods is reliable. Besides, the previously reported gene General Transcription Factor IIA Subunit 1 (GTF2A1) (Chromosome5: 40868271- 40894704 bp) known to be involved in the production of eggs in birds is also under strong selection pressure in this population (Lawal *et al*., 2018; Yuan *et al*., 2015).

Another interesting phenomenon is the presence of Myozenin 1 (MYOZ1) gene is also found to be under the pressure of the ongoing selection program. Myoz1 gene under the candidate

signatures of selection which plays a crucial role in signal transduction and muscle fiber type differentiation. The Myoz1 gene is a potential candidate for affecting carcass and meat quality traits in animals (Luo *et al*., 2018). Among other numerous genes in this study, the previously reported ovostatin (OVST) gene which is associated with the formation of eggshells by regulating eggshell matrix protein secretion is also under strong selection (Cordeiro and Hincke, 2016). Angiotensin II Type 1 Receptor (AGTR1) (Chromosome 9: 12398415- 12430615 bp) gene is the other gene available in the selective sweeps of this specific population. This gene is also reported heavily involved in Ascites in commercial broilers (Krishnamoorthy *et al*., 2014). Ascites refers to abnormal accumulation fluid in the abdominal (peritoneal) cavity and it is a disease of modern days in the poultry industry (Qanbari *et al*., 2015b; Wideman *et al*., 2013). In humans, AGTR1 (Chromosome 9: 12398415- 12430615 bp) is a strong candidate for the pulmonary arterial hypertension (Burks, 2011; Chung *et al*., 2014; Crossley and Altimiras, 2012). The Immunoglobin Superfamily Member 21 (IGSF21) (Chromosome 21: 23092- 65640 bp) which promotes differentiation of inhibitory synapses via binding to neurexin2α is also under selection pressure (Tanabe *et al*., 2017). Coordinated development of excitatory and inhibitory synapses is essential for higher brain function, and impairment in this development is associated with neuropsychiatric disorders. The most selected chromosome in Improved Horro is chromosome 1. Genes of interest that contain statistically significant include the DnaJ heat shock protein family (Hsp40) member C12 (DNAJC12) (Chromosome 6: 6666081- 6675111 bp) in Improved Horro chicken population. The DNAJC12 gene plays a pivotal role in the negative regulation of neuron apoptotic process (Fleming *et al*., 2017).

On top of TSHR, GTF2A1, AGTR1, and many other genes, the Beta-Carotene Dioxygenase 2 (BCDO2) (Chromosome24: 6130965 -6110301) gene is the only gene uniquely available in the candidate signature of selection in Local Horro. This gene is known to express in the skin where it encodes an enzyme that cleaves colorful carotenoids into colorless apocarotenoids, and polymorphisms in the BCDO2 gene have well-known effects on skin pigmentation in birds (Eriksson *et al*., 2008). To this end, it looks that the ongoing Improved Horro selection and improvement operation is working against this specific gene as it is not found in the selection signature regions of Improved Horro.

Unlike other populations, Jarso chicken populations have a fewer number of variants under strong selection of signature. In addition to the common genes TSHR and GTF2A1, many other genes are under strong selection signature. These include: Amyloid beta Precursor Protein (APP), Ankyrin Repeat And KH Domain Containing 1 (ANKHD1), Glycerol Kinase 5 (GK5), Heat shock factor protein 2 (HSF2), Steroid Receptor RNA Activator 1 (SRA1), tachykinin receptor 3 (TACR3), Transcription factor Dp-2 (TFDP2), and T-SNARE Domain Containing 1 (TSNARE1) are also the genes under strong selection of signature in Jarso chicken populations.

Hugub chicken was also having the OVST gene together with TSHR and GTF2A1 genes. Protein kinase C epsilon (PRKCE) (Chromosome 3: 26395277-26573746) gene is also another gene of interest in Hugub chicken population. In humans, PRKCE is considered as a stress response gene involved in cardiac tissue (Fleming *et al*., 2017) however its impact is less defined in chicken. Considering the hot arid environment of the home habitat of the population the later function makes much more sense to justify the findings of this study. Enrichment of go term functions

shows leucine-rich regions involved in Heparin binding in Hugub populations. According to Munoz and Linhardt (2004), Heparin is a major anticoagulant with activity mediated primarily through its interaction with antithrombin (AT).

Apart from, the TSHR (Chromosome 5: 40811286- 40858950 bp), and GTF2A1 (Chromosome 5: 40868271- 40894704) Arabo population also possess many other genes as candidate signatures of selection. Ankyrin Repeat And KH Domain Containing 1 (ANKHD1), bone morphogenetic protein receptor type 2 (BMPR2), Diaphanous-Related Formin 3 (DIAPH3), DLC1, echinoderm microtubule-associated protein like 4 (EML4), Phosphodiesterase 1C (PDE1C), regulating synaptic membrane exocytosis 1 (RIMS1), Steroid Receptor RNA Activator 1 (SRA1), and Tudor domain-containing protein 3 (TDRD3) are also the annotated genes under strong signature of selection in Arabo chicken populations. Functional annotation of signature of selection regions also shows various functions like Caveola cellular component functions. Caveolae are spherical invaginations of the plasma membrane and associated vesicles that are found at high surface densities in most cells, endothelia included (Thomson, 2002). Caveolae are known to involve in many cellular functions such as endocytosis, signal transduction, mechanotransduction, potocytosis, and cholesterol trafficking.

5.4.2. Candidate of selection signals based on Fst method

Signal transducer and activator of transcription 5b (STAT5b), the gene responsible for bone allocation and fecundity trait is found between Improved and Local Horro (Fu *et al*., 2016). Signal transducer and activator of transcription 5b (STAT5b) gene is found candidate gene and it is

associated with body weight and reproductive traits of Jinghai Yellow chicken (Luo *et al*., 2018; Zhou *et al*., 2005).

The only gene found in significant regions between these two populations is a gene called AGTR1 (Angiotensin II (Ang II)) which is an important regulator of cardiovascular function in adult vertebrates and have roles in thermoregulation (Crossley *et al*., 2010). This gene is known to heavily involve in Ascites in commercial broilers (Krishnamoorthy *et al*., 2014). The other gene is roundabout guidance receptor 2 (ROBO2) (96895939- 97053385 bp) gene which belongs to the immunoglobulin superfamily and plays functions associated in axon guidance and cell migration and are involved in SLIT/ROBO signaling (Wang *et al*., 2014). The ROBO2 gene has a strong effect on the antibody response to the NDV in chickens (Luo *et al*., 2013). The RALGAPA1 (36275772-36390043 bp) gene which is known to play a pivotal role in reproductive traits and broodiness is also under strong selection in Improved Horro and Local Horro chicken populations (Shen *et al*., 2012).

A gene called unconventional myosin-VI; MYO6 (80736607-80807004 bp) which serve in intracellular movements are also found between the high confidence selection regions of Improved Horro and Jarso chicken populations. Myosin 6 is a reverse-direction motor protein that moves towards the minus-end of actin filaments. The gene of interest is Ankyrin 2 (ANK2) (57097275-57432432 bp) which was reported by Fan *et al*. (2013) previously which Ankyrins play key roles in activities such as cell motility, activation, proliferation, contact and the maintenance of specialized membrane domains. Like the ROBO2 gene, the ROBO1 gene is known to have a strong effect on the antibody response to the NDV in chicken (Luo *et al*., 2013). Another

interesting gene in these populations is Interleukin-15 (IL-15) are T-cell growth factors potentially capable of enhancing cell-mediated immunity in vivo and plays a critical role in immune system function (Lillehoj *et al*., 2001). It is related cytokines that stimulate the activity and proliferation of T cells in mammals. Three functional genes Hippocalcin like 4 (HPCAL4; involved in the calcium-dependent regulation of rhodopsin phosphorylation), TRITI, and MYCL (MYCL proto-oncogene, bHLH transcription factor; implicated in lung cancer) which are reported in Horro and Jarso chicken populations by Lawal *et al*. (2018) is not found in the candidate of selection region between these populations which probably could be the variation in analysis method. The functional annotation analysis shows that the genes that displayed evidence of positive selection are mainly involved in protein transport and other biological processes. Integrin alpha-8/beta-1 (ITGA8) functions in the genesis of kidney and probably of other organs by regulating the recruitment of mesenchymal cells into epithelial structures (https://www.uniprot.org/uniprot/P26009).

On top of Syntaxin Binding Protein 6 (STXBP6), TBC1 Domain Family Member 30 (TBC1D30), TBC1, Domain Family Member 7 (TBC1D7) genes, candidate Fst signals between IH and Hugub population, also evidences the presence of stress-related genes, Hypocretin (orexin) neuropeptide (HCRT) (Fleming *et al*., 2015). Syntaxin-binding protein 6 (STXBP6) in chromosome 5, the gene responsible for bone allocation and fecundity trait is not found between Improved and Hugub chicken populations (Fu *et al*., 2016). Chicken interleukin-21 (IL21) is costimulatory for T cells and blocks maturation of dendritic cells. In mammals and chicken, interleukin-21 (IL-21) is an immunomodulatory cytokine with pleiotropic effects on the proliferation, differentiation and effector functions of T, B, NK and dendritic cells (Rothwell *et al*., 2012)Among many other genes,

Toll-like receptor 2 family member B (TLR2B) gene is under strong selection pressure in Improved Horro and Hugub chicken populations. Toll-like receptors (TLRs) are a group of highly conserved molecules that initiate innate immune responses to pathogens by recognizing structural motifs (Kannaki *et al*., 2010). In response to pathogen-associated molecular patterns, TLRs induce the production of reactive oxygen and nitrogen intermediates, inflammatory cytokines and up-regulate the expression of co-stimulatory molecules, subsequently initiating adaptive immunity (Ibid).

Among other genes, the Insulin-like Growth Factor 1 Receptor (IGF1R) and Insulin-like Growth factor 2 mRNA-Binding Protein 3 (IGF2BP3) genes, which are necessary for formal growth (Rubin *et al*., 2010; Stainton *et al*., 2015; Yang *et al*., 2014), is found between Improved Horro and Arabo chicken populations. Between these populations, the myosin-binding protein C, cardiac-type (MYBPC3) and GATA binding protein 3 (GATA3) genes are under strong pressure of selection. MYBPC3 gene is known as an accessory protein of vertebrate striated muscle thick filaments that modulate cardiac muscle contraction (Carrier *et al*., 2015). Haploinsufficiency for the transcription factor GATA3 leads to hearing the loss in humans. It is expressed throughout the auditory sensory epithelium (SE) (Alvarado, 2009; Alvarado *et al*., 2009). Integrin alpha-8/beta-1 (ITGA8) functions in the genesis of kidney and probably of other organs by regulating the recruitment of mesenchymal cells into epithelial structures. Candidate Fst signals between IH and Arabo population also evidences the presence of stress-related genes, Hypocretin (orexin) neuropeptide (HCRT) (Fleming *et al*., 2017) in the candidate signature of the selection region. The previously reported genes, TBC1 domain family member 7 (TBC1D7) and TBC1 domain family

member 30 (TBC1D30) genes which are associated with hypothermia and stress are found in this population (Fleming *et al*., 2017).

5.5. Conclusions

Since most of the candidate genes identified in the present study are novel and have probably been under recent selection, they should be of great interest for future research. Neural crest Hypothesis Domestication (FGFR-I) and Gonadotrophin-releasing hormone I (GnRH-I) genes are not in the candidates of signature of selection in Improved Horro and other indigenous chicken populations of Ethiopia. Much of the positive selection signals here, is related to immune-defense functions than to productivity and production. Future works should emphasize to map candidate genes responsible for egg and meat production. Besides, chores in the on-going improved Horro program should be based on genome-wide association studies and emphasize towards egg and weight production traits. In other words, the phenotypic records for body weight and egg production should be evaluated against the genomic regions of Improved Horo to exactly target genes for further selection. Besides, using the current data it is also important to check if the regions under the current selection pressure overlap to the Quantitative Trait Loci (QTLs) available on the online animal QTL data base.

CHAPTER 6. SUMMARY, CONCLUSION AND RECOMMENDATIONS

6.1. Implications for indigenous chicken improvement

Characterization of farm animal genetic resources is a prerequisite for any improvement, conservation and sustainable utilization of these resources (Al-Qamashoui *et al*., 2014). According to Kristensen *et al*. (2015), genetic improvement of animals is dependent on the existence of genetic variation existing between species, between breeds, within species and among animals within breeds. The genetic diversity comprised in farm animal species and breed is an important resource in livestock systems (Oldenbroek, 2007). However, as species and breeds are adapted to certain environments through centuries of natural and artificial selection, it may be difficult to restore genetic variation that may still be desired, but that has been lost by breed replacements in certain regions or environments (Kristensen *et al*., 2015). These days, global climate change is increasing the magnitude of environmental stressors, such as temperature, pathogens, and drought that limit the survivability and sustainability of livestock production (Fleming *et al*., 2017). This scenario has demanded the poultry industry to heavily depend upon robust animals that are able to cope with multiple environmental stressors. In this regard, indigenous chickens are endowed with high genetic variation and high local adaptation caliber which forms the basis of selective breeding and genetic improvement strategies through prioritizing and making informed decisions (Desta, 2015; Lawal *et al*., 2018).

Besides, to meet the future food demand and ensure plane of family nutrition in low input poultry systems, it is important to improve the productivity of indigenous chickens (Al-Qamashoui *et al*., 2014). Chicken is a major protein source and intensively selected for economically important traits

by humans (Desta, 2015). However, for a multitude of facts within the different species used for food production, only a few breeds are developed towards high-output breed fitting in high input systems leaving aside enormous breeds from the food producing livestock systems and exposing to high danger of extinction (Oldenbroek, 2007). Indigenous chicken is endowed with a multitude of important traits with a high reputation for hardiness and resistance to diseases which needs to be better characterized for better utilization and conservation (Ngeno *et al*., 2014). Years of natural selection, under scavenging conditions, has made them robust and resistant to various diseases, especially to those caused by bacteria, and protozoa and other internal and external parasites; they have better survival than the commercial hybrid strains under village production conditions (Besbes *et al*., n.d.). The village chicken is very alert and has long shanks to run away from predators and multiple colors to serve as camouflage against aerial predators. Indigenous chickens appear to have an inherent scavenging and nesting habit.

Although, purebred selection in indigenous chicken (IC) population require more time to improve performance than crossbreeding and breed substitution, nevertheless, it can be tailored to fit the needs of local farmers and the prevailing environmental conditions (Ngeno *et al*., 2015). Besbes *et al*. (n.d.) also highlight the existence of a considerable scope for improving the performance of local breeds by identifying alternative breeding goals and capitalize on the breeds' specific attributes. Chicken breeding programs should not solely focus on the importation of non-adapted improved chicken and should pay attention to the improvement of IC through selective breeding, as it is more rewarding for the low input and tropical systems than the former. For instance, selection within Ethiopian IC population, called Horro has been implemented successfully in Ethiopia and has resulted in better egg production, compared to unimproved village chicken

(Woldegiorgiss, 2015; Wondmeneh *et al*., 2016). Ethiopian Horro IC has increased egg production by 123.5% (75 eggs) by week 45 and age at first egg reduced to 148 from 203 days by generation five in five generations of selection for egg numbers.

To date, few and non-exhaustive studies have been carried out to characterize and unravel the genomic potential of indigenous chicken in Ethiopia using the state of the art technologies. Understanding the phenotypic and genomic diversity is a prerequisite for proper utilization and improvement of indigenous chicken in Ethiopia. Understanding the functional basis of the genetic variants that underlie these traits, however, remains a formidable endeavour particularly for complex traits. Nonetheless, molecular phenotyping of an organism from sequenced data is doable with the advances in bioinformatics analysis and unparalleled surveys of genome-wide genetic variants (Khoo, 2017). The aim of this study was therefore to undertake genome characterization of indigenous chicken in Ethiopia. The findings in this thesis provide knowledge on the genomic diversity, and regions under positive selection pressure adapted to different agro-ecological environments in different geographically distributed indigenous chicken in Ethiopia.

In chapter 1, we have tried to emphasize the pinning problems that justify this work and gives backgrounds and objectives. The second chapter comprehensively revises basic concepts of chicken phenotypic and genome diversity and the molecular methods to tap these variations. In line with the previous studies (Alemayhu, 2003; Bekerie, 2015; Desta *et al*., 2013; Hassen *et al*., 2009; Lawal *et al*., 2018; Mwacharo *et al*., 2013, 2007; Wragg *et al*., 2012), this review evidences the high phenomic and genomic diversity of IC chicken in Ethiopia. Here has been built on high diversity of IC chicken in terms of both phenotypic and molecular traits and their relationship

across physical factors to explore the variations in the physical features and the useful attributes of different populations of indigenous chicken. The 3rd chapter highlights and discusses the findings on the genomic variability of LEI0258 microsatellite locus and its implication on breed improvement operations. The work discussed in this chapter is also the first of its kind in addressing the LEI0258 diversity and signatures of selection in Improved Horro and indigenous chicken populations of Ethiopia. High LEI0258 polymorphism is also revealed in indigenous chicken populations of Ethiopia. In chapter 5, the SNP based characterization of IC chicken genomic variants were illustrated. As evidenced in this study, Ethiopian IC are diverse which will grant a greater advantage in developing sustainable breed improvement strategies through selection. This could be exemplified by the fact that abought 21 million SNPs have been obtained in IC populations of Ethiopia which out excels 3.6 to 5 million SNPs reported by Gheyas *et al*. (2015). This genetic divergence could be due to limited gene flow, ecological variability, variation in demographic history, route and time of introduction, and the populations might be descended from different ancestral origins and they have been under different management histories (Desta *et al*., 2014). The putative signatures of positive selection under strong selection pressure in Improved Horro and indigenous chicken populations of Ethiopia where also mapped and discussed in chapter 5. Here, since most of the candidate genes identified in the present study are novel and have probably been under recent selection, they should be of great interest for future research. Johnsson *et al* (2018) has identified the genes Trafficking Kinesin Protein 1 (TRAK1), Oxysterol Binding Protein-Like 8 (OSBPL8), YEATS Domain Containing 4 (YEATS4), Centrosomal Protein 55 (CEP55), and Phosphatidylinositol-5-phosphate 4-kinase type-2 beta (PIP4K2B) as strong candidates for growth loci in the chicken using linkage mapping approach to map growth traits in an advanced intercross of wild red jungle fowl and domestic white leghorn layer chickens.

Of which only the gene, CEP55, has been found in our list of genes as non-synonymous deleterious variants across 27 populations. Our informed analysis of a previously reported gene, Neural crest Hypothesis Domestication (FGFR-I) and Gonadotrophin-releasing hormone I (GnRH-I) doesn't ascertain its presence in the candidates of signature of selection in Improved Horro and other indigenous chicken populations of Ethiopia. In A similar fasion, the vasoactive intestinal poly-peptide receptor-1 (VIPR-1) and dopamine D2 receptor (DRD2) genes reported by Xu *et al* (2011) as having an association to chicken egg number at 300 days of age is reported.

6.2. Conclusions and recommendation

In general, genomic regions have ascertained high diversity and selection regions under strong selection pressure in indigenous chicken populations of Ethiopia. Besides, unlike previous molecular findings, this study has clustered the Ethiopian IC gene pool into 4. Due to the localized preference of chicken genotype among the tribal community in Ethiopia, low genetic diversity within the population and high genetic variation between populations have been confirmed. Chicken populations show geographic structuring. Based on the findings of this study the following recommendations worth emphasis.

- Future works should emphasize to map candidate genes responsible for egg and meat production.
- Chicken improvement programs ahead should consider the 4 gene pools revealed in this study.
- Various characterization studies have been done here and there on a piecemeal basis. Hence, concerted efforts should gear towards Genetic improvement programs through selection.

- Using the current data it is also important to check if the regions under the current selection pressure overlap to the Quantitative Trait Loci (QTLs) available on the online animal QTL data base.

- Sequence data management of this finding was based on Gal gal 5.0 version and thus future works should also consider re-analysis based on the upcoming version Gal gal 6.0 which is not yet publicized for use.

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Table S 1. List of sampling sites of the reported study

ID	Sites	ID	Sites	ID	Sites	ID	sites	ID	Sites
1	Alefa	24	Dawo	47	Gondar	70	Kombolcha	93	Seden Sodo
2	Tach Armachiho	25	Dawro	48	Gondar Zuria	71	Konso	94	Selti
3	Ada'a	26	Debre Elias	49	Gorogutu	72	Kembata Tembaro	95	Shalla
4	Adami tulu	27	Debrebirhan	50	Guangua	73	Loka abaya	96	Sheka
5	Adwa	28	Dejen	51	Guba	74	Lume	97	Sheko
6	Alaba	29	Dembiya	52	Guraferda	75	Machakel	98	Sidama
7	Amaro	30	Dera	53	Guragie	76	Mandura	99	Siraro shalla
8	Arbaminch Zuria	31	Dibate	54	Hadero Tunto	77	Mao-Komo	100	South bench
9	Arbegona	32	Dirashe	55	Hadiya	78	Mecha	101	South Omo
10	Assossa	33	Dodota	56	Halaba	79	Mehal Amiba	102	Tanqua Abergellie
11	Awabel	34	Duna	57	Haramaya	80	Melo Hamusit	103	Tembein
12	Benchi Maji	35	Endamehoni	58	Hawzein	81	Menz gera	104	Tenta
13	Beresa watershed	36	Enebise Sar Midir	59	Hitossa	82	Mereb lehe	105	Tepi
14	Bishoftu	37	Farta	60	Horro	83	Meta	106	Tillili
15	Boloso Sore	38	Fogera	61	Humbo	84	Moretinajiru	107	Tiyo
16	Boset	39	Gamogofa	62	Jamma	85	Muhor Na aklil	108	Wensho
17	Bure	40	Gantaafeshum	63	Jarso	86	Nole Kaba	109	Wogera
18	Burji	41	Gasay	64	Jimma	87	North Bench	110	Wolaita
19	Chefe	42	Gedeo	65	Kamash	88	North Mekelle	111	Wonbera
20	Cheliya	43	Gelila	66	Kefa	89	Ofla	112	Worabe
21	Chena	44	Gidan	67	Kersa	90	Pawe	113	Yem
22	Dale	45	Gimbo	68	Kewot	91	Quara	114	Ziqualla
23	Damot Gale	46	Goma	69	Kimbibit	92	Raya-azebo	115	Zombati

Table S 2. Phenotypic and/or genotypic studies investigated.

No.	Phenotypic	Populations (N=89)	Genotypic	Populations (N=32)
1	Aklilu *et al*., 2013	2	Alemayehu *et al*., 2003	5
2	Alemayehu *et al*., 2003	5	Mwacharo *et al*., 2007	2
3	Bekele, 2015	3	Hassen *et al*., 2009	9
4	Bekerie *et al*., 2015	4	Goraga *et al*., 2011	5
5	Bogale, 2011	1	Wragg *et al*., 2012	5
6	Dana *et al*., 2010	5	Bekerie *et al*., 2015	4
7	Desta *et al*., 2013	2	Desta *et al*., 2015	2
10	Duguma, 2006	3		
11	Getachew *et al*., 2016	3		
12	Getu *et al*., 2014a	3		
13	Getu *et al*., 2014b	3		
14	Hailu *et al*., 2013	3		
15	Halima *et al*., 2007	9		
16	Kibret, 2008	1		
17	Lemlem and Tesfaye, 2010	2		
20	Melesse and Negesse, 2011	19		
21	Moges *et al*., 2010	3		
22	Moges, 2014	1		
23	Muhiye, 2007	3		
24	Negassa *et al*., 2014	3		
25	Nigussie *et al*., 2013	3		
26	Yisma, 2015	3		
27	Yitbarek and Zewudu, 2013	1		
28	Zewdu *et al*., 2013	4		

N = Number of populations

Table S 3. Studies in relation to dominant religion.

No.	Dominant religion	Phenotypic studies	N	Genotypic studies	N
1	Muslim	Aklilu, 2013; Alemayehu *et al*., 2015; Bekerie, 2015; Bogale, 2011; Desta, 2013; Duguma, 2006; Halima *et al*., 2007; Nagussie, 2013; Negassa *et al*., 2014.	9	Alemayhu, 2003; Bekerie, 2015; Goraga *et al*., 2012; Desta *et al*., 2014.	4
2	Protestant	Dana, 2010; Bekele *et al*., 2015; Muhiye, 2007; Melesse and Negesse, 2011	4	Alemayhu, 2003; Dana, 2010; Goraga *et al*., 2012; Wragg *et al*., 2012.	4
3	Traditional	Alemayehu, 2015; Dana, 2010; Halima *et al*., 2007.	3	-	-
4	Orthodox	Aklilu, 2013; Alemayhu, 2003; Bekerie, 2015; Dana, 2010; Desta *et al*., 2013; Moges *et al*., 2010; Getu *et al*., 2014a, 2014b; Hailu, *et al*., 2013; Halima *et al*., 2007; Kibret, 2008; Moges, 2014; Lemlem and Tesfaye, 2010; Negassa *et al*., 2014; Yitbarek and Zewudu; Zewdu, 2013	16	Alemayhu, 2003; Bekerie, 2015; Dana, 2010; Goraga *et al*., 2012; Hassen *et al*., 2009; Mwacharo *et al*., 2007; Desta *et al*., 2014; Wragg *et al*., 2012	8

N = number of studies

Table S 4. Studies in relation to altitude.

Elevation (masl)	Phenotypic studies	N	Genotypic studies	N
500 - 1800	Alemayhu, 2003; Bekele *et al*., 2015; Bogale, 2011; Dana *et al*., 2010; Duguma, 2006; Getachew *et al*., 2016; Halima *et al*., 2007; Nigussie, 2013; Yitbarek and Zewudu, 2013; Yisma, 2015; Zewdu *et al*., 2013.	10	Alemayhu, 2003; Hassen *et al*., 2009; Wragg *et al*., 2012.	4
1800 - 2400	Aklilu, 2013; Alemayhu, 2003; Bekerie, 2015; Bikila, 2013; Dana, 2010; Duguma, 2006; Getachew *et al*., 2016; Getu *et al*., 2014b; Hailu *et al*., 2013; Halima, 2007; Kibret, 2008; Lemlem and Tesfaye, 2010; Mogess *et al*., 2014; Negassa *et al*., 2014; Nigussie, 2013; Yisma, 2015.	18	Alemayhu, 2003; Goraga *et al*., 2012a; Hassen *et al*., 2009; Mwacharo *et al*., 2007; Desta *et al*., 2014; Wragg *et al*., 2012.	6
2400 - 3200	Aklilu, 2013; Bekerie, 2015; Dana *et al*., 2010; Duguma *et al*., 2006; Getu *et al*., 2014b; Halima, 2007; Mogess, 2014; Nigussie, 2013; Dessie *et al*., 2013; Yisma, 2015.	10	Alemayhu, 2003; Bekerie, 2015; Mwacharo *et al*., 2007; Desta *et al*., 2014; Wragg *et al*., 2012.	5

N = number of studies

Table S 5. List of studies across agro – ecologies.

Symbol	Major agro-ecology	Phenotypic studies	N	Genotypic studies	N
SM1	Hot to warm sub-moist lowlands	Dana *et al*., 2010; Moges, 2014; Nigussie, 2013.	3	No data	-
SM2	Tepid to cool sub-moist mid highlands	Nigussie, 2013.	1	Dana, 2011a; Goraga *et al*., 2012; Mwacharo *et al*., 2007.	3
SM3	Cold to very cold sub-moist sub-afro-alpine to afro alpine	Aklilu, 2013; Getu *et al*., 2014a; Hailu *et al*., 2013.	3	-	-
M1	Hot to warm moist lowlands	Aklilu, 2013; Alemayhu, 2003; Duguma, 2006; Getachew *et al*., 2016; Kibret, 2008; Negassa *et al*., 2014; Zewdu *et al*., 2013.	7	Dana, 2011a; Hassen *et al*., 2009.	2
M2	Tepid to cool moist mid highlands	Alemayhu, 2003; Bekerie, 2015; Dana *et al*., 2010; Duguma, 2006; Getachew *et al*., 2016; Getu *et al*., 2014a; Moges, 2014; Yitbarek and Zewdu., 2013; Yisma, 2015.	9	Hassen *et al*., 2009; Wragg *et al*., 2012.	2
SH1	Hot to warm sub-humid lowlands	Halima *et al*., 2007.	1	Hassen *et al*., 2009.	1
SH2	Tepid to cool sub-humid mid highlands	Aklilu, 2013; Alemayhu, 2003; Bekerie, 2015; Bogale, 2011; Dana *et al*., 2010; Duguma, 2006; Melesse and Negesse, 2011; Zewdu *et al*., 2013.	8	Bekerie, 2015; Desta, 2015.	2
H1	Hot to warm humid lowlands	Bekele *et al*., 2015; Nigussie, 2013.	2	Wragg *et al*., 2012.	1
H2	Tepid to cool humid mid highlands	Melesse and Negesse, 2010; Negassa *et al*., 2014.	2	Alemayhu, 2003; Mwacharo *et al*., 2007.	2
Ph1	Hot to warm per humid lowlands	Melesse and Negesse, 2011.	1	-	

N = Number of studies

Table S 6. List of qualitative traits considered.

No.	Qualitative traits	N	Studies
1	Plumage colour	14	Aklilu, 2013; Bekele *et al*., 2015; Bekerie, 2015; Dana, 2011a; Duguma, 2006; Getachew *et al*., 2016; Getu *et al*., 2014a, 2014b; Halima *et al*., 2007; Kibret, 2008; Melesse and Negesse, 2011; Negassa *et al*., 2014; Nigussie, 2013; Yisma, 2015.
2	Comb type	15	Aklilu, 2013; Bekele *et al*., 2015; Bekerie, 2015; Dana, 2011a; Desta *et al*., 2013; Duguma, 2006; Getu *et al*., 2014a, 2014b; Halima *et al*., 2007; Kibret, 2008; Melesse and Negesse, 2011; Nigussie, 2013; Yisma, 2015, Getachew *et al*., 2016; Negassa *et al*., 2014.
3	Earlobe colour	13	Aklilu, 2013; Bekele *et al*., 2015; Bekerie, 2015; Dana, 2011a; Desta *et al*., 2013; Duguma, 2006; Getu *et al*., 2014a, 2014b; Kibret, 2008; Melesse and Negesse, 2011; Negassa *et al*., 2014; Nigussie, 2013; Yisma, 2015.
4	Eye colour	6	Aklilu, 2013; Duguma, 2006; Getu *et al*., 2014a, 2014b; Negassa *et al*., 2014; Yisma, 2015.
5	Shank colour	12	Aklilu, 2013; Bekele *et al*., 2015; Bekerie, 2015; Dana, 2011a; Desta *et al*., 2013; Duguma, 2006; Getu *et al*., 2014b; Halima *et al*., 2007; Kibret, 2008; Melesse and Negesse, 2011; Negassa *et al*., 2014; Yisma, 2015.
6	Skin colour	9	Aklilu, 2013; Bekele *et al*., 2015; Dana, 2011a; Duguma, 2006; Getu *et al*., 2014; Kibret, 2008; Negassa *et al*., 2014; Nigussie, 2013; Yisma, 2015.
7	Shank feather	4	Bekele *et al*., 2015; Bekerie, 2015; Kibret, 2008; Mogesse, 2007.
8	Hen spur	3	Bekele *et al*., 2015; Kibret, 2008; Nigussie, 2013.
9	Body shape	4	Dana, 2011a; Getu *et al*., 2014a, 2014b; Kibret, 2008.
10	Head shape	8	Aklilu, 2013; Alemayhu, 2003a; Bekerie, 2015; Getu *et al*., 2014b; Melesse and Negesse, 2011; Negassa *et al*., 2014; Nigussie, 2013; Yisma, 2015.
11	Neck feather colour	2	Dana, 2011; Negassa *et al*., 2014.
12	Feather morphology	5	Bekele *et al*., 2015; Dana, 2011a; Kibret, 2008; Melesse and Negesse, 2011; Nigussie, 2013.
13	Feather colour	2	Dana, 2011a; Negassa *et al*., 2014.
14	Feather distribution	2	Melesse and Negesse, 2011a; Negassa *et al*., 2014.

N = number of studies

Table S 7. Plumage colour descriptions as reported in various studies.

Local colour naming	Description	Source
Gebisma	Wheaten strips on black background	Dana *et al*., 2010
	Greyish mixture	Getu *et al*., 2014a, 2014b; Halima *et al*., 2007)
	Red brownish with black	Bekerie, 2015)
	Reddish grey	Duguma, 2006)
	Greyish with varying mixture	Bekerie, 2015; Nigussie *et al*., 2015
	Mixtures of white and black with varying shades of multicolours	Melesse and Negesse, 2011
Tikur gebsat	Black with wheaten or red strips	Nigussie *et al*., 2015
Teterima	Black or red speckles on white background	Dana *et al*., 2010
	Black with white tips	Getu *et al*., 2014a, 2014b; Halima *et al*., 2007
	Black with white or red spots	Nigussie *et al*., 2015
Black red teterima	White black and red trips	Getu *et al*., 2014a, 2014b
Red teterima	White with red tips	Getu *et al*., 2014a, 2014b
Key teterima	Red with white or black spots	Nigussie *et al*., 2015
Netch teterima	White with black or red spots	Nigussie *et al*., 2015
Kokima	Red brownish	Getu *et al*., 2014a, 2014b
	Greyish strips on brown background	Nigussie *et al*., 2015
	Greyish plumage, white or greyish strips on brown or reddish background	Dana *et al*., 2010; Melesse and Negesse, 2011
Kokima/Giracha	Grey	Duguma, 2006
Zigrima	Black and white spotted feather	Dana *et al*., 2010; Nigussie *et al*., 2015
	Black and white spotted feathers on red background	(Melesse and Negesse, 2011
Kuarichama	White with red strips	Nigussie *et al*., 2015
Wosera	Mixture of white and red with varying shades of multi-colours	Melesse and Negesse, 2011
Zagolima	White or red speckles on black background	Melesse and Negesse, 2011
Seran	White with red striped	Halima *et al*., 2007
Key dama	Red brown	Duguma, 2006; Halima *et al*., 2007
Libework	White with golden breast colour	Nigussie *et al*., 2015

Table S 8. List of quantitative traits considered.

No.	Traits	N	Studies
1	Body weight	15	Lemlem and Tesfaye, 2010; Aklilu, 2013; Bekele *et al*., 2015; Bekerie, 2015; Dana, 2011a; Duguma, 2006; Getachew *et al*., 2015; Getu *et al*., 2014a, 2014b; Halima *et al*., 2007; Kibret, 2008; Melesse and Negesse, 2011; Negassa *et al*., 2014; Nigussie, 2013; Yisma, 2015.
2	Egg/hen/year	15	Lemlem and Tesfaye, 2010; Aklilu, 2013; Bekele *et al*., 2015; Bekerie, 2015; Dana, 2011a; Duguma, 2006; Getachew *et al*., 2015; Getu *et al*., 2014a, 2014b; Halima *et al*., 2007; Kibret, 2008; Melesse and Negesse, 2011; Negassa *et al*., 2014; Nigussie, 2013; Yisma, 2015.
3	Body length	8	Bekele *et al*., 2015; Bekerie, 2015; Getu *et al*., 2014a, 2014c; Kibret, 2008; Negassa *et al*., 2014; Nigussie, 2013; Yisma, 2015.
4	Wing span	8	Bekele *et al*., 2015; Getu *et al*., 2014a, 2014c; Kibret, 2008; Mogesse, 2007; Negassa *et al*., 2014; Nigussie, 2013; Yisma, 2015.
5	Back length	4	Aklilu, 2013; Bekele *et al*., 2015; Nigussie, 2013; Yisma, 2015.
6	Beak length	3	Getu *et al*., 2014a, 2014b; Negassa *et al*., 2014.
7	Chest circumference	4	Aklilu, 2013; Getachew *et al*., 2016; Nigussie, 2013; Yisma, 2015.
8	Comb height	7	Bekele *et al*., 2015; Getu *et al*., 2014a, 2014b; Kibret, 2008; Negassa *et al*., 2014; Nigussie, 2013; Yisma, 2015.
9	Comb length	7	Bekele *et al*., 2015; Getu *et al*., 2014a, 2014b; Kibret, 2008, 2008; Negassa *et al*., 2014; Nigussie, 2013; Yisma, 2015.
10	Keel bone length	7	Aklilu, 2013; Bekele *et al*., 2015; Getu *et al*., 2014a, 2014c; Negassa *et al*., 2014; Nigussie, 2013; Yisma, 2015.
11	Neck length	2	Bekele *et al*., 2015; Yisma, 2015.
12	Shank circumference	4	Getachew *et al*., 2016; Getu *et al*., 2014a; Halima*et al*., 2007; Negassa *et al*., 2014.
13	Shank length	10	Bekele *et al*., 2015; Bekerie, 2015; Dana *et al*., 2010a; Getu *et al*., 2014a, 2014c; Halima *et al*., 2007; Melesse and Negesse, 2011; Negassa *et al*., 2014; Nigussie, 2013.
14	Spur length	7	Getu *et al*., 2014a, 2014c; Kibret, 2008.
15	Wattle length	3	Bekele *et al*., 2015; Bekerie, 2015; Nigussie, 2013.

N = number of studies

Table S 9. List of genotypic parameters considered.

No.	Parameter	N	Studies
1	Mean number of alleles	4	Alemayhu, 2003; Bekerie, 2015; Halima *et al*., 2007; Mwacharo *et al*., 2007)
2	Effective number of alleles	1	Mwacharo *et al*., 2007.
3	Alleles per locus	2	Goraga *et al*., 2012; Wragg *et al*., 2012.
4	Private Alleles	3	Goraga *et al*., 2012; Mwacharo *et al*., 2007; Wragg *et al*., 2012.
5	Observed Heterozygosity	6	Alemayhu, 2003; Bekerie, 2015; Goraga *et al*., 2012; Halima *et al*., 2007; Mwacharo *et al*., 2007; Wragg *et al*., 2012.
6	Expected heterozygosity	7	Alemayhu, 2003; Bekerie, 2015; Goraga *et al*., 2012; Halima *et al*., 2007; Mwacharo *et al*., 2007; Desta *et al*., 2014; Wragg *et al*., 2012.
7	Coefficient of Inbreeding	4	Goraga *et al*., 2012; Mwacharo *et al*., 2007; Desta *et al*., 2014; Wragg *et al*., 2012.
8	Polymorphic Information Content	3	Alemayhu, 2003; Bekerie, 2015; Halima *et al*., 2007.
9	Identity By Descent	2	Desta *et al*., 2014; Wragg *et al*., 2012.

N = number of studies

Table S 10. Average plumage colour variants (%) of indigenous chicken (N=9491).

Plumage	NP	N	%	Sources
Red	52	2378	27.8	Aklilu, 2013; Bekele *et al*., 2015; Bekerie, 2015; Dana *et al*., 2010; Getachew *et al*., 2016; Getu *et al*., 2014a, 2014b; Halima *et al*., 2007; Melesse and Negesse, 2011; Negassa *et al*., 2014; Nigussie *et al*., 2015; Yisma, 2015
Black	53	1506	15.28	Aklilu, 2013; Bekele *et al*., 2015; Bekerie, 2015; Dana *et al*., 2010; Getachew *et al*., 2016; Getu *et al*., 2014a, 2014b; Halima *et al*., 2007; Melesse and Negesse, 201; Negassa *et al*., 2014; Nigussie *et al*., 2015; Yisma, 2011
White	49	1392	14.13	Aklilu, 2013; Bekele *et al*., 2015; Bekerie, 2015; Dana *et al*., 2010; Getachew *et al*., 2016; Getu *et al*., 2014a, 2014b; Halima *et al*., 2007; Melesse and Negesse, 2011; Negassa *et al*., 2014; Yisma, 2015
Gebsima	51	1156	11.74	Aklilu, 2013; Bekele *et al*., 2015; Bekerie, 2015; Dana *et al*., 2010; Getachew *et al*., 2016; Getu *et al*., 2014a, 2014b; Halima *et al*., 2007; Kibret, 2008; Melesse and Negesse, 2011; Nigussie *et al*., 2015)
Teterima	34	516	5.24	Aklilu, 2013; Bekele *et al*., 2015; Bekerie, 2015; Dana *et al*., 2010; Getachew *et al*., 2016; Getu *et al*., 2014a, 2014b; Halima *et al*., 2007; Kibret, 2008; Melesse and Negesse, 2011; Nigussie *et al*., 2015
Kokima	32	497	5.05	Bekele *et al*., 2015; Dana *et al*., 2010; Getu *et al*., 2014; Kibret, 2008; Melesse and Negesse, 2011; Nigussie *et al*., 2015)
Grey	13	147	1.49	Aklilu, 2013; Bekele *et al*., 2015; Dana *et al*., 2010; Nigussie *et al*., 2015
Wosera	18	300	3.05	Halima *et al*., 2007; Melesse and Negesse, 2011; Negassa *et al*., 2014
Seran	16	71	0.72	Halima *et al*., 2007; Kibret, 2008; Nigussie *et al*., 2015; Yisma, 2015
Zigirima	71	176	1.79	Bekele *et al*., 2015; Dana *et al*., 2010; Halima *et al*., 2007; Melesse and Negesse, 2011; Nigussie *et al*., 2015
Zagolima	2	62	0.6	Halima *et al*., 2007; Melesse and Negesse, 2011
Anbesima	8	63	0.64	Getu *et al*., 2014; Halima *et al*., 2007; Kibret, 2008; Nigussie *et al*., 2015; Yisma, 2015
Aserima	3	46	0.47	Yisma, 2015
Brownish	52	886	8.99	Bekele *et al*., 2015; Bekerie, 2015; Dana *et al*., 2010; Getachew *et al*., 2016; Halima *et al*., 2007; Negassa *et al*., 2014; Nigussie, 2013; Nigussie *et al*., 2015)
Libework	13	193	1.96	Bekele *et al*., 2015; Bekerie, 2015; Dana *et al*., 2010; Getachew *et al*., 2016; Getu *et al*., 2014b; Halima *et al*., 2007; Negassa *et al*., 2014; Nigussie *et al*., 2015
Multicolor	26	102	1.04	Dana *et al*., 2010; Getu *et al*., 2014; Halima *et al*., 2007; Negassa *et al*., 2014; Nigussie *et al*., 2015)

N = number of chicken sampled; NP = Number of populations considered by investigated studies.

Table S 11. Earlobe colour variants of indigenous chicken (N=9624).

Earlobe color	NP	N	%	Sources
Red	52	4402	45.74	Aklilu, 2013; Bekele *et al*., 2015; Bekerie, 2015; Dana *et al*., 2010; Melesse and Negesse, 2011; Nigussie *et al*., 2015
Black	6	147	1.53	Bekerie, 2015; Getu *et al*., 2014; Nigussie *et al*., 2015
White	47	3434	35.68	Aklilu, 2013; Bekele *et al*., 2015; Bekerie, 2015; Dana *et al*., 2010; Desta *et al*., 2013; Kibret, 2008; Negassa *et al*., 2014; Nigussie *et al*., 2015; Yisma, 2015
Yellow	35	9.8	0.10	Aklilu, 2013; Bekele *et al*., 2015; Bekerie, 2015; Dana *et al*., 2010; Desta *et al*., 2013; Melesse and Negesse, 2011; Nigussie *et al*., 2015
White and red	7	559	5.81	Bekele *et al*., 2015; Kibret, 2008; Nigussie *et al*., 2015
Red and white	11	581	6.04	Aklilu, 2013; Bekerie, 2015; Desta *et al*., 2013
Purl	2	32	0.33	Getu *et al*., 2014
Green	3	41	0.43	Yisma, 2015
Grey	3	75	0.78	Yisma, 2015
Orange	3	55	0.57	Desta *et al*., 2013
Pink	2	119	1.24	Desta *et al*., 2013
Pink and yellow	1	6	0.06	Desta *et al*., 2013
Pink and white	2	138	1.43	Desta *et al*., 2013
Dark brown	1	1	0.01	Desta *et al*., 2013
Unclassified	3	24	0.25	Negassa *et al*., 2014

N = number of chicken sampled; NP = Number of populations considered by investigated studies.

Table S 12. Shank (N=9014) and skin (N= 6313) colour variants of indigenous chicken.

Shank color	NP	N	%	Sources
Yellow	57	4993	55.39	Bekele *et al*., 2015; Bekerie, 2015; Dana *et al*., 2010; Desta *et al*., 2013; Getu *et al*., 2014; Halima *et al*., 2007; Kibret, 2008; Melesse and Negesse, 2011; Negassa *et al*., 2014
White	58	2506	27.80	Bekele *et al*., 2015; Bekerie, 2015; Dana *et al*., 2010; Desta *et al*., 2013; Getu *et al*., 2014; Halima *et al*., 2007; Kibret, 2008; Melesse and Negesse, 2011; Negassa *et al*., 2014
Black	55	10.59	0.12	Bekele *et al*., 2015; Bekerie, 2015; Dana *et al*., 2010a; Desta *et al*., 2013; Getu *et al*., 2014b; Halima *et al*., 2007; Melesse and Negesse, 2011; Negassa *et al*., 2014
Brown	4	42	0.47	Bekerie, 2015
Bluish black	3	35	0.39	Aklilu, 2013; Kibret, 2008
Grey blue	17	530	5.88	Bekele *et al*., 2015; Negassa *et al*., 2014
Green	28	290	3.22	Aklilu, 2013; Desta *et al*., 2013; Getu *et al*., 2014; Halima *et al*., 2007; Melesse and Negesse, 2011; Negassa *et al*., 2014
Green blue	7	15	0.17	Aklilu, 2013
Slated blue	2	41	0.45	Desta *et al*., 2013
Red	9	217	2.41	Bekele *et al*., 2015; Getu *et al*., 2014
Pale	3	320	3.55	Duguma, 2006
Mottled	2	14	0.16	Desta *et al*., 2013
Skin colour	**NP**	**N**	**%**	**Sources**
Black	3	19	0.30	Duguma, 2006; Aklilu *et al*., 2013; Negassa *et al*., 2014; Agide, 2015; Bekele *et al*., 2015
Blue black	6	320	5.07	Kibret, 2008; Aklilu *et al*., 2013; Negassa *et al*., 2014
Green	2	726	11.50	Kibret, 2008; Agide, 2015; Negassa *et al*., 2014; Aklilu *et al*., 2013; Bekele *et al*., 2015
Red	9	774	12.27	Duguma, 2006; Aklilu *et al*., 2013; Negassa *et al*., 2014;Agide, 2015; Bekele *et al*., 2015
White	26	2709	42.92	Kibret, 2008; Agide, 2015; Negassa *et al*., 2014; Aklilu *et al*., 2013; Bekele *et al*., 2015
Yellow	23	1661	26.31	Kibret, 2008; Dana *et al*., 2010; Aklilu *et al*., 2013; Negassa *et al*., 2014; Bekele *et al*., 2015; Agide, 2015
Pink	3	104	1.65	Bekele *et al*., 2015

N = Number of chicken sampled; NP = Number of populations considered by investigated studies.

Table S 13. Eye colour variants of indigenous chicken populations across (N = 3248).

Eye color	NP	N	%	Sources
Orange	6	388	11.95	Aklilu, 2013; Getu *et al*., 2014a, 2014b
Black	8	773	23.80	Duguma, 2007; Getu *et al*., 2014b; Negassa *et al*., 2014
Pearl	4	19	0.58	Aklilu, 2013; Getu *et al*., 2014
Red	11	1200	36.95	Aklilu, 2013; Getu *et al*., 2014a, 2014b; Yisma, 2015
Brown	5	438	13.49	Aklilu, 2013; Yisma, 2015
Blue black	3	367	11.30	Negassa *et al*., 2014
Dark brown	3	63	1.94	Negassa *et al*., 2014

N = Number of chicken sampled; NP = Number of populations considered by investigated studies.

Table S 14. Neck feather colour variants of indigenous chicken (N = 1235).

Neck feather color	NP	N	%	Sources
White	7	256	20.73	Dana *et al*., 2010; Negassa *et al*., 2014
Black	7	139	11.26	Dana *et al*., 2010; Negassa *et al*., 2014
Red	7	210	17.00	Dana *et al*., 2010; Negassa *et al*., 2014
Gebsima	5	22	1.78	Desta *et al*., 2013
Teterima	5	18	1.46	Desta *et al*., 2013
Brown	8	311	25.18	Dana *et al*., 2010; Negassa *et al*., 2014
Kokima	5	4	0.32	Desta *et al*., 2013
Grey	7	32	2.59	Dana *et al*., 2010; Negassa *et al*., 2014
Zigirima	5	47	3.81	Desta *et al*., 2013
Gold	5	129	10.45	Desta *et al*., 2013
Multiple	5	37	3.00	Desta *et al*., 2013
Reddish brown	3	30	2.43	Desta *et al*., 2013

N=number of chicken sampled; NP=Number of populations considered by investigated studies.

Table S 15. Comb type variants in indigenous chicken (N=1071).

Comb type	NP	N	%	Sources
Single	11	4279	42.07	Bekele *et al*., 2015; Bekerie, 2015; Dana *et al*., 2010; Desta *et al*., 2013; Getachew *et al*., 2016; Getu *et al*., 2014a, 2014b; Halima *et al*., 2007; Kibret, 2008; Melesse and Negesse, 2011; Negassa *et al*., 2014; Nigussie *et al*., 2015; Yisma, 2015)
Rose	59	3132	30.79	Bekele *et al*., 2015; Bekerie, 2015; Dana *et al*., 2010; Desta *et al*., 2013; Getachew *et al*., 2016; Getu *et al*., 2014a, 2014b; Halima *et al*., 2007; Kibret, 2008; Melesse and Negesse, 2011; Negassa *et al*., 2014; Nigussie *et al*., 2015; Yisma, 2015
Pea	60	2136	21.00	Bekele *et al*., 2015; Bekerie, 2015; Dana *et al*., 2010; Desta *et al*., 2013; Getachew *et al*., 2016; Getu *et al*., 2014a, 2014b; Halima *et al*., 2007; Kibret, 2008; Melesse and Negesse, 2011; Negassa *et al*., 2014; Nigussie *et al*., 2015; Yisma, 2015
Strawberry	9	35	0.34	Bekele *et al*., 2015; Bekerie, 2015; Desta *et al*., 2013; Getachew *et al*., 2016; Nigussie *et al*., 2015
Walnut	9	246	2.42	Dana *et al*., 2010; Desta *et al*., 2013; Getachew *et al*., 2016; Getu *et al*., 2014; Halima *et al*., 2007; Melesse and Negesse, 2011; Negassa *et al*., 2014; Nigussie, 2013; Nigussie *et al*., 2015
Cushion	2	39	0.38	Aklilu, 2013
V-shape	8	222	2.18	Desta *et al*., 2013; Halima *et al*., 2007; Nigussie, 2013; Nigussie *et al*., 2015
Duplex	27	70	0.69	Dana *et al*., 2010; Desta *et al*., 2013; Getu *et al*., 2014a, 2014b; Melesse and Negesse, 2011
Butter cup	3	9	0.09	Desta *et al*., 2013; Getachew *et al*., 2016
Unclassified	2	3	0.03	Desta *et al*., 2013

N=number of chicken sampled; NP=Number of populations considered by investigated studies.

Table S 16. Feather distribution (N=12624) and motrphology (N=11455) variants of indigenous chicken.

Feather distribution	**NP**	**N**	**%**	**Sources**
Normal	37	10715	84.88	Bekele *et al*., 2015; Dana *et al*., 2010; Kibret, 2008; Melesse and Negesse, 2011; Nigussie *et al*., 2015
Necked Neck	19	347	2.75	Bekele *et al*., 2015; Dana *et al*., 2010; Kibret, 2008; Melesse and Negesse, 2011; Nigussie *et al*., 2015
Crest	6	547	4.33	Bekele *et al*., 2015; Dana *et al*., 2010; Kibret, 2008; Melesse and Negesse, 2011; Nigussie *et al*., 2015
Shank and feet	9	76	0.60	Melesse and Negesse, 2011
Muff and beard	12	82	0.65	Melesse and Negesse, 2011
Silky	9	623	4.94	Melesse and Negesse, 2011
Frizzle	6	234	1.85	Melesse and Negesse, 2011
Feather morphology	**NP**	**N**	**%**	**References**
Normal	25	5492	89.82	Kibret, 2008; Nigussie *et al*, 2010; Abera and Tegegne, 2011; Nigussie *et al*., 2015
Frizzel	9	29	0.47	Abera and Teggne, 2011
Silky	8	5934	9.71	Dana *et al*., 2010; Abera and Tegegne, 2011

N = number of chicken sampled; NP = Number of populations considered by investigated studies.

Table S 17. Shank feather (N=1231), hen spur (N=1480) and body shaper (N=2123) variants of indigenous chicken.

Shank feather	**NP**	**N**	**%**	**Sources**
Present	8	28	2.27	Bekele *et al*., 2015; Bekerie, 2015; Halima *et al*., 2007
Absent	16	1203	97.73	
Hen spur	**NP**	**N**	**%**	
Present	7	646	43.65	Bekele *et al*., 2015; Kibret, 2008; Nigussie *et al*., 2015
Absent	7	834	56.35	
Body shape	NP	N	%	Sources
Triangular	12	435	20.50	Dana *et al*., 2010 ; Getu et al., 2014b; Getu *et al*., 2014C
Blocky	12	1262	59.42	Kibret, 2008, Dana *et al*., 2010 ; Getu *et al*., 2014b; Getu et al., 2014C
Wedge	12	426	20.09	Kibret, 2008, Dana *et al*., 2010 ; Getu *et al*., 2014b; Getu *et al*., 2014C

N = Number of chicken sampled; NP = Number of populations considered by investigated studies.

Table S 18. Significance test and LS means of plumage colour across dominant religion and elevation

Religion	Red	Black	White	Green	Teterima	Kokima	Green	Wesera	Seran	Zig		Anb	AS	Br	LI	MC
Muslim	43^{a}	32^{a}	29^{a}	23^{a}	14^{a}	28^{a}	20^{a}	34^{a}	5^{a}	9^{a}		9^{a}	15^{a}	30^{a}	3^{a}	4^{a}
Protestant	96^{a}	48^{a}	29^{a}	38^{a}	19^{a}	23^{a}	5^{a}	3^{a}	5^{a}	3^{a}		9^{a}	15^{a}	33^{a}	14^{a}	3^{a}
Orthodox	32^{a}	17^{a}	27^{a}	16^{a}	17^{a}	10^{a}	8^{a}	23^{a}	5^{a}	11^{a}		9^{a}	15^{a}	25^{a}	21^{a}	5^{a}
Traditional	37^{a}	10^{a}	41^{a}				17^{a}		5^{a}	4^{a}		9^{a}	15^{a}	35^{a}	14^{a}	
Elevation	**Red**	**Brown**	**White**	**Green**	**Teterima**	**Kokima**	**Green**	**Wesera**	**Seran**	**Zig**	**Za**	**A**	**AS**	**BR**	**LI**	**MC**
500-1500	45^{a}	25^{ab}	25^{a}	21^{a}	14^{a}	15^{a}	7^{a}	19^{a}	6^{a}	8^{a}	2^{a}	17^{a}		33^{a}	16^{a}	5^{a}
1501-2400	66^{a}	35^{a}	28^{a}	28^{a}	14^{a}	19^{a}	11^{a}	17^{a}	5^{a}	9^{a}	7^{a}	6^{a}		21^{a}	17^{a}	4^{a}
2401-3200	27^{a}	13^{b}	31^{a}	11^{a}	29^{a}	10^{a}	6^{a}	18^{a}	0.6^{a}	8^{a}	4^{a}	3^{a}		43^{a}	14^{a}	2^{a}

Za = Zagolima; A = Anbesima; AS = Aserima; Br = Brown; LI = Libework; MC = Multicolour. Values with different letter superscripts across columns are significantly different ($P < 0.05$).

Table S 19. Significance test and LS means of comb types across dominant religion and elevation.

Religion	Single	Rose	Pea	Strawberry	Walnut	V-shape	Duplex
Orthodox	42.40^{b}	64.96^{a}	36.28^{a}	3.06^{a}	11.27^{a}	6.22^{a}	22.64^{a}
Protestant	122.48^{a}	44.29^{a}	27.76^{a}	4.04^{a}	7.79^{a}	6.05^{a}	11.47^{a}
Traditional	8.79^{b}	6.80^{a}	43.85^{a}	3.76^{a}	2.80^{a}	6.05^{a}	36.94^{a}
Muslim	57.00^{b}	39.89^{a}	53.03^{a}	3.76^{a}	5.46^{a}	0.07^{a}	3.18^{a}
Elevation	**Single**	**Rose**	**Pea**	**Strawberry**	**Walnut**	**V-shape**	**Duplex**
500-1500	53.40^{ab}	45.66^{a}	32.53^{a}	2.98^{a}	9.16^{a}	8.48^{a}	8.11^{a}
1501-2400	88.26^{a}	51.28^{a}	35.52^{a}	3.50^{a}	8.13^{a}	1.75^{a}	17.57^{a}
2401-3200	28.10^{b}	60.08^{a}	48.04^{a}	4.30^{a}	9.86^{a}	8.48^{a}	29.46^{a}

Values with different letter superscripts across columns are significantly different ($P < 0.05$).

Table S 20. Significance test and LS means of Earlobe colour across dominant religion and elevation.

Dominant Religion	Black	White	Red	Yellow	White and Red	Red and white	Green	Grey	Orange	others
Muslim	61.95[a]	61.42[a]	71.99[a]	38.39[a]	90.82[a]	72.75[a]	13.67[a]	15.67[a]	18.39[a]	11.84[a]
Protestant	30.13[a]	87.61[a]	79.62[a]	30.78[a]	93.36[a]	55.81[a]	13.67[a]	15.67[a]	18.39[a]	8.58[a]
Traditional	30.13[a]	144.55[a]	89.23[a]	26.88[a]	90.82[a]	55.81[a]	13.67[a]	15.67[a]	18.39[a]	8.58[a]
Orthodox	6.35[a]	63.37[a]	92.77[a]	17.67[a]	65.21[a]	43.15[a]	13.67[a]	15.67[a]	18.39[a]	6.15[a]
Elevation	**Black**	**White**	**Red**	**Yellow**	**White and Red**	**red and white**	**Green**	**Grey**	**Orange**	**others**
500-1800	1.48[a]	61.83[a]	70.05[a]	21.98[a]	72.18[a]	39.23[a]	16.75[a]	21.40[a]	6.97[a]	8[a]
1800-2400	45.74[a]	84.44[a]	92.34[a]	33.34[a]	69.01[a]	56.28[a]	12.37[a]	13.25[a]	35.99[a]	8[a]
2400-3200	1.43[a]	59.27[a]	86.29[a]	11.38[a]	122.50[a]	64.60[a]	12.37[a]	13.25[a]	9.68[a]	8[a]

Values with different letter superscripts across columns are significantly different ($P < 0.05$).

Table S 21. Significance test and LS means of eye colour across dominant religion and elevation.

Dominant religion	Orange	Black	pearl	Red	Brown	blue black	
Muslim	144.62[a]	126.14[a]	6.21[a]	76.53[a]	2.93[a]	97.09 [a]	
Orthodox	39.96[a]	87.54[a]	4.28[a]	119.04[a]	113.65[a]	130.10 [a]	
Elevation	**Orange**	**Black**	**pearl**	**Red**	**Brown**	**blue black**	**Dark brown**
500-1800	5.95[a]	59.87[a]	1.99[a]	131.32[a]	146.75[a]	122.33[a]	21[a]
1800-2400	78.86[a]	73.57[a]	5.61[a]	105.95[a]	78.11[a]	122.33[a]	21[a]
2400-3200	124.18[a]	188.65[a]	6.41[a]	87.38[a]	32.64[a]	122.33[a]	21[a]

Values with different letter superscripts across columns are significantly different ($P < 0.05$).

Table S 22. Significance test and LS means of shank colour across dominant religion and elevation.

Dominant religion	Yellow	White	Black	Brown	Bluish black	Grey blue	Green	Red	Pale	Grey blue
Muslim	86.90[a]	42.46[a]	14.65[a]	12.26[a]	8.82[a]	67.90[a]	18.22[a]	31.56[a]	182.35[a]	11.25[a]
Orthodox	86.38[a]	42.23[a]	17.91[a]	8.05[a]	21.79[a]	73.99[a]	11.61[a]	39.55[a]	69.23[a]	4.92[a]
Protestant	97.98[a]	51.67[a]	23.63[a]	10.30[a]	8.68[a]	57.49[a]	6.43[a]	0.77[a]	117.68[a]	4.55[a]
Traditional	48.25[a]	11.81[a]	12.89[a]	11.45[a]	8.68[a]	73.99[a]	1.20[a]	19.48[a]	117.68[a]	7.64[a]
Elevation	**Yellow**	**White**	**Black**	**brown**	**bluish black**	**Grey blue**	**Green**	**Red**	**Pale**	**Grey blue**
500-1800	65.88[a]	34.49[a]	15.31[a]	13.74[a]	2.95[a]	72.22[a]	7.74[a]	13.7[a]	41.6[a]	0.06[a]
1800-2400	97.40[a]	51.47[a]	22.57[a]	7.43[a]	19.82[a]	65.03[a]	14.07[a]	10.4[a]	139.4[a]	9.68[a]
2400-3200	93.05[a]	34.33[a]	14.21[a]	13.74[a]	2.95[a]	68.44[a]	4.57[a]	74.3[a]	114.3[a]	5.11[a]

Values with different letter superscripts across columns are significantly different ($P < 0.05$).

Table S 23. Significance test and LS means of skin colour across dominant religion and elevation.

Dominant religion	Yellow	White	Black	Bluish black	Pink	Red
Muslim	101.56[a]	53.73[a]	6.34[a]	55.18[a]	34.67[a]	177.31[a]
Traditional	59.38[a]	153.00[a]	6.34[a]	37.13[a]	34.67[a]	106.36[a]
Protestant	54.25[a]	146.20[a]	6.34[a]	37.13[a]	34.67[a]	106.36[a]
Orthodox	66.14[a]	95.25[a]	6.34[a]	23.74[a]	34.67[a]	53.75[a]
Elevation	**Yellow**	**White**	**Black**	**Bluish black**	**Pink**	**Red**
500-1800	69.62[a]	113.11[a]	0.28[a]	7.51[a]	14.05[a]	27.81[a]
1800-2400	77.53[a]	81.39[a]	11.53[a]	59.85[a]	50.87[a]	95.59[a]
2400-3200	47.66[a]	125.64[a]	5.77[a]	7.51[a]	32.89[a]	162.00[a]

Values with different letter superscripts across columns are significantly different ($P < 0.05$).

Table S 24. Significance test and LS means of feather distribution across dominant religion and elevation.

Dominant religion	Normal	Naked Neck	Crest	Shank and feet	Muff and beard
Protestant	225.31[a]	17.80[a]	17.31[a]	10.04[a]	7.60[a]
Traditional	218.25[a]	11.15[a]	19.67[a]	12.05[a]	10.48[a]
Muslim	238.38[a]	29.65[a]	13.72[a]	7.32[a]	7.45[a]
Orthodox	170.13[a]	17.22[a]	86.37[a]	4.84[a]	3.91[a]
Elevation	**Normal**	**Naked Neck**	**Crest**	**Shank and feet**	**Muff and beard**
500-1800	208.42[a]	9.19[a]	55.74[a]	12.70[a]	6.67[a]
1800-2400	215.42[a]	22.59[a]	20.44[a]	6.46[a]	6.67[a]
2400-3200	180.00[a]	16.11[a]	97.11[a]	9.47[a]	6.67[a]

Values with different letter superscripts across columns are significantly different ($P < 0.05$).

Table S 25. Significance test and LS means of feather morphology across dominant religion and elevation.

Dominant religion	Normal	Silky	Frizzle
Muslim	290.00[a]	174.28[a]	27.99[a]
Protestant	231.08[a]	54.24[a]	34.57[a]
Traditional	115.31[a]	174.28[a]	27.99[a]
Orthodox	184.20[a]	56.41[a]	25.92[a]
Elevation	**Normal**	**Silky**	**Frizzle**
500-1800	197.14[a]	106.82[a]	31.52[a]
1801-2400	231.07[a]	48.77[a]	31.28[a]
2401-3200	186.94[a]	101.61[a]	31.40[a]

Values with different letter superscripts across columns are significantly different ($P < 0.05$).

Table S 26. Significance test and LS means of neck feather across dominant religion and elevation.

Dominant religion	White	Black	Red	Gebsima	Teterima	Brown	kok	Grey	Zigirima	Reddish brown
Orthodox	41.16[a]	13.05[a]	30.51[a]	5.66[a]	3.36[a]	35.69[a]	0.78[a]	5.40[a]	11.76[a]	13.14[a]
Muslim	23.50[a]	40.50[a]	65.00[a]	2.52[a]	3.82[a]	53.50[a]	0.13[a]	9.51[a]	8.76[a]	5.79[a]
Protestant	21.32[a]	6.93[a]	35.47[a]	5.34[a]	3.34[a]	35.47[a]	0.22[a]	0.30[a]	7.12[a]	9.67[a]
Traditional	42.63[a]	6.16[a]	22.49[a]	2.52[a]	3.82[a]	25.95[a]	0.13[a]	0.66[a]	8.76[a]	9.67[a]
Elevation	**White**	**Black**	**Red**	**Gebsima**		**Brown**	**kokima**	**Grey**		**Reddish brown**
500-1800	28.42[b]	6.67[a]	31.14[a]	3.78[a]		32.29[a]	0.10[a]	0.39[a]		10[a]
1800-2400	24.86[b]	28.89[a]	51.06[a]	4.70[a]		50.06[a]	0.76[a]	7.83[a]		10[a]
2400-3200	71.05[a]	4.62[a]	17.30[a]	5.09[a]		13.84[a]	0.20[a]	3.79[a]		10[a]

Values with different letter superscripts across columns are significantly different ($P < 0.05$).

Table S 27. Significance test and LS means of body shape across dominant religion and elevation.

Dominant religion	**Blocky**	**Triangular**	**Wedge**
Orthodox	76.04[a]	40.12[a]	36.94[a]
Protestant	191.25[a]	29.25[a]	4.50[a]
Traditional	189.00[a]	18.00[a]	18.00[a]
Elevation	**Blocky**	**Triangular**	**Wedge**
500-1800	193.50[a]	23.6[a]	7.9[a]
1800-2400	48.57[b]	47.0[a]	40.0[a]
2400-3200	79.67[ab]	36.0[a]	42.7[a]

Values with different letter superscripts across columns are significantly different ($P < 0.05$).

Table S 28. Significance test and LS means of plumage colour variants (%) AEZ (N=9850).

Plumage	**AEZ**	**N**	**LSM**	**P-value**
Red (n=2738)	H1	678	84.72[a]	0.001
	H2	65	99.78[a]	
	M1	169	31.70[bc]	
	M2	174	33.43[bc]	
	PH1	98	97.73[a]	
	SH1	70	14.01[c]	
	SH2	1075	72.23[a]	
	SM1	99	24.80[bc]	
	SM2	300	70.43[ab]	
	SM3	10	20.88[bc]	
Black (n=1505)	H1	330	41.30[a]	0.07
	H2	39	43.86[a]	
	M1	97	17.82[a]	
	M2	114	18.92[a]	
	PH1	50	49.59[a]	
	SH1	45	14.60[a]	
	SH2	589	38.49[a]	
	SM1	40	9.93[a]	
	SM2	118	29.20[a]	
	SM3	83	27.50[a]	
White (n=1392)	H1	165	20.64[a]	0.05
	H2	15	34.76[a]	
	M1	121	21.26[a]	
	M2	262	32.57[a]	
	SH1	36	27.29[a]	
	SH2	481	12.80[a]	
	SM1	92	28.71[a]	
	SM2	29	29.94[a]	

Plumage	AEZ	N	LSM	P-value
	SM3	191	22.51[a]	
Gebsima (n=1156)	H1	174	21.72[a]	0.10
	H2	17	23.00[a]	
	M2	99	11.57[a]	
	PH1	42	13.65[a]	
	SH1	52	41.76[a]	
	SH2	520	10.46[a]	
	SH3	12	36.76[a]	
	SM1	13	7.475[a]	
	SM2	191	42.72[a]	
	SM3	36	19.54[a]	
Teterima (n=516)	H1	103	18.99[a]	0.05
	M1	59	13.13[a]	
	M2	105	12.24[a]	
	SH1	24	16.44[a]	
	SH3	1	8.11[a]	
	SM1	50	13.74[a]	
	SM3	174	12.45[a]	
Kokima (n=497)	H1	217	27.14[a]	0.12
	M1	4	14.32[a]	
	M2	38	12.39[a]	
	PH1	43	43.21[a]	
	SH2	167	16.15[a]	
	SM1	6	9.50[a]	
	SM2	14	12.42[a]	
	SM3	8	8.01[a]	
Grey (n=147)	H1	11	6.84[a]	0.67
	M1	52	6.84[a]	
	M2	8	13.74[a]	
	SH1	35	7.89[a]	
	SH2	39	10.53[a]	
	SM1	2	9.79[a]	
Wosera (n=300)	H1	12	19.04[a]	0.55
	H2	49	24.50[a]	
	M1	48	24.02[a]	
	PH1	27	27.26 [a]	
	SH1	11	18.19[a]	
	SH2	98	15.71[a]	
	SM2	55	27.02[a]	
Seran (n=71)	M1	9	4.16[a]	0.27
	M2	18	5.30[a]	
	SH1	1	4.23[a]	
	SM1	13	4.48[a]	
	SM2	7	4.42[a]	

Plumage	AEZ	N	LSM	P-value
	SM3	23	9.35[a]	
Zigirima (n=176)	H1	44	7.89[a]	0.44
	M1	13	9.38[a]	
	PH1	2	1.74[a]	
	SH1	41	15.69[a]	
	SH2	72	8.94[a]	
	SM2	4	8.31[a]	
Zagolima (n=62)	PH1	42	41.76[a]	0.0001
	SH1	20	21.61[a]	
Anbesima (n=63)	M1	2	8.01[a]	0.37
	M2	29	11.01[a]	
	SH1	12	9.01[a]	
	SM1	4	9.63[a]	
	SM2	3	7.76 [a]	
	SM3	13	6.01[a]	
Aserima (n=46)	M2	14	15.20[a]	0.99
	SM3	32	15.78[a]	
Brownish (n=886)	H1	113	31.78[a]	0.31
	H2	12	20.11[a]	
	M1	129	22.57[a]	
	M2	85	23.46[a]	
	SH1	95	24.64[a]	
	SH2	318	42.41[a]	
	SM1	42	10.52[a]	
	SM2	92	24.04[a]	
Libework (n=193)	M1	11	13.06[a]	0.11
	M2	49	17.77[a]	
	SH1	26	14.85[a]	
	SM1	21	16.08[a]	
	SM2	25	13.29[a]	
	SM3	61	14.65[a]	
Multicolor (n=102)	H1	3	3.40[a]	0.67
	H2	3	3.54[a]	
	M1	8	2.36[a]	
	M2	51	6.74[a]	
	SH1	2	2.85[a]	
	SH2	6	3.89[a]	
	SM1	8	2.06[a]	
	SM2	21	5.83[a]	

AEZ = Agro ecologic Zone; N = Number of chicken reported with a given plumage in a given agro-ecology; Values with $P < 0.05$ are significantly different.

Table S 29. Significance test and LS means of shank colour variants across AEZ.

Shank color	AEZ	N	LSM	P-value
Yellow (n=4993)	H1	812	101.47[a]	0.49
	H2	233	77.83[a]	
	M1	578	64.20[a]	
	M2	520	65.02[a]	
	PH1	95	94.95[a]	
	SH1	49	24.70[a]	
	SH2	1752	109.52[a]	
	SH3	25	24.56[a]	
	SM1	379	94.67[a]	
	SM2	324	108.00[a]	
	SM3	226	113.00[a]	
White (n=2506)	H1	432	54.03[ab]	0.001
	H2	74	36.88[ab]	
	M1	244	24.43[ab]	
	M2	238	29.81[ab]	
	PH1	96	96.30[a]	
	SH1	13	4.306[b]	
	SH2	929	54.66[ab]	
	SH3	4	4.000[b]	
	SM1	100	25.03[ab]	
	SM2	217	108.50[a]	
	SM3	159	79.50[ab]	
Black (n=1036)	H1	114	22.76[a]	0.13
	H2	120	40.07[a]	
	M1	84	9.36[a]	
	M2	172	21.49[a]	
	PH1	28	28.35[a]	
	SH1	12	6.01[a]	
	SH2	313	18.39[a]	
	SH3	5	5.44[a]	
	SM1	31	7.73[a]	
	SM2	77	25.67[a]	
	SM3	80	40.00[a]	
Brown (n=42)	M2	20	20.30[a]	0.11
	SH2	22	7.21[a]	
Bluish black (n=35)	M1	29	14.50[a]	0.78
	SH2	6	6.00[a]	
Grey blue (n= 268)	H1	199	35.74[a]	0.52
	H2	262	5.55[a]	
	M1	8	25.08[a]	
	M2	2	1.61[a]	
	PH1	5	5.423[a]	

Shank color	AEZ	N	LSM	P-value
	SH2	54	8.96 [a]	
Green (n=290)	H1	20	10.22[b]	0.0001
	H2	64	64.00[a]	
	M1	42	6.93[b]	
	M2	46	9.22[b]	
	SH1	6	3.09[b]	
	SH2	18	3.05[b]	
	SH3	8	8.00[b]	
	SM1	5	2.50[b]	
	SM2	62	62.00[a]	
	SM3	19	9.500[b]	
Green blue (n=32)	H1	15		
	H2	11		
	M1	5		
	SH2	1		
Slated blue (n=41)	M1	37		
	SH2	4		
Red (n=217)	H1	4	1.33[c]	0.0001
	M1	33	33.07[b]	
	M2	10	3.34[c]	
	SH1	36	36.02[b]	
	SH2	134	133.90[a]	
Pale (n=320)	M1	146		
	SH1	59		
	SH2	115		
Mottled (n=14)	M1	13		
	SH2	1		

AEZ=Agro ecologic Zone; N= Number of chicken reported with a given shank colour in a given agro-ecology; Values with different letter superscripts across columns are significantly different (P<0.05).

Table S 30. Significance test and LS means of eye colour variants across AEZ.

Eye color	AEZ	N	LSM	P-value
Orange (n=388)	M1	158	95.72[a]	0.19
	M2	15	19.90[a]	
	SH2	195	129.79[a]	
	SM3	20	49.56[a]	
Black (n=773)	H2	46	46.00[a]	0.35
	M1	284	126.87[a]	
	M2	14	51.80[a]	
	SH1	105	105.00[a]	
	SH2	257	176.81	
	SM2	67	86.75[a]	
Pearl (n=19)	M1	6	5.16[a]	0.71
	M2	7	4.10[a]	
	SH2	6	5.37[a]	
Red (n=1200)	M1	53	90.36[a]	0.35
	M2	499	124.75[a]	
	SH2	20	109.05[a]	
	SM2	300	64.52[a]	
	SM3	328	136.35[a]	
Brown (n=438)	M1	1	58.73[a]	0.35
	M2	154	104.20[a]	
	SH2	1	44.30[a]	
	SM3	282	123.20[a]	
Blue black (n=367)	H2	139	139.00[a]	0.02
	M1	119	121.22[b]	
	SM2	109	117.89[b]	
Dark brown (n=63)	H2	15	22.00[a]	0.01
	M1	24	22.00[a]	
	SM2	24	15.00[b]	

AEZ=Agro ecologic Zone; N= Number of chicken reported with a given plumage in a given agro-ecology. Values with different letter superscripts across columns are significantly different ($P < 0.05$).

Table S 31. Significance test and LS means of neck feather colour variants across AEZ.

Neck feather color	AEZ	N	LSM	P-value
White (n=256)	H1	43	21.32[a]	0.28
	H2	24	24.00[a]	
	M1	19	19.00 [a]	
	M2	43	42.63[a]	
	SH2	28	28.42[a]	
	SM1	71	71.05[a]	
	SM2	28	28.00 [a]	
Black (n=139)	H1	14		
	H2	33		
	M1	43		
	M2	6		
	SM1	5		
	SM2	38		
Red (n=210)	H1	38	35.47 [a]	0.14
	H2	50	50.00 [a]	
	M1	59	59.00 [a]	
	M2	22	22.49 [a]	
	SH2	24	24.22 [a]	
	SM1	17	17.30 [a]	
Gebsima (n=22)	H1	9	4.62[a]	0.76
	M2	3	2.84[a]	
	SH2	5	4.97[a]	
	SM1	5	4.97[a]	
Teterima (n=18)	H1	7	3.47[a]	0.14
	M2	4	3.78[a]	
	SH2	1	0.63[a]	
	SM1	6	6.30[a]	
Brown (N=311)	H1	71	35.47[a]	0.23
	H2	69	69.00[a]	
	M1	58	58.00[a]	
	M2	26	25.95[a]	
	SH2	24	24.22[a]	
	SM1	14	13.84[a]	
	SM2	49	49.00[a]	
Kokima (n=4)	H1	1		
	M2	1		
	SH2	1		
	SM1	1		
Grey (n=32)	H1	1		
	H2	11		
	M1	10		
	M2	1		

Neck feather color	AEZ	N	LSM	P-value
	SH2	1		
	SM2	8		
Zigirima (n=47)	H1	15	7.73[a]	0.09
	M2	9	9.27[a]	
	SH2	19	18.54[a]	
	SM1	4	4.12[a]	
Gold (n=129)	H1	31	15.48[a]	0.16
	M2	31	30.96[a]	
	SH2	34	34.40[a]	
	SM1	33	32.68[a]	
Multiple (n=37)	H1	31	4.59[a]	0.29
	M2	2	2.04[a]	
	SH2	2	1.53[a]	
	SM1	2	2.04[a]	
Reddish brown (n=30)	H2	13		
	M1	11		
	SM2	6		

AEZ=Agro ecologic Zone; N= Number of chicken reported with a given plumage in a given agro-ecology; Values with different letter superscripts across columns are significantly different (P<0.05).

Table S 32. Significance test and LS means of skin colour variants across AEZ.

Skin color	AEZ	N	LSM	P-value
Yellow (N=1657)	H1	257	64.25[a]	0.66
	H2	125	125.00[a]	
	M1	208	69.33[a]	
	M2	344	68.81[a]	
	SH2	196	65.43[a]	
	SM1	204	101.88[a]	
	SM2	253	84.33[a]	
	SM3	70	23.33[a]	
White (N=2624)	H1	603	120.60[a]	0.57
	H2	28	28.00[a]	
	M1	226	56.48[a]	
	M2	423	84.60[a]	
	SH2	303	100.88[a]	
	SM1	262	130.63[a]	
	SM2	380	126.67[a]	
	SM3	399	133.00[a]	
Black (N=19)	M2	19		
Bluish black (n=190)	H2	20	20.00[a]	0.73
	M1	121	40.33[a]	

Skin color	AEZ	N	LSM	P-value
	SH2	2	2.00[a]	
	SM2	47	47.00[a]	
Pink (n=104)	H1	47		
	SM3	57		
Red (n=764)	H1	88	87.99[a]	0.07
	M1	192	192.06[a]	
	M2	117	29.25[a]	
	SH2	203	203.03[a]	
	SM3	164	82.00[a]	
Green (n=11; 0.20%)	M2	11		

AEZ = Agro ecologic Zone; N = Number of chicken reported with a given skin colour in a given agro-ecology; Values with different letter superscripts across columns are significantly different (P < 0.05).

Table S 33. Significance test and LS means of comb type variants across AEZ

Comb type	AEZ	N	LSM	P-value
Single (n=4279)	H1	1199	133.29[ab]	0.00
	H2	203	67.76[ab]	
	M1	434	47.22[ab]	
	M2	313	28.00[b]	
	PH1	190	39.15[b]	
	SH1	141	189.59[a]	
	SH2	1325	28.20[b]	
	SH3	7	88.35[ab]	
	SM1	39	7.00[b]	
	SM2	242	9.75[b]	
	SM3	186	40.33[b]	
Rose (n=3132)	H1	175	25.26[a]	0.03
	H2	200	66.56[ab]	
	M1	262	31.21[a]	
	M2	441	2.00[a]	
	PH1	57	61.59[ab]	
	SH1	51	56.55[a]	
	SH2	882	20.63[a]	
	SM1	193	62.27[ab]	
	SM1	519	48.25[a]	
	SM3	352	86.42[a]	
Pea (n=2136)	H1	322	35.73[a]	0.90
	H2	62	20.67[a]	
	M1	373	33.9[a]	
	M2	17	25.51[a]	
	PH1	23	23.16[a]	
	SH1	158	31.6[a]	

Comb type	AEZ	N	LSM	P-value
	SH2	686	45.72[a]	
	SM1	198	49.50[a]	
	SM3	297	20.83[a]	
Strawberry (n=35)	H1	12	4.00[a]	0.59
	M1	7	3.50[a]	
	M2	4	4.00[a]	
	SM1	3	8.00[a]	
	SH2	8	3.00 [a]	
	SM2	1	1.00[a]	
Walnut (n=246)	H1	43	21.50[a]	0.24
	H2	17	8.53[a]	
	M1	21	4.20[a]	
	M2	13	6.50[a]	
	SH1	2	1.00[a]	
	SH2	34	6.88[a]	
	SM1	9	4.50[a]	
	SM2	77	15.30[a]	
	SM3	30	30.00[a]	
Cushion (n=39)	M1	19		
	SH2	5		
V-shape (n=222)	H2	1	1.00[a]	0.43
	M1	15	3.75[a]	
	SH3	8	7.00[a]	
	SM1	15	8.00[a]	
Duplex (n=70)	H1	18	9.00[b]	0.03
	M1	13	6.50[b]	
	M2	82	27.32 [ab]	
	SH1	12	6.00 [b]	
	SH2	36	11.87[b]	
	SM3	61	61.00[a]	
Butter cup (n=9)	M1	3		
	SH2	6		
Unclassified (n=3)	M1	1		
	SM3	2		

AEZ = Agro ecologic Zone; N = Number of chicken reported with a given comb type in a given agro-ecology; Values with different letter superscripts across columns are significantly different ($P < 0.05$).

Table S 34. Significance test and LS means of feather distribution variants across AEZ.

Feather distribution	AEZ	N	LSM	P-value
Normal (n=10715)	H1	2925	205.90[ab]	0.001
	H2	523	249.98[a]	
	M1	150	100.00[b]	
	M2	333	218.25[ab]	
	PH1	513	254.91[a]	
	SH2	4806	239.01a	
	SM1	1090	158.67[ab]	
	SM2	375	135.00[ab]	
Necked Neck (n=347)	H1	86	12.34	0.59
	H2	8	8.41	
	M2	7	6.75	
	PH1	15	15.43	
	SH2	231	25.67	
Crest (n=547)	H1	39	19.43[b]	0.0001
	H2	22	22.04[b]	
	PH1	15	15.43[b]	
	SH2	137	17.06[b]	
	SM1	229	114.50[a]	
	SM2	105	105.00[a]	
Shank and feet (n=76)	H1	15	15.37[a]	0.71
	H2	10	9.57[a]	
	PH1	2	2.32[a]	
	SH2	49	8.12[a]	
Muff and beard (n=82)	PH1	2	2.32[a]	0.46
	SH2	36	7.13[a]	
	H1	44	7.69[a]	
Silky (n = 623)	H1	194	96.86[a]	0.28
	M2	110	109.69[a]	
	PH1	9	9.31[a]	
	SH2	219	54.86[a]	
	SM1	91	91.13[a]	
Frizzle (n = 234)	PH1	34	22.33[a]	0.52
	SH2	200	32.09[a]	
Body shape	**AEZ**		**LSM**	**P-value**
Blocky	H1		191.25[a]	0.06
	M1		11.00[a]	
	M2		99.23[a]	
	SH2		202.50[a]	
	SM1		198.00 [a]	
	SM2		30.00[a]	
	SM3		4.95[a]	

Triangle	H1	29.25[a]	0.21
	M1	9.00[a]	
	M2	37.01[a]	
	SH2	18.00[a]	
	SM1	9.00[a]	
	SM2	72.75[a]	
	SM3	49.50[a]	
Wedge	H1	4.50[ab]	0.02
	M1	80.00[ab]	
	M2	14.49[ab]	
	SH2	4.50[ab]	
	SM1	18.00[ab]	
	SM2	47.25[ab]	
	SM3	95.55[ab]	

AEZ=Agro ecologic Zone; N= Number of chicken reported with a given feather morphology in a given agro-ecology; Values with different letter superscripts across columns are significantly different ($P < 0.05$).

Table S 35. Significance test and LS means of morphometric traits of chicken across dominant religion.

Dominant religion	BW	EN	BDL	WS	NL	CH	CL	WL	SL	SC	KBL	CC	BAL	BKL	SPL
Protestant	1.66^{a}	59.48^{a}	35.71^{a}	48.43^{a}	14.82^{a}	1.63^{a}	3.64^{a}	2.12^{a}	8.79^{a}	2.34^{ab}	10.74^{a}	26.579^{a}	20.43^{a}	2.11^{a}	0.33^{a}
Muslim	1.53^{a}	56.62^{a}	27.97^{bc}	28.37^{a}	10.28^{a}	1.66^{a}	3.72^{a}	1.72^{a}	8.57^{a}	3.75^{a}	10.87^{a}	27.966^{a}	19.62 ^{ab}	1.89^{a}	0.33^{a}
Orthodox	1.47^{a}	52.59^{a}	33.39^{ab}	30.78^{a}	8.79^{a}	1.89^{a}	3.14^{a}	2.10^{a}	8.31^{a}	1.35^{b}	9.95^{a}	25.61^{a}	17.94^{b}	2.26^{a}	0.33^{a}
Traditional	1.47^{a}	59.48^{a}	13.39^{c}	19.86^{b}	12.35^{a}	2.12^{a}	2.84 ^{a}	1.16^{a}	6.44^{a}	2.33^{ab}	9.54^{a}	26.579^{a}	18.03^{ab}	2.11^{a}	0.33^{a}
P-value	0.77	0.73	0.00	0.002	0.78	0.79	0.61	0.68	0.16	0.04	0.70	0.432	0.02	0.83	1.00
Elevation(m)	**BW**	**EN**	**BDL**	**WS**	**NL**	**CH**	**CL**	**WL**	**SL**	**SC**	**KBL**	**CC**	**BAL**	**BKL**	**SPL**
500-1800	1.31^{a}	59.98^{a}	33.75^{a}	37.52^{a}	16.46^{a}	1.77^{a}	3.42^{a}	2.24^{a}	8.36^{b}	2.50^{a}	9.81^{a}	25.71^{a}	19.50^{a}	1.99^{a}	0.33^{a}
1800-2400	1.37^{a}	54.04^{a}	31.07^{a}	29.97^{a}	12.50^{a}	1.88^{a}	3.31^{a}	1.98^{a}	8.23^{ab}	1.89^{a}	10.41^{a}	26.49^{a}	18.54^{a}	2.31^{a}	0.33^{a}
2400-3200	1.36^{a}	43.16^{a}	34.98^{a}	37.83^{a}	9.71^{a}	1.64^{a}	3.33^{a}	1.93^{ab}	8.72^{b}	0.58^{a}	11.76^{a}	27.12^{a}	18.18^{a}	2.41^{a}	0.33^{a}
P-value	0.14	0.24	0.41	0.71	0.05	0.93	0.99	0.02	0.00	0.17	0.29	0.52	0.56	0.62	1.00

Values with different superscripts across columns are significantly different ($P < 0.05$).

Table S 36. Significance test and LS means of morphometric traits of chicken across AEZ.

Traits	AEZ	Minimum	Maximum	Mean	SD	LS means	SE	P-value
Body weight	H1	1.21	1.61	1.34	0.153	1.35[a]	0.11	0.82
	H2	1.24	1.24	1.24	0.153	1.04[a]	0.17	
	M1	0.95	1.52	1.22	0.220	1.22[a]	0.10	
	M2	0.84	1.54	1.27	0.195	1.28[a]	0.07	
	SH1	1.18	1.40	1.29	0.111	1.29[a]	0.17	
	SH2	0.98	1.54	1.25	0.222	1.25[a]	0.08	
	SM1	0.90	1.98	1.35	0.323	1.35[a]	0.09	
	SM2	1.05	1.58	1.20	0.195	1.19[a]	0.11	
	SM3	1.18	1.22	1.20	0.015	1.20[a]	0.14	
No. of eggs/hen/year	H2	62.95	62.95	62.95	0.00	62.95[a]	8.24	0.08
	M1	53.00	76.00	63.00	9.63	63.00[a]	4.76	
	M2	47.51	61.30	53.81	5.07	53.81[a]	4.12	
	SH1	75.00	75.00	75.00	5.07	75.00[a]	8.24	
	SH2	72.00	75.60	73.57	1.51	73.57[a]	4.76	
	SM1	54.90	75.96	65.43	10.53	65.43[a]	5.83	
	SM2	55.98	58.77	57.38	1.40	55.98[a]	8.24	
	SM3	47.35	49.13	48.24	0.89	48.24[a]	5.83	
Body length	H1	17.73	38.80	29.91	9.59	36.32[a]	3.19	0.03
	H2	18.67	23.35	21.77	2.20	35.23[a]	4.12	
	M1	18.92	34.40	22.19	4.50	35.15[a]	2.38	
	M2	17.58	37.51	27.40	8.38	29.91[a]	2.52	
	PH1	18.00	35.35	26.68	8.68	27.40[a]	5.04	
	SH2	18.28	37.57	24.19	6.69	26.68[a]	2.38	
	SM1	34.60	35.85	35.23	0.63	24.19[a]	5.04	
	SM2	33.75	36.80	35.15	1.26	22.19[a]	4.12	
	SM3	35.15	37.28	36.32	0.88	21.77[a]	4.12	
Wing span	H1	59.50	61.83	60.86	0.99	60.86[ab]	9.24	0.01
	H2	7.42	7.76	7.59	0.17	7.59[b]	11.32	
	M1	7.64	66.77	25.83	18.94	25.83[ab]	5.34	
	M2	35.50	46.15	39.56	3.98	39.56[ab]	8.00	
	PH1	38.49	38.49	38.49	3.98	38.49[ab]	16.01	
	SH1	14.09	14.85	14.47	0.38	14.47[b]	11.32	
	SH2	73.92	73.92	73.92	0.38	73.9152[a]	16.01	
	SM1	13.84	69.90	50.76	26.12	50.76[ab]	9.24	
	SM2	35.75	43.80	38.95	3.49	38.95[ab]	9.24	
	SM3	38.05	40.59	39.16	1.06	39.16[ab]	9.24	
Shank length	H1	8.60	9.45	9.00	0.34	9.33[a]	0.44	0.06
	H2	6.98	9.02	7.67	0.95	9.00[a]	0.57	
	M1	6.95	9.94	8.84	0.75	9.00[a]	0.31	
	M2	6.36	11.23	8.67	1.58	8.84[a]	0.38	

Traits	AEZ	Minimum	Maximum	Mean	SD	LS means	SE	P-value
	PH1	7.03	7.03	7.03	1.58	8.67[a]	0.99	
	SH1	9.15	9.50	9.33	0.18	8.16[a]	0.70	
	SH2	7.80	10.27	9.00	0.69	7.94[a]	0.35	
	SM1	7.40	9.42	8.16	0.77	7.67[a]	0.50	
	SM2	7.65	8.35	7.94	0.30	7.03[a]	0.57	
	SM3	6.26	8.40	7.03	0.97	7.03[a]	0.57	
Comb height	H1	1.48	1.61	1.56	0.06	2.38[a]	0.32	0.47
	M1	1.58	1.68	1.63	0.05	1.56[a]	0.39	
	M2	1.89	2.05	1.96	0.06	1.63[a]	0.32	
	PH1	1.50	1.50	1.50	0.06	1.96[a]	0.56	
	SH2	1.47	1.47	1.47	0.06	1.50[a]	0.56	
	SM1	1.06	1.41	1.23	0.18	1.47[a]	0.39	
	SM2	1.30	2.95	2.38	0.77	1.23[a]	0.32	
	SM3	1.19	2.75	1.90	0.64	1.90[a]	0.32	
Comb length	H1	3.57	3.93	3.80	0.17	3.80[a]	0.23	0.02
	H2	3.65	3.96	3.80	0.16	3.80[a]	0.28	
	M1	3.41	4.09	3.77	0.28	3.77[a]	0.23	
	M2	2.15	3.12	2.67	0.40	2.67[a]	0.23	
	PH1	2.72	2.72	2.72	0.40	2.72[a]	0.40	
	SH2	4.13	4.13	4.13	0.40	4.13[a]	0.40	
	SM1	3.48	3.85	3.67	0.19	3.67[a]	0.28	
	SM2	2.75	3.64	3.18	0.36	3.18[a]	0.23	
	SM3	2.30	3.28	2.92	0.44	2.92[a]	0.23	
Wattle length	H1	2.01	2.34	2.19	0.14	2.19[a]	0.28	0.42
	H2	2.09	2.12	2.10	0.01	2.10[a]	0.34	
	M1	1.85	2.05	1.94	0.08	1.94[a]	0.28	
	M2	0.92	2.60	1.62	0.66	1.62[a]	0.24	
	PH1	2.27	2.27	2.27	0.66	2.27[a]	0.49	
	SH2	1.35	2.16	1.73	0.34	1.73[a]	0.24	
	SM1	1.80	1.96	1.88	0.08	1.88[a]	0.34	
	SM2	1.84	3.50	2.56	0.69	2.56[a]	0.28	
	SM3	1.92	2.25	2.07	0.14	2.07[a]	0.28	
Keel bone length	H1	10.92	11.07	11.00	0.06	11.0[ab]	0.85	0.03
	H2	9.17	9.36	9.26	0.10	9.26[ab]	1.05	
	M1	9.35	13.82	11.58	2.24	11.58[ab]	1.05	
	M2	7.80	8.84	8.36	0.43	8.36[b]	0.85	
	PH1	9.41	9.41	9.41	0.43	9.41[ab]	1.48	
	SH2	15.00	15.00	15.00	0.43	15.00 [a]	1.48	
	SM1	12.70	13.05	12.88	0.18	12.88[ab]	1.05	
	SM2	8.05	12.75	9.93	2.03	9.93[ab]	0.85	
	SM3	8.44	9.75	8.90	0.60	8.90[ab]	0.85	
Shank circumference	H2	3.64	3.71	3.68	0.04	3.68[a]	0.87	0.1

Traits	AEZ	Minimum	Maximum	Mean	SD	LS means	SE	P-value
	M1	0.65	3.77	1.97	1.46	1.97[a]	0.46	
	M2	3.45	4.08	3.71	0.27	3.71[a]	0.71	
	PH1	3.18	3.18	3.18	0.27	3.18[a]	1.23	
	SH1	0.72	0.75	0.73	0.02	0.73[a]	0.87	
	SM1	0.62	0.62	0.62	0.02	0.61[a]	1.23	
Neck length	H1	16.66	18.03	17.17	0.61	17.17[a]	0.47	0.04
	M2	11.73	11.73	11.73	0.61	11.73[b]	0.81	
	SM3	10.28	11.58	10.93	0.65	10.93[b]	0.57	
Chest circumference	M1	25.39	28.04	26.57	1.10	26.57[a]	0.82	0.31
	M2	25.48	28.81	27.14	1.67	27.14[a]	1.00	
	SH2	29.15	29.15	29.15	1.67	29.15[a]	1.42	
	SM1	25.85	26.60	26.23	0.38	26.23[a]	1.00	
	SM2	25.85	25.85	25.85	0.38	25.85[a]	1.42	
	SM3	24.03	25.11	24.57	0.54	24.57[a]	1.00	
Back length	H1	20.02	20.90	20.55	0.38	20.55[a]	0.28	0.01
	M1	19.79	19.79	19.79	0.38	19.79[ab]	0.49	
	M2	17.63	17.63	17.63	0.38	17.63[ab]	0.49	
	SH2	20.55	20.55	20.55	0.38	20.55[a]	0.49	
	SM1	18.10	18.85	18.48	0.38	18.48[ab]	0.35	
	SM2	18.25	18.25	18.25	0.38	18.25[ab]	0.49	
	SM3	16.56	17.27	16.91	0.36	16.91 b	0.35	
Beak length	H2	1.87	1.92	1.90	0.02	1.90	0.97	0.39
	M1	1.93	1.93	1.93	0.02	1.93	1.37	
	M2	1.45	4.70	3.08	1.63	3.08	0.97	
	PH1	3.51	3.51	3.51	1.63	3.51	1.37	
	SM2	4.60	5.40	5.00	0.40	5.00	0.97	
	SM3	4.80	4.80	4.80	0.40	4.80	1.37	
Spur length	M1	0.80	2.90	2.14	0.95	2.14	0.89	0.69
	M2	0.17	3.62	1.51	1.51	1.51	0.89	
	PH1	0.57	0.57	0.57	1.51	0.57	1.54	

NS = Number of sample birds; Values with different letter superscripts across columns are significantly different ($P < 0.05$).

Table S 37. Significant test and LS means of genetic parameters across religion

Religion	MNA	ENA	APL	PA	OH	EH	FIS	PIC	IBS
Traditional	5.01[a]	10.62[b]	4.68[a]	2.81[a]	0.53[a]	0.62[a]	0.08[a]	0.65[a]	0.73[a]
Orthodox	5.39[a]	3.39 [a]	5.00[a]	2.75[a]	0.90[a]	0.44[a]	0.08[a]	0.63[a]	0.73[a]
Muslim	4.90[a]	10.62[b]	4.79[a]	3.19[a]	0.48[a]	0.55[a]	0.07[a]	0.53[a]	0.74[a]
Protestant	5.29[a]	5.10[a]	4.66[a]	3.56[a]	0.58[a]	0.57[a]	0.06[a]	0.52[a]	0.73[a]
P-value	0.70	0.01	0.77	0.81	0.40	0.29	0.94	0.32	0.99
Elevation	**MNA**	**ENA**	**APL**	**PA**	**OH**	**EH**	**FIS**	**PIC**	**IBS**
1	5.25[a]	5.05[a]	4.84[a]	3.53[a]	0.87[a]	0.47[a]	0.09[a]	0.63[a]	0.00[a]
2	5.45[a]	5.78[a]	4.96[a]	2.74[a]	0.88[a]	0.45[a]	0.06[a]	0.62[a]	0.00[a]
3	5.13[a]	3.75[a]	4.90[a]	2.41[a]	0.50[a]	0.55[a]	0.07[a]	0.51[a]	0.00[a]
P-value	0.68	0.58	0.93	0.210	0.29	0.42	0.48	0.11	1.00

Table S 38. Significance test and LS means of genetic parameter estimate variation across AEZ

Parameters	AEZ	Min	Max	Mean	SD	LS means	SE	P-value
Mean number of alleles	H1	5.00	5.00	5.00	0.00	5.00[a]	0.23	0.04
	H2	5.20	5.30	5.25	0.05	5.25[a]	0.36	
	M1	4.85	4.85	4.85	0.00	4.85[a]	0.36	
	M2	4.20	6.29	5.60	0.75	5.60[a]	0.16	
	SH1	6.15	6.15	6.15	0.75	6.15[a]	0.50	
	SH2	4.60	5.50	4.86	0.37	4.86[a]	0.17	
	SM2	5.27	5.43	5.30	0.06	5.30[a]	0.23	
Observed Homozygosity	H1	0.27	0.55	0.38	0.14	0.38[a]	0.07	0.07
	H2	0.45	0.55	0.50	0.05	0.50[a]	0.11	
	M1	0.57	0.93	0.75	0.18	0.75[a]	0.11	
	M2	0.27	0.84	0.60	0.19	0.60[a]	0.05	
	SH1	0.79	0.79	0.79	0.19	0.79[a]	0.16	
	SH2	0.27	0.63	0.49	0.12	0.49[a]	0.05	
	SM2	0.49	0.75	0.58	0.09	0.58[a]	0.07	
Expected heterozygosity	H1	0.59	0.59	0.59	0.00	0.59[a]	0.04	0.19
	H2	0.54	0.55	0.55	0.01	0.55[a]	0.06	
	M1	0.54	0.61	0.58	0.04	0.58[a]	0.06	
	M2	0.32	0.61	0.57	0.09	0.57[a]	0.03	
	SH1	0.32	0.32	0.32	0.09	0.32[a]	0.09	
	SH2	0.33	0.63	0.56	0.09	0.56[a]	0.03	
	SM2	0.33	0.62	0.53	0.10	0.53[a]	0.04	
Polymorphic information content	H1	0.47	0.47	0.47	0.00	0.47[a]	0.02	0.0001
	H2	0.47	0.47	0.47	0.00	0.47[a]	0.04	

Parameters	AEZ	Min	Max	Mean	SD	LS means	SE	P-value
	M1	0.67	0.67	0.67	0.00	0.67[a]	0.04	
	M2	0.49	0.71	0.64	0.08	0.64[a]	0.02	
	SH1	0.72	0.72	0.72	0.08	0.72[a]	0.05	
	SH2	0.52	0.54	0.54	0.01	0.54[a]	0.02	
	SM2	0.68	0.68	0.68	0.00	0.68[a]	0.02	
Coefficient of inbreeding	H1	0.07	0.08	0.07	0.01	0.07[ab]	0.02	0.03
	H2	0.17	0.17	0.17	0.01	0.17[a]	0.02	
	M1	0.08	0.08	0.08	0.01	0.08[ab]	0.02	
	M2	0.06	0.09	0.07	0.01	0.07[ab]	0.02	
	SH2	0.02	0.08	0.05	0.02	0.05[b]	0.01	
	SM2	0.05	0.11	0.08	0.02	0.08[ab]	0.01	
Effective number of alleles	H1	5.35	6.10	5.73	0.38	5.73[a]	1.33	0.68
	H2	2.53	2.53	2.53	0.38	2.53[a]	1.88	
	M1	6.10	6.10	6.10	0.38	6.1[a]	1.88	
	SH2	5.65	5.65	5.65	0.38	5.65[a]	1.88	
	SM2	2.67	6.35	4.51	1.84	4.5[a]	1.33	
Alleles per locus	M2	5.00	5.00	5.00	1.84	5.00[ab]	0.05	0.04
	SH2	4.70	4.70	4.70	0.00	4.70[b]	0.04	
	SM2	5.00	5.10	5.05	0.05	5.05[a]	0.04	
Private alleles	H2	3.00	3.00	3.00	0.05	3.00[a]	0.87	0.94
	M2	3.35	3.35	3.35	0.05	3.35[a]	0.87	
	SH2	2.45	3.60	3.03	0.58	3.03[a]	0.61	
	SM2	2.00	3.75	2.77	0.73	2.77[a]	0.50	
Identity buy state	H1	0.74	0.74	0.74	0.00	0.74[a]	0.01	0.55
	M2	0.73	0.74	0.74	0.00	0.74[a]	0.01	
	SH2	0.72	0.74	0.73	0.01	0.73[a]	0.01	

N = No. of sampled birds; Values with P < 0.05 are significant difference.

Table S 39. Overall allele frequency (%) of LEI0258 in indigenous chicken by allele size.

Allele	Count	Frequency	Standard deviation
185	1	0.002	0.002
197	57	0.121	0.015
209	9	0.019	0.006
221	11	0.023	0.008
245	3	0.006	0.002
253	36	0.076	0.012
263	37	0.078	0.012
289	1	0.002	0.002
300	29	0.061	0.012
302	21	0.045	0.010
312	4	0.009	0.005
315	39	0.083	0.014
325	77	0.163	0.018
327	3	0.006	0.004
340	12	0.025	0.008
351	20	0.042	0.010
363	15	0.032	0.010
375	42	0.089	0.014
385	21	0.045	0.009
397	8	0.017	0.007
411	3	0.006	0.004
426	2	0.004	0.003
450	4	0.009	0.004
460	2	0.004	0.003
465	5	0.012	0.005
472	1	0.002	0.002
485	2	0.004	0.003
525	3	0.006	0.004
569	4	0.009	0.006

Table S 40. Pairwise population matrix of Nei Unbiased Genetic Distance across populations.

Pop	BA	SU	AS	GA	AD	EN	HU	KE	GE	KI	TT	AR	AS	DI	BG	SG	KU	LO	HA	MI	GI	ME	AL	NA
BA	1.00																							
SU	0.62	1.00																						
ASH	0.55	0.56	1.00																					
GA	0.88	0.60	0.66	1.00																				
AD	0.39	0.34	0.31	0.39	1.00																			
EN	0.78	0.62	0.67	0.81	0.58	1.00																		
HU	0.14	0.08	0.33	0.20	0.28	0.29	1.00																	
KE	0.46	0.60	0.56	0.41	0.51	0.42	0.33	1.00																
GE	0.70	0.54	0.37	0.54	0.22	0.37	0.29	0.44	1.00															
KI	0.61	0.51	0.52	0.58	0.24	0.40	0.24	0.49	0.71	1.00														
TT	0.43	0.61	0.57	0.60	0.39	0.66	0.10	0.49	0.33	0.45	1.00													
AR	0.59	0.55	0.65	0.59	0.38	0.46	0.36	0.59	0.79	0.61	0.42	1.00												
AS	0.71	0.59	0.57	0.79	0.38	0.78	0.20	0.40	0.53	0.67	0.64	0.58	1.00											
DI	0.63	0.63	0.58	0.74	0.39	0.70	0.24	0.39	0.60	0.78	0.76	0.60	0.80	1.00										
BG	0.71	0.59	0.50	0.73	0.32	0.62	0.21	0.59	0.59	0.41	0.62	0.57	0.55	0.54	1.00									
SG	0.21	0.44	0.38	0.26	0.19	0.28	0.05	0.50	0.33	0.21	0.63	0.44	0.30	0.33	0.65	1.00								
KU	0.67	0.57	0.87	0.74	0.41	0.69	0.28	0.52	0.36	0.47	0.41	0.60	0.56	0.52	0.54	0.20	1.00							
LO	0.70	0.56	0.72	0.71	0.25	0.63	0.21	0.49	0.59	0.77	0.59	0.70	0.75	0.78	0.59	0.43	0.63	1.00						
HA	0.73	0.56	0.76	0.71	0.38	0.65	0.37	0.62	0.75	0.63	0.47	0.85	0.63	0.64	0.67	0.48	0.68	0.75	1.00					
MI	0.46	0.66	0.61	0.58	0.35	0.59	0.44	0.64	0.54	0.60	0.84	0.64	0.67	0.78	0.64	0.58	0.47	0.69	0.57	1.00				
GI	0.67	0.55	0.52	0.75	0.40	0.76	0.19	0.36	0.55	0.66	0.85	0.49	0.78	0.92	0.58	0.35	0.43	0.73	0.58	0.75	1.00			
ME	0.83	0.56	0.62	0.82	0.32	0.65	0.25	0.44	0.80	0.65	0.56	0.77	0.67	0.71	0.70	0.30	0.62	0.73	0.80	0.61	0.76	1.00		
AL	0.94	0.61	0.61	0.90	0.34	0.75	0.18	0.46	0.77	0.72	0.59	0.68	0.78	0.77	0.72	0.29	0.62	0.78	0.77	0.61	0.82	0.93	1.00	
NA	0.36	0.30	0.27	0.37	0.64	0.29	0.35	0.57	0.55	0.36	0.17	0.67	0.31	0.38	0.32	0.13	0.29	0.28	0.60	0.31	0.31	0.49	0.41	1.00

BA = Batambe; SU = Surta; ASH = Amesha Shinkuri; GA = Gafera; AD = 025-Adane; ME= Meseret; HU= Hugub; KE = Kefis; GE = Gesses; KI = Kido; TT = Tsion Teguaz; AR = Arabo; AS = Ashuda; DI = Dikuli; BG = Bekele Girisa; SG = Shumbi Gemo; KU = Kumato; LO = Loya; HA = Hadushi Adi; MI = Mihiquan; GI = Gijet; ME = Metkilimat; AL = Alifa Midir; NA = Negasi Amba.

Table S 41. Pairwise population matrix of Nei Unbiased Genetic Distance across MAEZ.

MEZ	A1	M1	M2	M3	SA2	SH1	SH2	SM2
A1	0.000							
M1	1.040	0.000						
M2	1.299	0.356	0.000					
M3	1.239	0.687	0.000	0.000				
SA2	2.851	1.382	0.798	0.860	0.000			
SH1	1.054	1.378	0.024	0.008	1.146	0.000		
SH2	1.373	0.735	0.109	0.041	0.985	0.146	0.000	
SM2	1.362	0.490	0.000	0.000	0.669	0.000	0.000	0.000

A1 = Hot to warm arid lowland plains; M1 = Hot to warm moist lowlands; M2 = Tepid to cool moist mid highlands; M3 = Cold to very cold moist sub-afro-alpine to afro-alpine; SA2 = Tepid to cool semi-arid mid highlands; SH1 = Hot to warm sub-humid lowlands; SH2 = Tepid to cool sub humid mid highlands; SM2 = Tepid to cool sub-moist mid highlands.

Table S 42. Pairwise population F_{ST} values.

PO	BA	SU	AS	GA	AD	EN	HU	KE	GE	KI	TT	AR	AS	DI	BG	SG	KU	LO	HA	MI	GI	ME	AL	NA
BA	0																							
SU	0.04	0																						
ASH	0.05	0.04	0																					
GA	0.02	0.04	0.03	0																				
AD	0.07	0.06	0.06	0.06	0																			
EN	0.05	0.03	0.02	0.03	0.04	0																		
HU	0.12	0.11	0.08	0.10	0.09	0.08	0																	
KE	0.06	0.03	0.04	0.05	0.04	0.04	0.07	0																
GE	0.04	0.05	0.06	0.05	0.08	0.06	0.09	0.05	0															
KI	0.04	0.04	0.04	0.04	0.07	0.05	0.08	0.04	0.03	0														
TT	0.07	0.04	0.04	0.04	0.06	0.02	0.11	0.04	0.07	0.05	0													
AR	0.04	0.03	0.02	0.03	0.05	0.03	0.06	0.02	0.02	0.02	0.04	0												
AS	0.03	0.03	0.04	0.02	0.05	0.02	0.09	0.04	0.04	0.03	0.03	0.03	0											
DI	0.04	0.03	0.04	0.02	0.05	0.03	0.09	0.05	0.04	0.02	0.02	0.03	0.02	0										
BG	0.03	0.03	0.04	0.02	0.06	0.03	0.08	0.03	0.04	0.04	0.03	0.02	0.03	0.03	0									
SG	0.09	0.06	0.06	0.08	0.08	0.05	0.12	0.05	0.07	0.07	0.04	0.04	0.06	0.06	0.03	0								
KU	0.04	0.04	0.01	0.02	0.05	0.03	0.08	0.04	0.06	0.04	0.05	0.03	0.03	0.04	0.03	0.07	0							
LO	0.03	0.03	0.02	0.03	0.06	0.02	0.08	0.03	0.03	0.02	0.03	0.01	0.02	0.02	0.02	0.05	0.02	0						
HA	0.03	0.03	0.02	0.03	0.05	0.03	0.07	0.02	0.02	0.02	0.04	0.01	0.02	0.03	0.02	0.04	0.02	0.01	0					
MI	0.05	0.03	0.03	0.03	0.05	0.02	0.06	0.02	0.04	0.03	0.01	0.02	0.02	0.02	0.02	0.04	0.03	0.02	0.02	0				
GI	0.04	0.04	0.04	0.02	0.06	0.03	0.10	0.05	0.04	0.03	0.01	0.04	0.02	0.01	0.03	0.06	0.05	0.02	0.03	0.02	0			
ME	0.02	0.04	0.03	0.02	0.06	0.03	0.08	0.04	0.02	0.03	0.04	0.01	0.02	0.02	0.02	0.06	0.03	0.02	0.01	0.02	0.02	0		
AL	0.01	0.04	0.04	0.01	0.07	0.04	0.10	0.05	0.02	0.03	0.04	0.03	0.02	0.02	0.02	0.07	0.03	0.02	0.02	0.03	0.02	0.01	0	
NA	0.09	0.08	0.08	0.08	0.05	0.08	0.10	0.05	0.06	0.07	0.10	0.04	0.08	0.07	0.07	0.11	0.08	0.07	0.04	0.07	0.08	0.06	0.07	0

BA = Batambe; SU = Surta; ASH = Amesha Shinkuri; GA = Gafera; AD = 025-Adane; ME= Meseret; HU= Hugub; KE = Kefis; GE = Gesses; KI = Kido; TT = Tsion Teguaz; AR = Arabo; AS = Ashuda; DI = Dikuli; BG = Bekele Girisa; SG = Shumbi Gemo; KU = Kumato; LO = Loya; HA = Hadushi Adi; MI = Mihiquan; GI = Gijet; ME = Metkilimat; AL = Alifa Midir; NA = Negasi Amba.

Table S 43. Pairwise Population FST values by MAEZ.

MAEZ	A1	M1	M2	M3	SA2	SH1	SH2	SM2
A1	0.000							
M1	0.090	0.000						
M2	0.079	0.042	0.000					
M3	0.090	0.059	0.018	0.000				
SA2	0.117	0.083	0.055	0.066	0.000			
SH1	0.081	0.071	0.024	0.023	0.068	0.000		
SH2	0.092	0.060	0.029	0.025	0.068	0.030	0.000	
SM2	0.081	0.047	0.015	0.013	0.052	0.016	0.018	0.000

A1 = Hot to warm arid lowland plains; M1 = Hot to warm moist lowlands; M2 = Tepid to cool moist mid highlands; M3 = Cold to very cold moist sub-afro-alpine to afro-alpine; SA2 = Tepid to cool semi-arid mid highlands; SH1 = Hot to warm sub-humid lowlands; SH2 = Tepid to cool sub humid mid highlands; SM2 = Tepid to cool sub-moist mid highlands.

Table S 44. Pair wise genetic distance between Ethiopian chickens based on microsatellite LEI0258 sequences.

1	3	4	5	6	7	8	9	10	11	12	13	14	15	17	18	19	20	21	22	23	Chickens
0	23.8	49.2	26.4	48.7	48.7	48.7	48.7	48.7	48.7	48.7	25.9	25.9	25.9	25.9	26.9	25.9	48.7	48.7	48.7	51.3	**Batanbe_4H 1**
	0	48.4	21.7	51.2	51.2	51.2	51.2	51.2	51.2	51.2	22.6	22.6	22.6	22.6	23.5	22.6	51.2	51.2	51.2	51.6	**Meseret_156b 3**
		0	46.2	50.4	50.4	49.6	50.0	50.0	50.4	50.4	48.3	48.3	48.3	48.3	48.3	48.3	50.4	50.4	50.4	60.2	**Hugub_H2 4**
			0	53.6	53.6	51.6	51.6	54.0	54.0	54.0	20.8	20.8	21.2	21.2	22.0	21.2	54.4	54.4	54.4	54.4	**Tsion_9C 5**
				0	0	15.2	14.8	17.3	16.6	16.6	51.6	51.6	53.4	51.9	53.7	53.7	19.4	19.4	19.4	51.6	**Ashuda_1C 6**
					0	15.2	14.8	17.3	16.6	16.6	51.6	51.6	53.4	51.9	53.7	53.7	19.4	19.4	19.4	51.6	**Kefis_12C 7**
						0	0.3	14.9	14.6	14.6	52.9	52.9	52.5	53.9	52.5	54.2	19.0	19.0	19.0	51.9	**BekeleGirisa_8H 8**
							0	15.3	14.2	14.2	52.9	52.9	52.5	53.9	52.5	54.2	18.6	18.6	18.6	52.2	**ShubiGemo_1H 9**
								0	1.0	1.0	54.1	54.1	53.1	53.1	54.7	53.4	18.6	18.6	18.6	53.1	**Ashuda_10H 10**
									0	0	54.1	54.1	53.1	52.8	54.4	53.1	17.9	17.9	17.9	53.1	**Dikuli_4H 11**
										0.0	54.1	54.1	53.1	52.8	54.4	53.1	17.9	17.9	17.9	53.1	**Gijet_49H 12**
											0	0	13.6	14.9	17.2	17.8	55.7	55.7	55.7	51.8	**Gafera_8C 13**
												0	13.6	14.9	17.2	17.8	55.7	55.7	55.7	51.8	**Ashuda_9C 14**
													0	13.1	15.3	15.9	57.0	56.7	56.7	52.0	**Dikuli_7H 15**
														0	12.9	13.8	55.9	56.2	56.2	53.5	**NgasiAmba_4H 17**
															0	12.8	58.0	58.0	58.0	55.1	**Hugub_H9 18**
																0	57.7	57.7	57.7	54.9	**Adane_9C 19**
																	0	0.3	0.3	55.4	**BekeleGirisa_H1 20**
																		0	0	55.2	**Kumato_2C 21**
																			0	55.2	**Kumato_5H 22**
																				0	**Surta_7H 23**

Appendix 1. Raw sequences of LEI0258 alleles in indigenous chicken of Ethiopia.

R13: ATGTCTTCTTTCT

R12: TTCCTTCTTTCT

>Batambe_4H (Accession No. MG495227)
CACGCAGCAGAACTTGGTAAGGGAATTCCCTCCCTGGGTTTGTTCTCTTGTTTTTCTCTTTTGGAGGGGGATTTTTTCTATGTCTTCTTTCTTTCCTT
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>Meseret_156b (Accession No. MG495229)
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>Hugub_H2 (Accession No. MG495230)
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>Tsion_9C (Accession No. MG495231)
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>Ashuda_1C ((Accession No. MG495232)
CACGCAGCAGAACTTGGTAAGGGAATTCCCTCCCTGGGTTTGTTCTCATTTTTCTCTTTTGGAGGGGGATTTTTTCTATGTCTTCTTTCTTTCCTTCT
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>Kefis_12C (Accession No. MG495233)
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>BekeleGirisa_8H (Accession No. MG495234)
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>ShubiGemo_1H (Accession No. MG495235)
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>NegasiAmba_4H (Accession No. MG495243)

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>Adane_9C (Accession No. MG495245)
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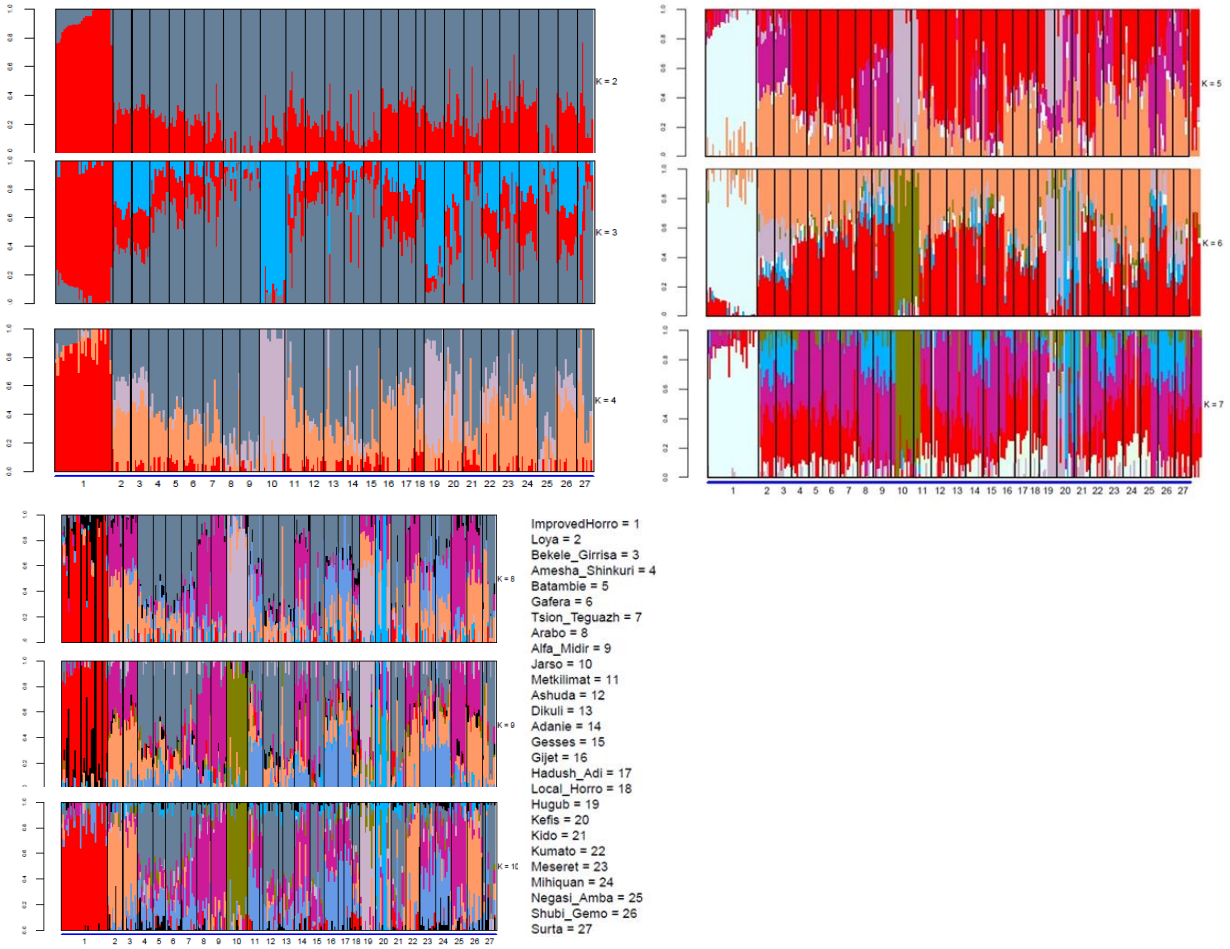
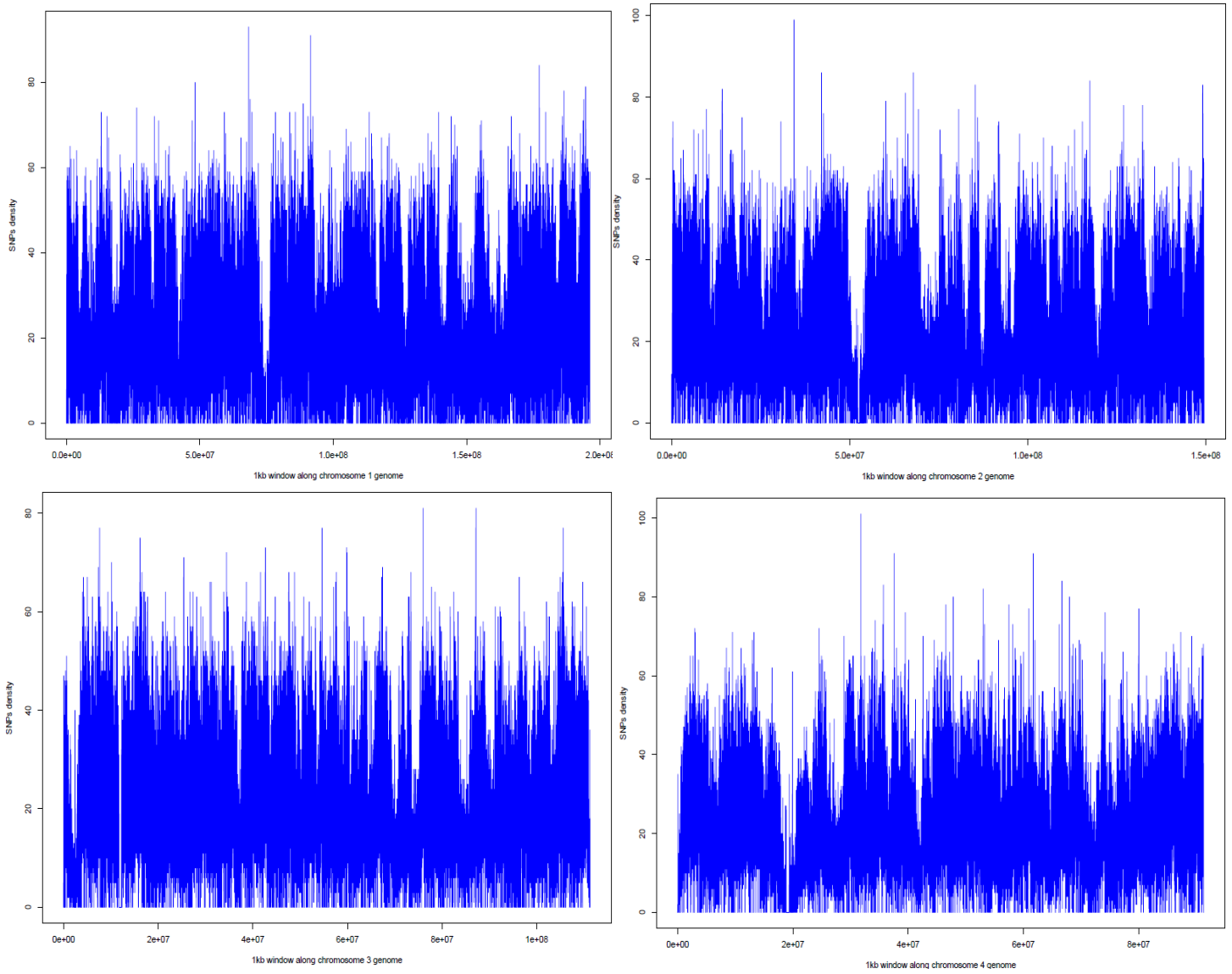


Figure S 1. The admixture plots for Ethiopian indigenous chicken populations (6 < K < 10).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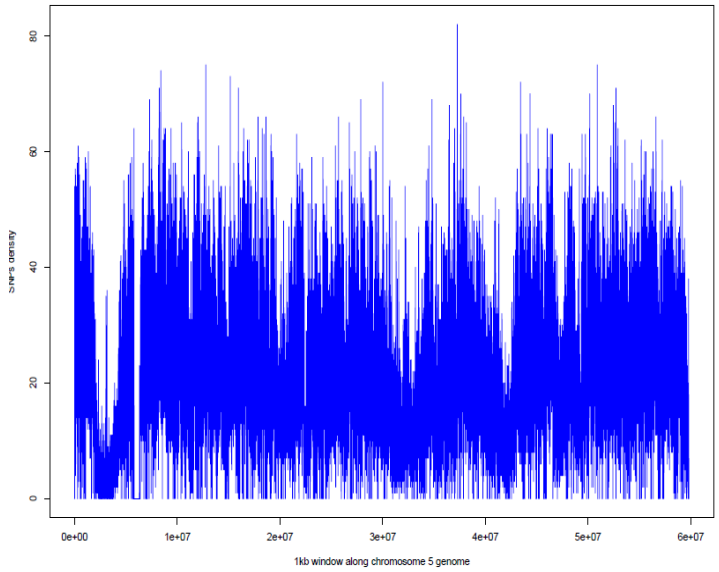
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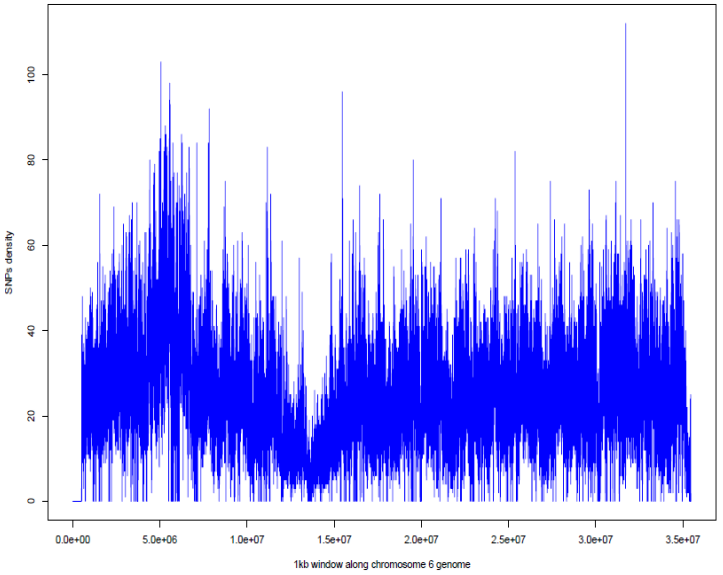
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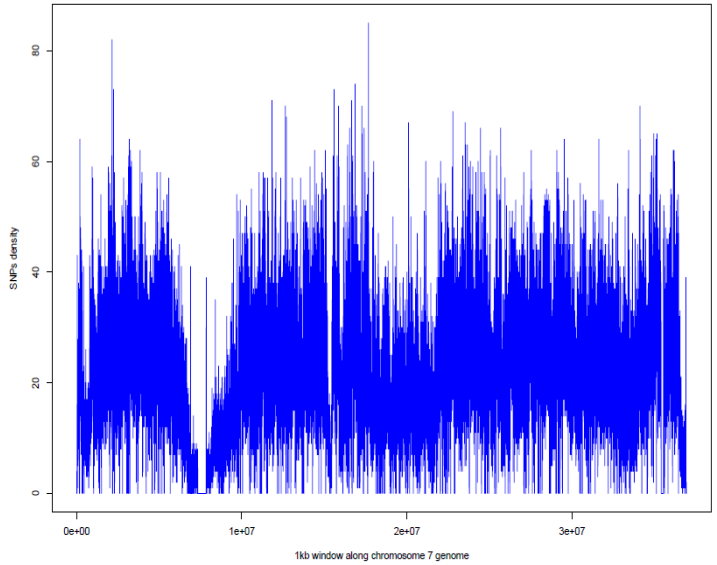
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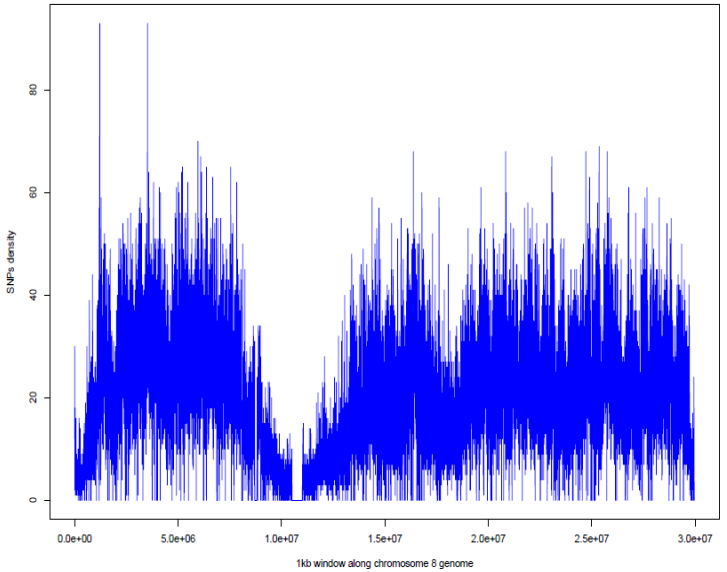
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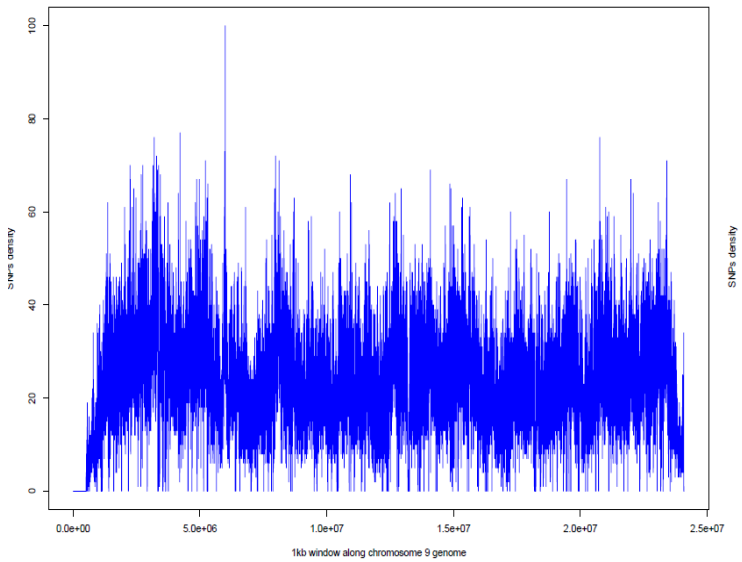
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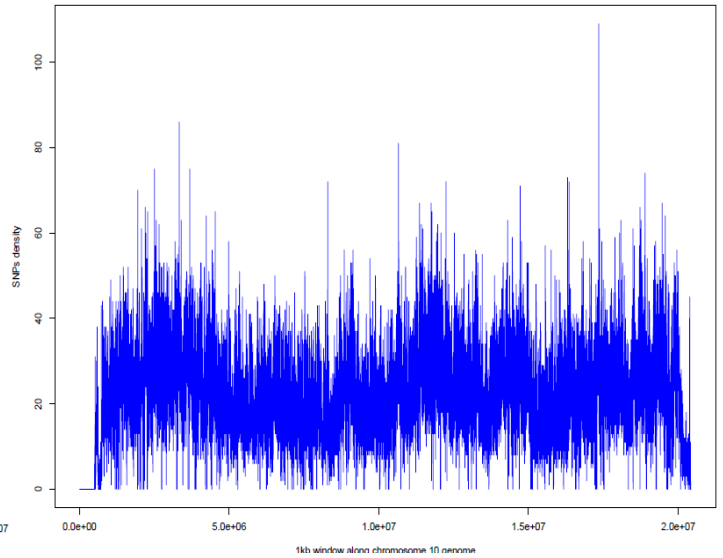
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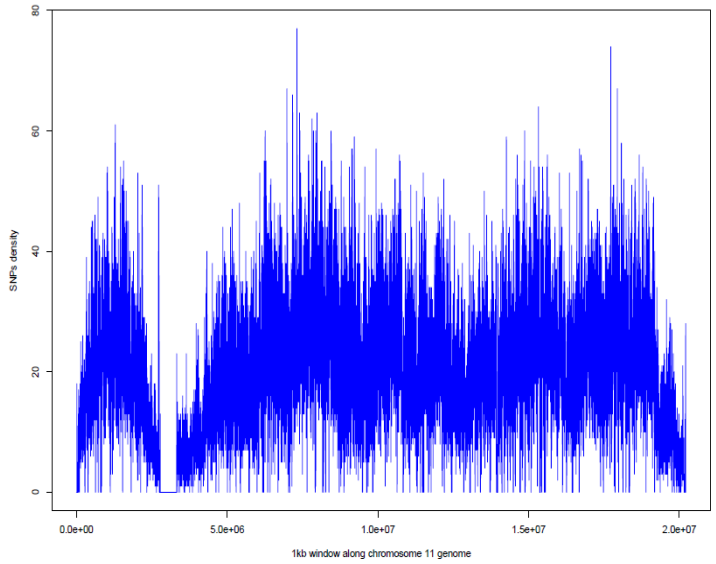
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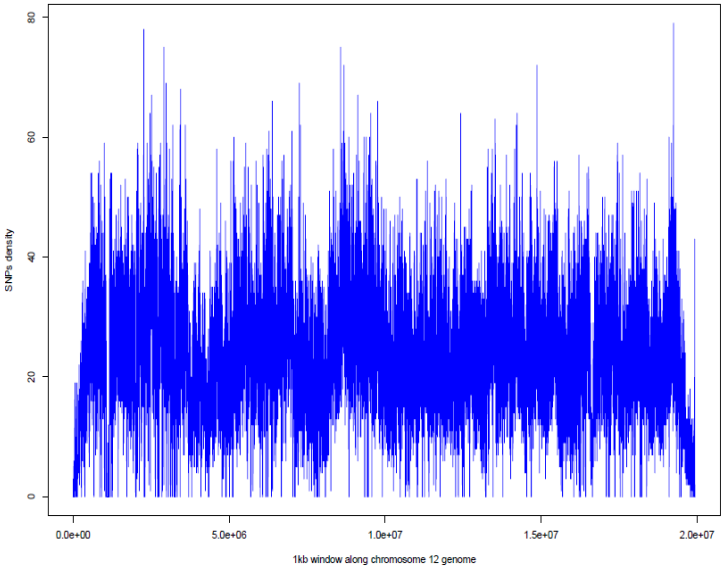
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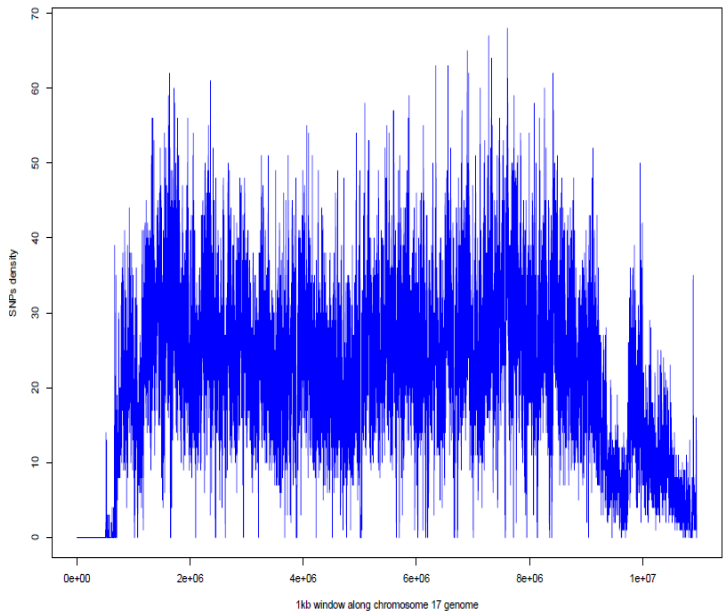
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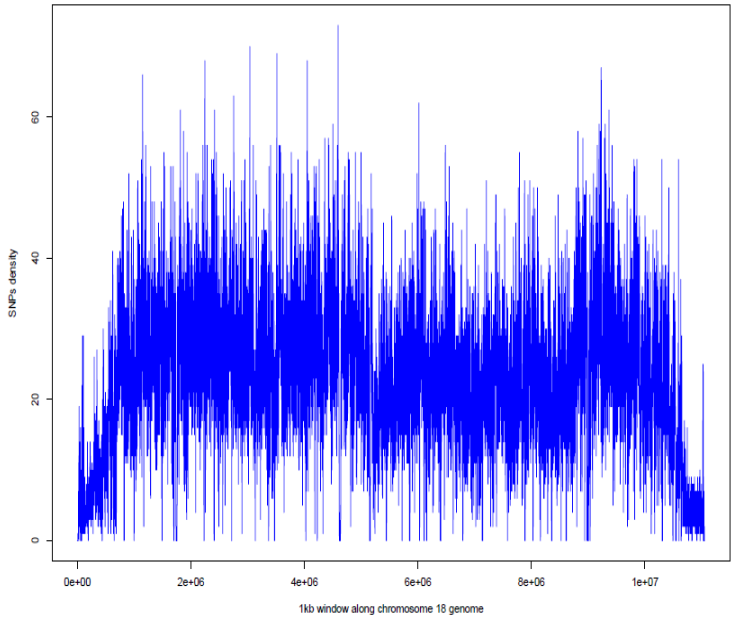
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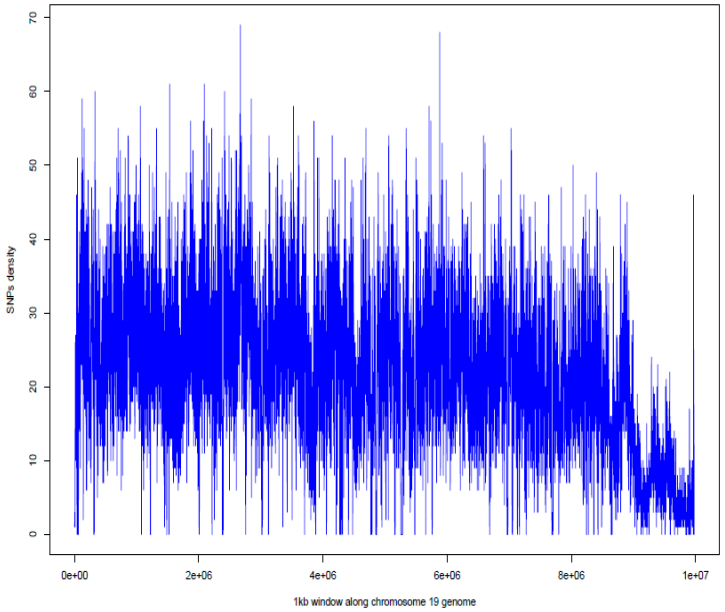
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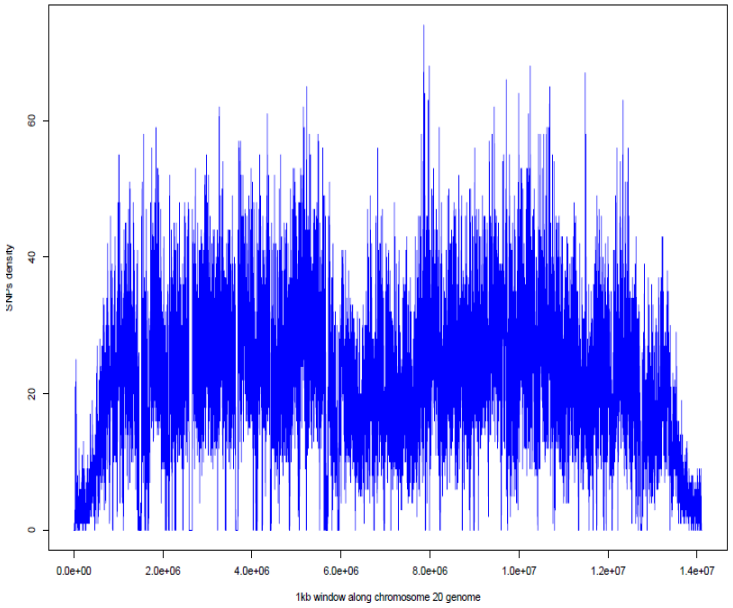
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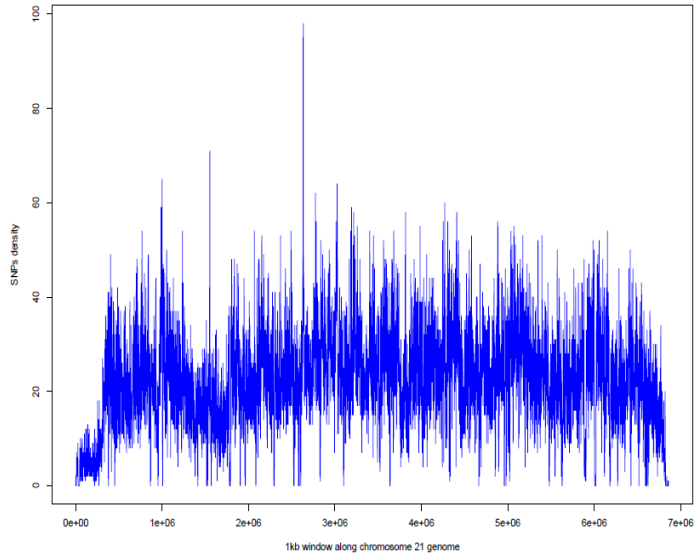
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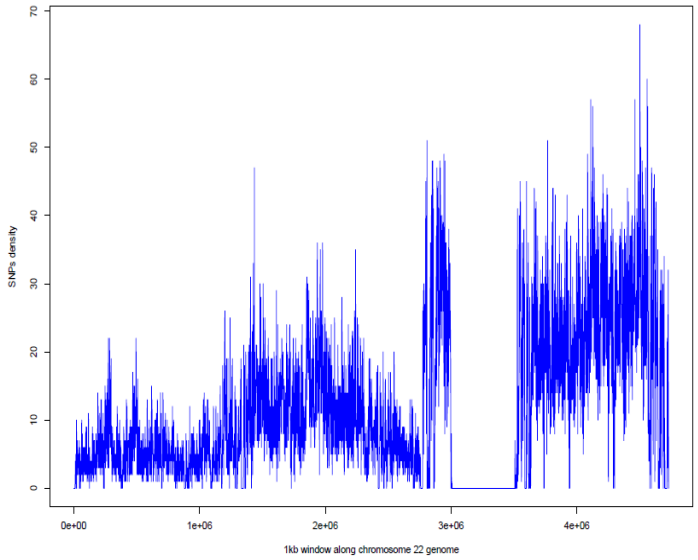
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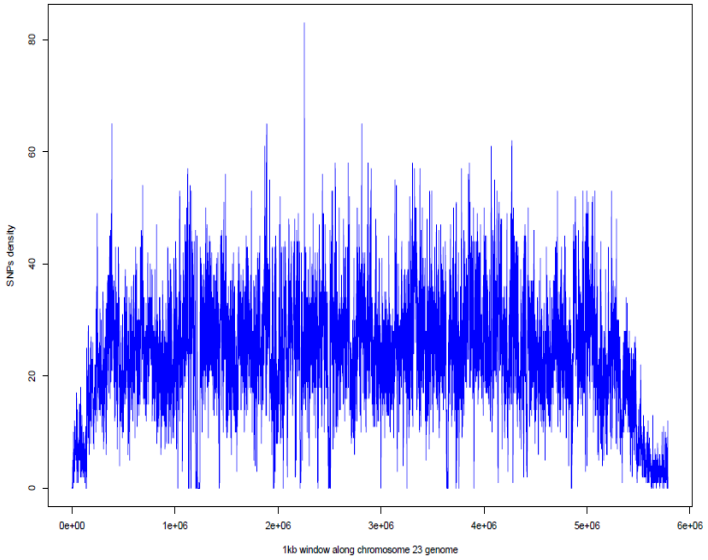
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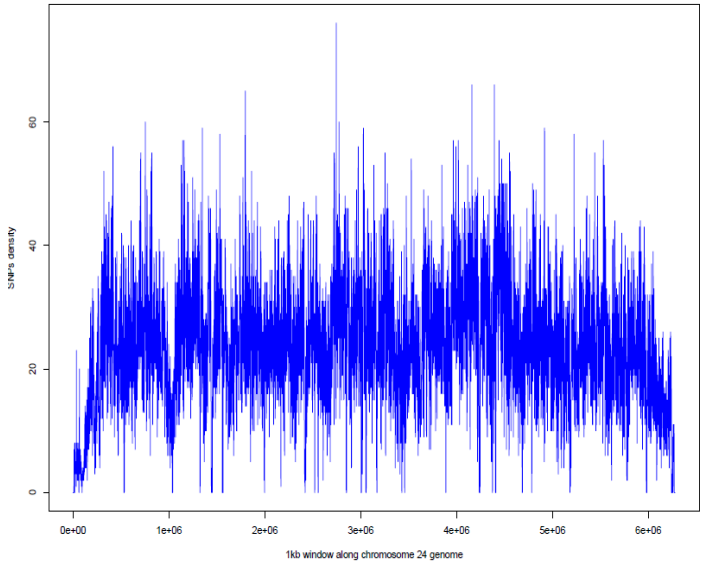
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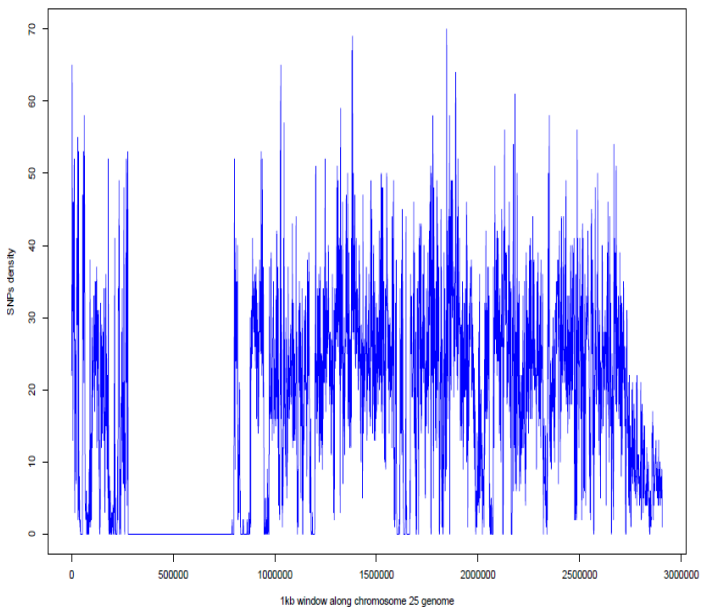
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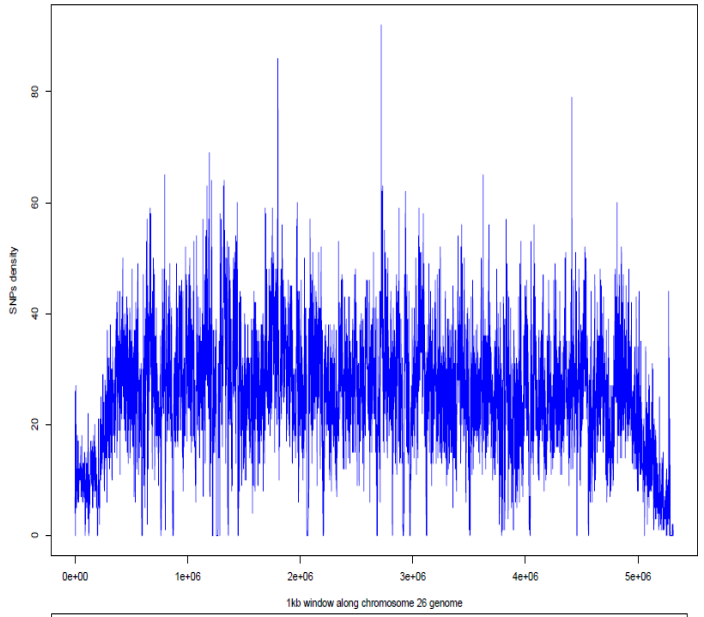
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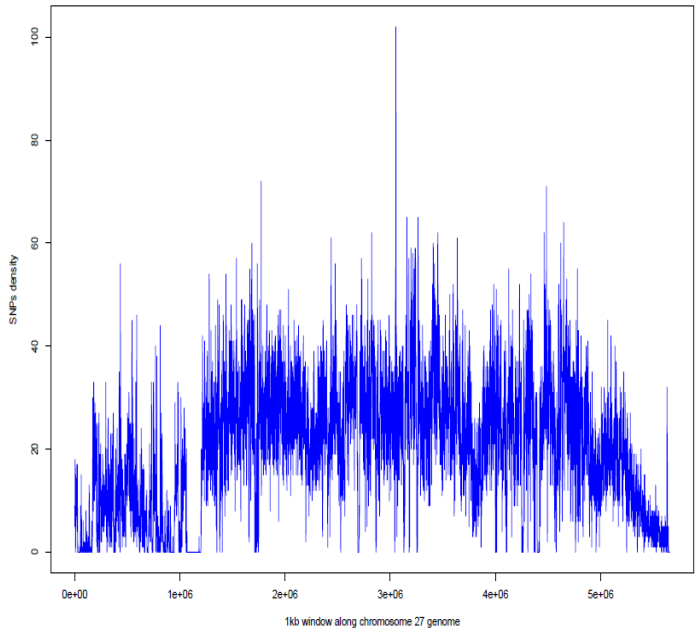
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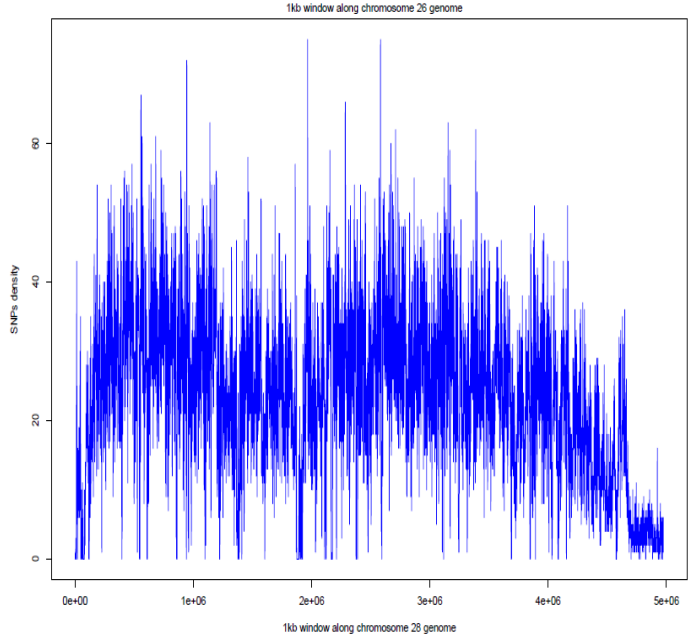
1kb window along chromosome 27 genome


SNPs density
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20
40
60
0e+00
1e+06
2e+06
3e+06
4e+06
5e+06
1kb window along chromosome 28 genome

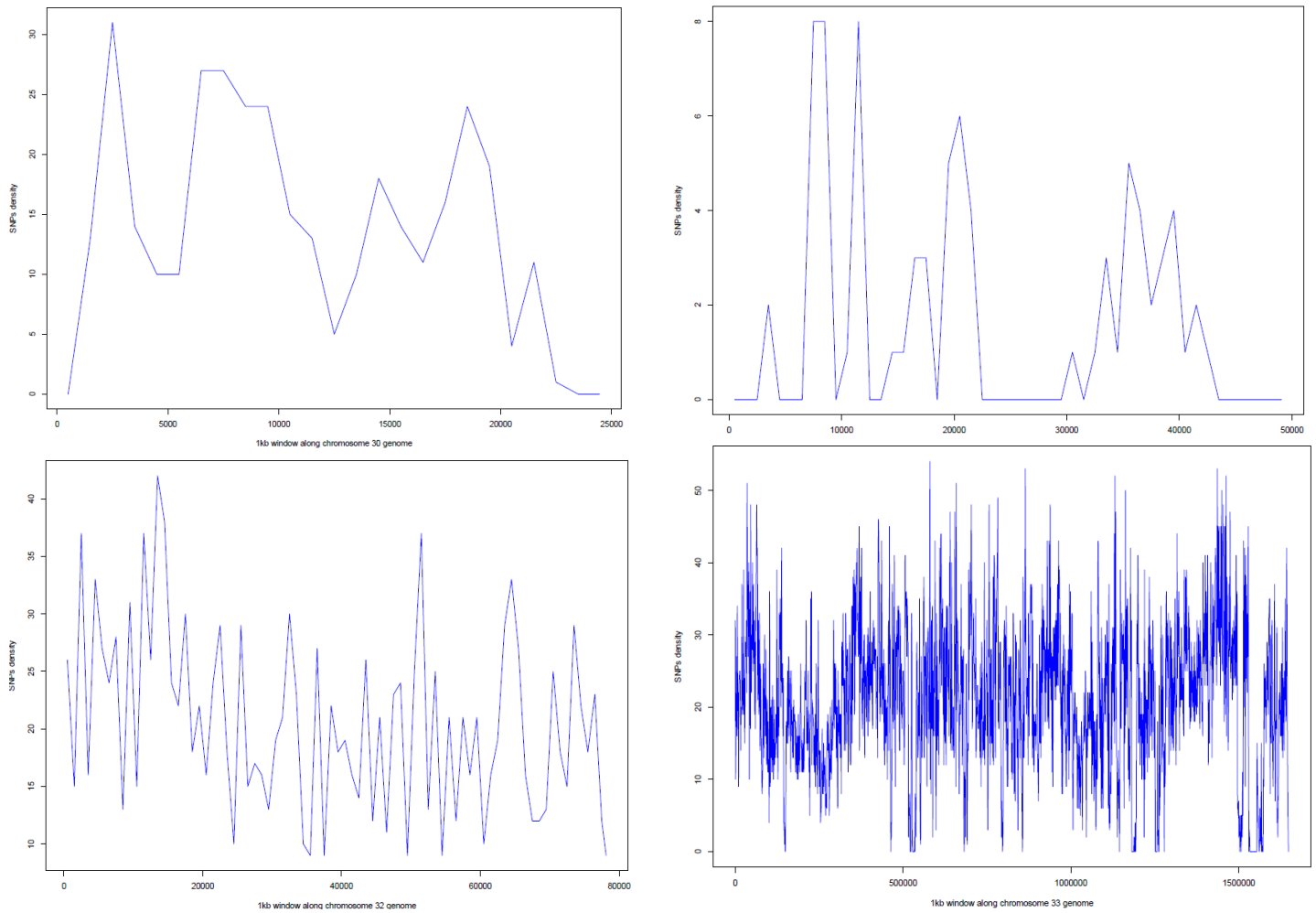

Figure S 2. SNP density for individual chromosomes across the genome

Chromosome positions (Mb) are presented on the x-axis and on the y-axis heterozygosity is given as the density of heterozygous SNPs corrected for the number of bases covered within a window size of 300 Kb.

chr11:2800000

2800001 2800011 2800021 2800031 2800041 2800051 2800061

NNNN

Table S 45. List of genes in nonsynonymous deleterious variants in 27 populations.

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000000071	189094840	189101813	DDIAS
ENSGALG00000000081	205312	210738	IL4I1
ENSGALG00000000104	1080122	1086604	CRY4
ENSGALG00000000109	9950627	9953475	AFMID
ENSGALG00000000123	134466	137899	
ENSGALG00000000168	981821	998840	ADORA1
ENSGALG00000000243	1782741	1787570	RDM1
ENSGALG00000000264	47377290	47399491	
ENSGALG00000000329	1288997	1307914	AHCYL1
ENSGALG00000000396	2503689	2516378	METTL2A
ENSGALG00000000399	2677578	2680770	DUSP28
ENSGALG00000000477	1508360	1510438	
ENSGALG00000000504	1529164	1533184	ETV7
ENSGALG00000000507	18986242	18989246	CPNE7
ENSGALG00000000516	19022589	19054970	FANCA
ENSGALG00000000521	19057727	19063586	SPIRE2
ENSGALG00000000584	375289	387140	
ENSGALG00000000611	1775328	1779751	PPP1R15B
ENSGALG00000000625	3126090	3162020	MAPT
ENSGALG00000000637	554292	560757	ZBTB48
ENSGALG00000000638	19158556	19163523	UTP4
ENSGALG00000000652	604020	610916	ACOT7
ENSGALG00000000699	19283823	19315488	WWP2
ENSGALG00000000720	1432743	1440630	
ENSGALG00000000722	900940	906771	
ENSGALG00000000761	193483508	193498274	TSKU
ENSGALG00000000803	1957157	1958826	
ENSGALG00000000845	194108535	194189490	UVRAG
ENSGALG00000000908	20121097	20141797	ADAT1
ENSGALG00000001025	10048762	10063018	GOLGA1
ENSGALG00000001028	527581	580075	RNF43
ENSGALG00000001049	657606	667042	
ENSGALG00000001062	502768	516984	GGT7
ENSGALG00000001076	776890	785744	LIMK1
ENSGALG00000001084	2286962	2297493	ATP8B3
ENSGALG00000001091	2605227	2608015	C1orf116
ENSGALG00000001111	1085143	1257267	
ENSGALG00000001158	10285736	10327040	UIMC1
ENSGALG00000001175	2686743	2697121	C4BPA
ENSGALG00000001181	1075877	1112534	KCNJ5
ENSGALG00000001206	8366752	8370140	
ENSGALG00000001235	2618283	2624077	ANKRD24
ENSGALG00000001252	2632685	2637600	CREB3L3
ENSGALG00000001267	2637819	2646108	MAP2K2

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000001332	663124	682263	RBL1
ENSGALG00000001412	2464702	2487049	SEMA7A
ENSGALG00000001446	8882615	8908331	GSN
ENSGALG00000001449	2519526	2529895	STRA6
ENSGALG00000001479	3177600	3181452	CYB5D2
ENSGALG00000001504	3284914	3291217	DDX20
ENSGALG00000001565	8801959	8828360	C5
ENSGALG00000001583	8783105	8792615	TRAF1
ENSGALG00000001586	2570401	2574557	NEIL1
ENSGALG00000001632	3387552	3388959	MIS12
ENSGALG00000001658	4534537	4536944	RPL19
ENSGALG00000001691	2335818	2343146	INTS11
ENSGALG00000001696	1187620	1202062	SAG
ENSGALG00000001697	815561	836748	
ENSGALG00000001723	4307425	4310801	
ENSGALG00000001749	1642902	1659177	ACSBG2
ENSGALG00000001765	68485992	68502940	CAAP1
ENSGALG00000001800	1559956	1567028	
ENSGALG00000001828	4089023	4097513	SH2B2
ENSGALG00000001857	2472220	2486139	C1QTNF12
ENSGALG00000001866	14407361	14411064	MCHR2
ENSGALG00000001895	4684399	4691245	
ENSGALG00000001912	3621009	3642966	
ENSGALG00000001936	1309264	1343370	MYO7B
ENSGALG00000002008	4517732	4531542	RNF157
ENSGALG00000002083	2149947	2153763	
ENSGALG00000002098	3867936	3937207	GRIK3
ENSGALG00000002106	1330224	1344472	CLCC1
ENSGALG00000002111	13364535	13374948	
ENSGALG00000002112	4028838	4033940	CSF3R
ENSGALG00000002138	1447839	1450278	HYAL2
ENSGALG00000002143	1431681	1447736	ANKLE2
ENSGALG00000002144	4072417	4093864	THRAP3
ENSGALG00000002175	1456284	1483196	KIF14
ENSGALG00000002179	4661984	4675773	FBF1
ENSGALG00000002199	2863974	2878026	KLHL17
ENSGALG00000002201	13315606	13335789	PPL
ENSGALG00000002253	1780053	1810653	HEMK1
ENSGALG00000002266	2853372	2902314	OGDHL
ENSGALG00000002276	13277094	13283352	EME2
ENSGALG00000002325	13259080	13261144	IGFALS
ENSGALG00000002403	2638997	2708090	ULK1
ENSGALG00000002447	2590011	2698188	CTNNA1
ENSGALG00000002453	2927136	2938279	ABCA7
ENSGALG00000002463	4879162	4882722	SUMF2
ENSGALG00000002470	22543083	22545995	CYP27A1
ENSGALG00000002489	8195255	8199280	PPP1R26

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000002504	3508644	3516114	TROVE2
ENSGALG00000002551	13130172	13153006	CFAP70
ENSGALG00000002561	4080350	4082578	
ENSGALG00000002563	4446782	4454984	TPM4
ENSGALG00000002570	1936311	1938756	
ENSGALG00000002587	4944774	4972405	CRCP
ENSGALG00000002591	2957605	2959977	POLR2E
ENSGALG00000002597	13126748	13129142	MSS51
ENSGALG00000002622	1930227	1934679	FCHSD1
ENSGALG00000002638	5116741	5157334	
ENSGALG00000002663	10472558	10508150	ATR
ENSGALG00000002678	2637608	2655172	CSPG4
ENSGALG00000002679	3736274	3781857	GLT1D1
ENSGALG00000002692	4177681	4185200	
ENSGALG00000002710	5253421	5283874	IPMK
ENSGALG00000002802	4361060	4364487	PACSIN1
ENSGALG00000002820	3732186	3735823	DFFA
ENSGALG00000002831	8853753	8918179	SH3PXD2B
ENSGALG00000002843	5340639	5344241	RILP
ENSGALG00000002845	6694536	7131100	CTNNA3
ENSGALG00000002849	5041127	5044158	DCXR
ENSGALG00000002853	2041059	2091973	CFDP1
ENSGALG00000002855	7501369	7519642	SARDH
ENSGALG00000002860	4573764	4579315	MLN
ENSGALG00000002877	5050116	5059719	LRRC45
ENSGALG00000002931	4258298	4259712	REG4
ENSGALG00000002932	5120226	5122254	NME2
ENSGALG00000002945	3328395	3380261	TMEM266
ENSGALG00000002955	7446665	7466142	ADAMTSL2
ENSGALG00000002971	10206726	10259504	NSD1
ENSGALG00000002980	8157125	8275706	RTKN2
ENSGALG00000003024	3671339	3676081	ARMC6
ENSGALG00000003031	5414295	5420886	SMYD4
ENSGALG00000003047	3676512	3687043	SUGP2
ENSGALG00000003058	3693225	3701042	
ENSGALG00000003105	6179731	6229305	ANKFN1
ENSGALG00000003126	3073321	3558739	ERBB4
ENSGALG00000003181	7348592	7351670	SURF2
ENSGALG00000003194	4955473	4970589	ATP6V0A2
ENSGALG00000003197	7341076	7344697	RPL7A
ENSGALG00000003285	10365016	10375987	CDHR2
ENSGALG00000003294	6696138	6712562	ATAD5
ENSGALG00000003337	5166291	5170582	EIF3I
ENSGALG00000003400	976634	979055	AIMP2
ENSGALG00000003403	5186133	5220676	ZNF385C
ENSGALG00000003412	7265700	7284064	
ENSGALG00000003419	5099849	5123800	MPHOSPH9

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000003435	4946918	4950939	PGC
ENSGALG00000003476	6829425	6861860	ERN1
ENSGALG00000003499	4037999	4047856	MAST3
ENSGALG00000003540	6970209	6982733	CEP95
ENSGALG00000003563	5279493	5284301	YARS
ENSGALG00000003569	1309031	1318031	TMEM130
ENSGALG00000003572	4085166	4125847	
ENSGALG00000003574	3756709	3784646	LPCAT2
ENSGALG00000003589	5643262	5647788	VTN
ENSGALG00000003661	6964407	6992177	SETX
ENSGALG00000003665	5732371	5736475	PIGS
ENSGALG00000003693	5359116	5470470	MACF1
ENSGALG00000003731	4331470	4369323	FBXO42
ENSGALG00000003742	4229272	4253848	CPAMD8
ENSGALG00000003774	4411149	4423378	ATP13A2
ENSGALG00000003777	2201059	2481132	NELL1
ENSGALG00000003815	5165779	5186674	RPN2
ENSGALG00000003833	5721919	5794586	CACNA1E
ENSGALG00000003849	5621877	5662732	TRPM1
ENSGALG00000003860	1738814	1777456	MID2
ENSGALG00000003863	5458325	5469803	P2RX7
ENSGALG00000003922	4838538	4857184	TOP2A
ENSGALG00000003937	12017387	12033276	GEMIN5
ENSGALG00000004017	6089879	6099342	TOR1AIP2
ENSGALG00000004028	5308806	5314214	
ENSGALG00000004037	10593818	10608366	DNA2
ENSGALG00000004052	6289263	6319401	GPR107
ENSGALG00000004087	6291473	6524226	THSD4
ENSGALG00000004102	5253737	5257097	C1orf158
ENSGALG00000004104	2565759	2592534	INTS1
ENSGALG00000004110	5370082	5373738	TOMM34
ENSGALG00000004162	7872473	7878562	SLC16A6
ENSGALG00000004167	10819703	10821527	SRGN
ENSGALG00000004169	1310797	1346333	
ENSGALG00000004216	6258254	6262709	TOR3A
ENSGALG00000004228	5873857	5902664	USP40
ENSGALG00000004251	1253552	1260151	ARR3
ENSGALG00000004260	1517982	1524901	PKP3
ENSGALG00000004262	6240247	6244176	TMIGD1
ENSGALG00000004267	1511993	1516792	SIGIRR
ENSGALG00000004280	1498469	1507574	ANO9
ENSGALG00000004286	11020202	11048579	COL13A1
ENSGALG00000004294	7259782	7315837	CGNL1
ENSGALG00000004297	3033149	3099125	DNAH1
ENSGALG00000004336	1242567	1251009	INPPL1
ENSGALG00000004360	13024860	13028805	
ENSGALG00000004365	5736958	5749931	WDR66

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000004368	3384941	3387376	GNA12
ENSGALG00000004375	7949456	7976331	VPS35
ENSGALG00000004390	22789995	22948814	AP3B1
ENSGALG00000004424	6631529	6642933	SEC16B
ENSGALG00000004428	7973018	7976373	
ENSGALG00000004475	1210009	1212138	
ENSGALG00000004496	13051554	13056671	TNIP1
ENSGALG00000004502	9210257	9213583	KIF19
ENSGALG00000004509	6584989	6587790	UBB
ENSGALG00000004515	5949198	5981021	KNTC1
ENSGALG00000004529	5981277	5986395	VPS29
ENSGALG00000004538	7096736	7113948	TNN
ENSGALG00000004542	5956857	5997973	ZMYND8
ENSGALG00000004591	7408662	7414693	SERPINC1
ENSGALG00000004594	13146841	13150694	CD74
ENSGALG00000004611	4163980	4187079	FBXL18
ENSGALG00000004621	6385508	6529830	PREX1
ENSGALG00000004627	7557778	7561205	
ENSGALG00000004637	6652849	6660676	
ENSGALG00000004660	6686185	6699711	TRPV3
ENSGALG00000004669	6702366	6708308	ASPA
ENSGALG00000004670	3281636	3298041	ATRIP
ENSGALG00000004683	9736236	9752383	TPD52L2
ENSGALG00000004711	4401977	4407450	
ENSGALG00000004742	1874383	1876926	BMP15
ENSGALG00000004750	3454111	3467101	NOL8
ENSGALG00000004767	5648047	5666048	ODF2
ENSGALG00000004798	4691169	4749364	MPRIP
ENSGALG00000004820	6935447	6938641	FAM57A
ENSGALG00000004825	1894128	1902643	HDAC8
ENSGALG00000004837	6899289	6906498	CCNDBP1
ENSGALG00000004848	6406970	6414976	YBX1
ENSGALG00000004859	6906827	6918959	ZNFX1
ENSGALG00000004888	4926676	4933844	RAI1
ENSGALG00000004921	4271288	4287004	SLC6A1
ENSGALG00000004953	5030233	5038727	DRG2
ENSGALG00000004965	5511456	5519318	SLC27A4
ENSGALG00000004978	5047798	5064630	MYO15A
ENSGALG00000005005	5104842	5107494	MIEF2
ENSGALG00000005006	11258200	11281700	UBA2
ENSGALG00000005012	5054111	5063325	
ENSGALG00000005014	2066138	2068061	AIPL1
ENSGALG00000005028	5109957	5121859	TOP3A
ENSGALG00000005031	2071935	2082734	DRP2
ENSGALG00000005043	6711180	6730689	
ENSGALG00000005046	5132126	5136038	SHMT1
ENSGALG00000005077	2154809	2178532	F8

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000005083	5163796	5192508	SLC5A10
ENSGALG00000005093	7209131	7215496	
ENSGALG00000005102	7546069	7840288	CDH4
ENSGALG00000005118	8396685	8397791	FAM124B
ENSGALG00000005122	6773611	6789221	MYO1H
ENSGALG00000005138	6792641	6799711	KCTD10
ENSGALG00000005146	11444091	11445695	PDP2
ENSGALG00000005188	998427	1065818	MINDY4
ENSGALG00000005253	5617810	5620433	
ENSGALG00000005279	7494633	7541587	BRIP1
ENSGALG00000005286	6425974	6434135	TRIM42
ENSGALG00000005315	6017339	6019278	RPUSD1
ENSGALG00000005336	2373286	2387260	GUK1
ENSGALG00000005349	6029103	6043043	
ENSGALG00000005361	14154543	14161749	
ENSGALG00000005426	31717648	31775857	FREM1
ENSGALG00000005434	31707297	31708392	CER1
ENSGALG00000005435	15636273	15670143	
ENSGALG00000005450	8379726	8395484	CCDC66
ENSGALG00000005467	15966703	15974642	HSD17B2
ENSGALG00000005468	8618892	8649089	SYNRG
ENSGALG00000005476	3598940	3705027	PTH1R
ENSGALG00000005499	8553006	8591010	IL17RD
ENSGALG00000005517	3971607	3992312	KIF9
ENSGALG00000005519	16594013	16673810	TLL2
ENSGALG00000005527	8610054	8639123	APPL1
ENSGALG00000005535	13151075	13168747	TCOF1
ENSGALG00000005572	6193969	6197292	NOXO1
ENSGALG00000005594	9057635	9058939	OMG
ENSGALG00000005595	7194104	7204732	HPS4
ENSGALG00000005599	16785354	16790215	
ENSGALG00000005609	8519646	8532665	OGFR
ENSGALG00000005618	8778424	8796646	CTR9
ENSGALG00000005621	13192090	13212308	CAMK2A
ENSGALG00000005634	7229327	7230473	CRYBA4
ENSGALG00000005654	7577645	7595931	PITPNB
ENSGALG00000005655	5184138	5190382	TSPEAR
ENSGALG00000005661	4362962	4364776	
ENSGALG00000005672	13218281	13226254	SLC6A7
ENSGALG00000005687	16983558	16994562	CUEDC2
ENSGALG00000005707	9325242	9327381	IFT20
ENSGALG00000005747	2451344	2452399	
ENSGALG00000005757	17821801	17827332	IRF8
ENSGALG00000005769	9313714	9322206	WEE1
ENSGALG00000005770	13295985	13313953	HMGXB3
ENSGALG00000005789	9059020	9068014	UQCRC1
ENSGALG00000005797	9022635	9065766	COL20A1

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000005801	9071546	9090148	CHRNA4
ENSGALG00000005826	4698534	4734741	DLEC1
ENSGALG00000005845	18186088	18218511	SLC7A5
ENSGALG00000005857	17636489	17657686	
ENSGALG00000005869	9103875	9122950	COPG1
ENSGALG00000005889	13985788	14013189	CCDC18
ENSGALG00000005914	17786239	17817301	WASHC2C
ENSGALG00000005947	4841182	4853799	MYD88
ENSGALG00000005968	8025665	8042567	MMP11
ENSGALG00000005977	14285091	14295767	BTBD8
ENSGALG00000005986	10199239	10319919	TUB
ENSGALG00000005999	9681793	9708956	ABTB1
ENSGALG00000006025	4992188	5013715	XIRP1
ENSGALG00000006038	14391623	14498728	TGFBR3
ENSGALG00000006044	4874387	4875766	
ENSGALG00000006052	5312695	5336291	WDR48
ENSGALG00000006078	6919383	6928668	PALB2
ENSGALG00000006095	18197465	18217445	FRMPD2
ENSGALG00000006099	18584503	18617687	ZFPM1
ENSGALG00000006119	11660424	11665477	SAXO2
ENSGALG00000006140	6966453	6978215	GGA2
ENSGALG00000006152	9988019	9990550	
ENSGALG00000006182	10008305	10014862	NSFL1C
ENSGALG00000006188	15173264	15196009	KYAT3
ENSGALG00000006208	11990010	12080323	OTOG
ENSGALG00000006229	1267434	1272776	
ENSGALG00000006239	18721562	18726300	
ENSGALG00000006273	10252718	10259735	MYLK2
ENSGALG00000006352	19330373	19331756	CH25H
ENSGALG00000006357	10801221	10810412	XPC
ENSGALG00000006376	12084067	12101401	TMC3
ENSGALG00000006378	19343210	19348438	LIPA
ENSGALG00000006392	4703951	4711851	RNF168
ENSGALG00000006417	15802894	15826139	SEC24A
ENSGALG00000006436	4624346	4626196	AQP12A
ENSGALG00000006445	12413427	12483133	ARNT2
ENSGALG00000006459	11270120	11281464	CCDC174
ENSGALG00000006521	13575719	13609829	TRPM5
ENSGALG00000006526	11332373	11363615	PLXNB1
ENSGALG00000006539	4383100	4389373	C9H21orf2
ENSGALG00000006540	20039179	20040556	DD1CR
ENSGALG00000006542	9522054	9589349	ESYT2
ENSGALG00000006543	4375703	4380667	PFKL
ENSGALG00000006558	9595575	9615165	
ENSGALG00000006560	8824964	8995709	SEMA3A
ENSGALG00000006597	4107760	4112433	
ENSGALG00000006607	8479513	8485340	GUCD1

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000006608	14113198	14118876	
ENSGALG00000006612	10358970	10373491	ASXL1
ENSGALG00000006631	12837819	12854365	TICRR
ENSGALG00000006632	3662350	3680002	CEP63
ENSGALG00000006639	20405524	20418860	CEP55
ENSGALG00000006651	11497919	11499883	OGG1
ENSGALG00000006652	9958497	10244031	DIP2C
ENSGALG00000006679	10519797	10524406	BPIFB4
ENSGALG00000006693	10526109	10530923	
ENSGALG00000006700	6195950	6208354	PROSER2
ENSGALG00000006724	3082800	3338435	
ENSGALG00000006755	4178788	4187152	USP2
ENSGALG00000006776	11553069	11555613	KLHDC8B
ENSGALG00000006783	11508788	11558301	PLOD2
ENSGALG00000006791	10603545	10615064	TTI1
ENSGALG00000006802	11573714	11594922	LAMB2
ENSGALG00000006804	16057748	16074923	ODF2L
ENSGALG00000006819	13624751	13893408	AGBL1
ENSGALG00000006821	5224423	5232217	TNMD
ENSGALG00000006834	12454619	12470944	CPB1
ENSGALG00000006876	10729767	10733859	CTSA
ENSGALG00000006910	11655848	11667410	IMPDH2
ENSGALG00000006911	8539866	8565249	TMC5
ENSGALG00000006963	9573525	9581879	ENDOV
ENSGALG00000006976	12679286	12696726	
ENSGALG00000007001	4083114	4088567	TLR4
ENSGALG00000007003	4069259	4077367	
ENSGALG00000007007	21518224	21579102	
ENSGALG00000007014	22240272	22243704	
ENSGALG00000007048	16877090	16897766	SYNM
ENSGALG00000007070	8795233	8824633	OTOA
ENSGALG00000007080	17126956	17144545	
ENSGALG00000007098	15350861	15434281	KIF21A
ENSGALG00000007125	13135663	13572700	PARD3
ENSGALG00000007168	11946151	11967925	
ENSGALG00000007169	14127254	14169164	EPC1
ENSGALG00000007438	5484062	5488400	
ENSGALG00000007525	17067826	17075764	
ENSGALG00000007531	22287005	22296037	ZFYVE27
ENSGALG00000007537	17085279	17109145	INCENP
ENSGALG00000007572	22321784	22335727	MMS19
ENSGALG00000007579	16147118	16204934	APBB1IP
ENSGALG00000007643	18467490	18482742	DIS3L
ENSGALG00000007645	22530257	22534464	
ENSGALG00000007661	10420643	10427959	MYCBPAP
ENSGALG00000007673	10471029	10475321	LRRC59
ENSGALG00000007676	10476723	10481875	EME1

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000007710	12285790	12294879	
ENSGALG00000007711	18528211	18534374	RPL4
ENSGALG00000007713	10504470	10508384	CD300LG
ENSGALG00000007766	16938374	17272982	KIAA1217
ENSGALG00000007777	9564789	9679908	SLC39A10
ENSGALG00000007815	5747940	5753666	ANKK1
ENSGALG00000007835	2071841	2105903	PUS10
ENSGALG00000007862	16927115	16996501	CNTN3
ENSGALG00000007864	17452004	17513814	ARMC3
ENSGALG00000007892	17711127	17743785	SPAG6
ENSGALG00000007907	10875974	10885281	CCDC157
ENSGALG00000007917	14926773	14978515	LAMB4
ENSGALG00000007970	19107954	19156499	PIAS1
ENSGALG00000007974	10782998	10794894	NUP85
ENSGALG00000008034	10931921	10957831	CASKIN2
ENSGALG00000008077	19355200	19358789	PAQR5
ENSGALG00000008109	14151339	14182335	CDHR3
ENSGALG00000008120	19501916	19520583	TLE3
ENSGALG00000008150	11256379	11267964	RASAL1
ENSGALG00000008155	11227663	11233652	KCTD18
ENSGALG00000008160	23400232	23499498	CNNM2
ENSGALG00000008172	3029721	3040592	ERLEC1
ENSGALG00000008176	3040531	3073125	ASB3
ENSGALG00000008180	19759094	19785369	SPG11
ENSGALG00000008185	11249381	11285636	AOX1
ENSGALG00000008256	19933508	19950517	BLM
ENSGALG00000008257	3200895	3221901	MERTK
ENSGALG00000008263	17898685	18121966	CNTN4
ENSGALG00000008266	14111920	14151756	COL4A6
ENSGALG00000008275	20020799	20022277	
ENSGALG00000008283	15737984	15742734	CYP2AB1
ENSGALG00000008312	12676726	12723229	GSAP
ENSGALG00000008359	3328455	3330821	CD93
ENSGALG00000008368	19335198	19369470	RAD18
ENSGALG00000008370	11515225	11532948	TRAK2
ENSGALG00000008416	3831127	3921447	CFAP61
ENSGALG00000008475	2456073	2482710	ARRDC1
ENSGALG00000008503	15914297	15916640	ALG3
ENSGALG00000008516	12407009	12420281	CPO
ENSGALG00000008529	12432880	12443438	FASTKD2
ENSGALG00000008537	16012725	16023253	EPHB3
ENSGALG00000008544	16328932	16398413	SLC8A1
ENSGALG00000008609	4399060	4424446	PTK7
ENSGALG00000008615	24709933	24791051	LTK
ENSGALG00000008618	16559396	16566077	UPF3B
ENSGALG00000008624	24855680	24884673	RPAP1
ENSGALG00000008638	19525053	19554688	MMR1L3

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000008645	16598334	16606619	NKRF
ENSGALG00000008646	16205261	16216585	
ENSGALG00000008692	25038945	25096118	
ENSGALG00000008725	5571728	5637205	KIF16B
ENSGALG00000008744	16272609	16420707	MCF2L2
ENSGALG00000008776	22165912	22185499	HYAL6
ENSGALG00000008780	16611056	16617553	CTBS
ENSGALG00000008786	13740109	13819369	NBEAL1
ENSGALG00000008791	20613975	20640410	NMT2
ENSGALG00000008803	13841905	13846428	
ENSGALG00000008810	15354761	15359822	FAM161A
ENSGALG00000008815	15330848	15337331	LRRN4
ENSGALG00000008819	2026955	2051551	LRSAM1
ENSGALG00000008885	14004793	14133988	PDE1A
ENSGALG00000008888	16915775	17249012	
ENSGALG00000008914	27468288	27513634	NRAP
ENSGALG00000008937	8953571	8983004	PPP1R21
ENSGALG00000008942	8915296	8942633	FOXN2
ENSGALG00000008946	27592399	27623494	NHLRC2
ENSGALG00000008962	8658316	8685996	MSH2
ENSGALG00000008974	19041884	19071668	USP33
ENSGALG00000008980	27760066	27774032	VWA2
ENSGALG00000008999	27778781	27799753	AFAP1L2
ENSGALG00000009001	14833295	14861223	CWC22
ENSGALG00000009004	21380802	21410300	ZNF804B
ENSGALG00000009017	21695262	21701570	STEAP2
ENSGALG00000009026	21710551	21734535	
ENSGALG00000009032	19675023	19681422	PIF1
ENSGALG00000009119	16761868	16770284	THUMPD2
ENSGALG00000009134	24474948	24550085	CTTNBP2
ENSGALG00000009145	25824681	25835329	
ENSGALG00000009205	14117925	14203370	
ENSGALG00000009250	15889941	15901595	HNRNPA3
ENSGALG00000009266	20484771	20491761	FGA
ENSGALG00000009301	16865856	16875595	CHRNA1
ENSGALG00000009315	26297611	26324915	PAPLN
ENSGALG00000009345	26454626	26467002	
ENSGALG00000009365	22521894	22535678	CYP51A1
ENSGALG00000009369	30049291	30054581	PRDX3
ENSGALG00000009415	27718429	27835276	SMOC1
ENSGALG00000009435	26361986	26387951	PPP1R3A
ENSGALG00000009441	18069988	18080140	TAF1A
ENSGALG00000009458	20403471	20563585	
ENSGALG00000009466	30394469	30410543	SEC23IP
ENSGALG00000009468	20640065	20645598	
ENSGALG00000009483	18659507	18713332	MARK1
ENSGALG00000009485	27299899	27307305	

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000009491	28406954	28747300	RAD51B
ENSGALG00000009496	23475697	23491768	NAF1
ENSGALG00000009507	28813891	28865737	PLEKHH1
ENSGALG00000009523	28757424	28995706	CNTN1
ENSGALG00000009556	29649659	29708429	PRICKLE1
ENSGALG00000009594	22539912	22550592	RARRES1
ENSGALG00000009598	18846482	18883499	EPRS
ENSGALG00000009601	30342085	30485295	NELL2
ENSGALG00000009611	29490434	29523553	EIF2AK4
ENSGALG00000009645	19997179	20358337	ESRRG
ENSGALG00000009669	22593316	22706455	RSRC1
ENSGALG00000009714	25756022	25763028	CBR4
ENSGALG00000009723	30438360	30554506	FMN1
ENSGALG00000009792	29559149	29561899	
ENSGALG00000009817	32206472	32209601	ZNF770
ENSGALG00000009837	22052274	22074536	DTL
ENSGALG00000009844	32283463	32288278	ACTC1
ENSGALG00000009855	29945818	29988757	TBC1D9
ENSGALG00000009877	22357077	22527887	
ENSGALG00000009885	34415870	34428812	HELB
ENSGALG00000009902	19691444	19711677	CFAP57
ENSGALG00000009904	35101235	35103693	IL22
ENSGALG00000009905	35112854	35137000	MDM1
ENSGALG00000009981	25557990	25574700	PREPL
ENSGALG00000009983	34519335	34601731	NUBPL
ENSGALG00000009995	34843920	35050252	AKAP6
ENSGALG00000010005	26625940	26701895	EPAS1
ENSGALG00000010022	32220976	32236070	PRMT9
ENSGALG00000010047	27857774	27873604	SLC4A1AP
ENSGALG00000010053	19988821	20225336	PTPRF
ENSGALG00000010081	33497816	33524132	SH3D19
ENSGALG00000010090	33605469	33679767	FAM160A1
ENSGALG00000010108	34283512	34287993	C4orf33
ENSGALG00000010116	29464746	29583035	DNAH8
ENSGALG00000010118	37030439	37188796	MIPOL1
ENSGALG00000010133	20869028	20884084	PTCH2
ENSGALG00000010154	37633590	37642338	GEMIN2
ENSGALG00000010193	37713774	37731357	ZNF410
ENSGALG00000010197	37740605	37748157	COQ6
ENSGALG00000010202	37750948	37767273	ENTPD5
ENSGALG00000010203	20988109	20994448	
ENSGALG00000010207	34656454	34689429	LARP1B
ENSGALG00000010224	37799941	37807895	GLIPR1L
ENSGALG00000010226	21101144	21106303	MUTYH
ENSGALG00000010230	21118192	21176057	TESK2
ENSGALG00000010242	4871480	4874774	
ENSGALG00000010258	37973837	38033648	LTBP2

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ENSGALG00000010268	34869460	34877868	PARM1
ENSGALG00000010276	21260097	21277121	GPBP1L1
ENSGALG00000010304	38176680	38194379	MLH3
ENSGALG00000010313	21323722	21490422	
ENSGALG00000010316	35018318	35181390	FRAS1
ENSGALG00000010323	38322143	38331207	BATF
ENSGALG00000010324	35192841	35208343	MRPL1
ENSGALG00000010325	39561955	39685625	PPP1R12A
ENSGALG00000010349	30993718	30997091	POLR1C
ENSGALG00000010360	21671551	21675013	NSUN4
ENSGALG00000010391	35737241	35779227	MMRN1
ENSGALG00000010392	35907697	35913582	
ENSGALG00000010440	21871550	21892367	MKNK1
ENSGALG00000010468	39289421	39292849	ISM2
ENSGALG00000010478	21991222	22008702	STIL
ENSGALG00000010572	40811286	40858950	TSHR
ENSGALG00000010577	38977102	39011532	
ENSGALG00000010601	39525695	39537283	UFSP2
ENSGALG00000010607	43079009	43113022	SPATA7
ENSGALG00000010609	33619026	33624917	NDUFAF7
ENSGALG00000010611	39613075	39632176	CFAP97
ENSGALG00000010627	24470877	24475138	PRPF38A
ENSGALG00000010630	33860673	33913598	AHCTF1
ENSGALG00000010636	39762374	39778389	PRIMPOL
ENSGALG00000010641	33936002	33945995	SCCPDH
ENSGALG00000010668	40162296	40247894	WWC2
ENSGALG00000010677	43865707	43890463	NRDE2
ENSGALG00000010691	34848623	34865195	
ENSGALG00000010703	44254119	44275768	DGLUCY
ENSGALG00000010749	25215563	25220131	TCEANC2
ENSGALG00000010763	44582962	44610633	TRIP11
ENSGALG00000010774	25250767	25301654	SSBP3
ENSGALG00000010927	45986045	45995778	DMP1
ENSGALG00000010933	19477509	19493971	
ENSGALG00000010934	27404833	27470245	
ENSGALG00000010935	39870775	39980929	PTPRQ
ENSGALG00000010939	40029520	40056169	LIN7A
ENSGALG00000010943	19691055	19747676	SCN1A
ENSGALG00000010949	31184795	31200167	GPNMB
ENSGALG00000010956	19751570	19782350	TTC21B
ENSGALG00000010969	45611921	45622004	SPIA4
ENSGALG00000010995	27910149	27935026	ITGB3BP
ENSGALG00000011000	38573516	38605829	TARBP1
ENSGALG00000011058	28434800	28465001	LEPR
ENSGALG00000011076	46084881	46114497	SYNE3
ENSGALG00000011078	46127455	46159442	PTPN13
ENSGALG00000011149	21941750	21977517	PLA2R1

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ENSGALG00000011178	46716267	46721036	ENOPH1
ENSGALG00000011180	40904572	40967021	FAM120B
ENSGALG00000011186	41248476	41263775	ERMARD
ENSGALG00000011235	34327646	34349885	GALNT15
ENSGALG00000011269	43925156	43947733	EPYC
ENSGALG00000011277	44602930	44615820	PLEKHG7
ENSGALG00000011298	37655934	37978166	RARB
ENSGALG00000011304	38055640	38075203	NGLY1
ENSGALG00000011332	22332671	22343840	ANKZF1
ENSGALG00000011342	45374215	45438791	FGD6
ENSGALG00000011386	22592086	22597668	BCS1L
ENSGALG00000011391	49969802	49986553	AMN
ENSGALG00000011413	26796821	26810573	
ENSGALG00000011446	50222277	50231944	TNFAIP2
ENSGALG00000011459	45924074	45955569	
ENSGALG00000011492	23625446	23667655	XRCC5
ENSGALG00000011499	50249539	50270243	SCARB2
ENSGALG00000011531	46718811	46744193	APAF1
ENSGALG00000011557	47186191	47253542	UHRF1BP1L
ENSGALG00000011565	50651466	50702881	TDRD9
ENSGALG00000011615	45598072	45610154	
ENSGALG00000011621	45625353	45679661	IGF2R
ENSGALG00000011643	47672512	47732097	UTP20
ENSGALG00000011683	51915873	51947769	CENPC
ENSGALG00000011687	51898823	51911235	
ENSGALG00000011696	52195852	52255454	JAG2
ENSGALG00000011708	27324149	27507722	MYLK
ENSGALG00000011742	48069970	48074563	ART4
ENSGALG00000011744	27566419	28008798	KALRN
ENSGALG00000011849	54073440	54076485	IL2
ENSGALG00000011866	49224852	49228486	RRP7A
ENSGALG00000011961	54501619	54521075	TNIP3
ENSGALG00000011966	49768544	49787684	RANGAP1
ENSGALG00000011970	49788795	49792401	CHADL
ENSGALG00000011990	55086276	55109473	USP53
ENSGALG00000011994	55168618	55260528	SYNPO2
ENSGALG00000012005	54717088	54736656	LRRC9
ENSGALG00000012010	55453742	55481442	
ENSGALG00000012023	55232337	55241595	DACT1
ENSGALG00000012025	55274097	55338508	TA3
ENSGALG00000012044	57097275	57432432	ANK2
ENSGALG00000012072	28389233	28403654	
ENSGALG00000012074	57505958	57539448	ALPK1
ENSGALG00000012076	57543611	57548315	TIFA
ENSGALG00000012089	55450095	55492082	C14orf37
ENSGALG00000012095	55629271	55635045	CCDC198
ENSGALG00000012100	28481649	28499392	CFAP221

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000012101	55699101	55709296	AP5M1
ENSGALG00000012103	5540164	5584404	CCDC73
ENSGALG00000012118	56011682	56040330	TMEM260
ENSGALG00000012129	29030066	29062387	CCDC93
ENSGALG00000012147	29074922	29083226	DDX18
ENSGALG00000012155	58394125	58445817	EGF
ENSGALG00000012177	29971539	29999038	NCKAP5
ENSGALG00000012196	58526506	58553506	MCUB
ENSGALG00000012245	60334644	60342396	ADH5
ENSGALG00000012260	30797938	30815468	LCT
ENSGALG00000012263	57806860	57827533	NEMF
ENSGALG00000012293	51105368	51109027	C22orf23
ENSGALG00000012317	47035043	47108957	ADGB
ENSGALG00000012321	57934324	57991948	MAP4K5
ENSGALG00000012361	58040392	58064238	NIN
ENSGALG00000012362	31073812	31346787	THSD7B
ENSGALG00000012377	31413137	31428256	HNMT
ENSGALG00000012407	32016417	32446623	LRP1B
ENSGALG00000012412	48792857	48928383	MTHFD1L
ENSGALG00000012422	51220223	51226301	
ENSGALG00000012472	51492000	51505358	IL2RB
ENSGALG00000012484	35331804	35359923	RIF1
ENSGALG00000012488	51546120	51553306	TST
ENSGALG00000012593	40166144	40179451	SLC28A3
ENSGALG00000012689	60597695	60709367	KIF13A
ENSGALG00000012720	62240247	62268129	NUP153
ENSGALG00000012731	62416160	62431263	TBC1D7
ENSGALG00000012768	63420678	63425726	GCM2
ENSGALG00000012860	1327076	1332053	HSD11B1L
ENSGALG00000012866	67896375	67905857	SERPINB6L
ENSGALG00000012903	68591175	68684088	PIGN
ENSGALG00000012932	59021804	59039816	FGD4
ENSGALG00000012984	1185316	1196659	
ENSGALG00000012987	60351125	60361329	CCDC77
ENSGALG00000013005	78491436	78497046	SNRNP48
ENSGALG00000013006	78498575	78505697	ROPN1L
ENSGALG00000013034	61754952	61846994	CECR2
ENSGALG00000013035	78614461	78623745	SBK2
ENSGALG00000013058	62161773	62170124	
ENSGALG00000013060	79496841	79702592	ADCY2
ENSGALG00000013079	80294941	80381834	
ENSGALG00000013090	22249905	22254300	LOXL4
ENSGALG00000013117	64035202	64232501	PIK3C2G
ENSGALG00000013131	83841416	83847040	C18orf21
ENSGALG00000013169	11854602	11862668	IL20RB
ENSGALG00000013174	65371068	65390497	RECQL
ENSGALG00000013177	65432216	65472333	BCAT1

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000013218	66846831	66850139	C3AR1
ENSGALG00000013232	1490889	1495432	RHBG
ENSGALG00000013253	1402697	1413677	INSRR
ENSGALG00000013268	89063802	89211727	
ENSGALG00000013294	9208018	9221830	CYP19A1
ENSGALG00000013400	89230899	89237386	PDCD6
ENSGALG00000013402	89281165	89346954	AHRR
ENSGALG00000013468	61707202	61720669	TLR3
ENSGALG00000013495	4726168	4730946	GSDMA
ENSGALG00000013503	61727991	61741835	FAM149A
ENSGALG00000013548	16662049	16666243	GZMA
ENSGALG00000013600	63214032	63216773	
ENSGALG00000013624	90472344	90506067	FAM65B
ENSGALG00000013627	63439358	63479725	SLC7A2
ENSGALG00000013661	63627699	63673835	MICU3
ENSGALG00000013697	92127902	92139467	CNDP1
ENSGALG00000013720	92301222	92334345	FBXO15
ENSGALG00000013727	51934949	51998398	SYNJ2
ENSGALG00000013738	6691790	6711192	OPTN
ENSGALG00000013745	93915972	93996632	RTTN
ENSGALG00000013804	65542342	65548565	SRD5A3
ENSGALG00000013822	54155137	54192103	TXLNB
ENSGALG00000013853	97433438	97456386	AFG3L2
ENSGALG00000013879	3565948	3577370	TIA1
ENSGALG00000013893	7620168	7625810	MNS1
ENSGALG00000013962	55939197	56007426	HBS1L
ENSGALG00000014071	67751004	67983940	
ENSGALG00000014083	68025368	68044088	INTS13
ENSGALG00000014192	67190626	67220017	ATP10D
ENSGALG00000014200	67270708	67291796	
ENSGALG00000014217	68026814	68043002	GUF1
ENSGALG00000014227	70416011	70422094	UPK3A
ENSGALG00000014261	69068033	69072673	UCHL1
ENSGALG00000014267	69357333	69363626	RBM47
ENSGALG00000014298	69760276	69796593	RFC1
ENSGALG00000014455	77027981	77029234	LPAR5
ENSGALG00000014603	77379603	77388708	C1S
ENSGALG00000014615	99747385	99848774	LAMA1
ENSGALG00000014642	51274317	51349988	CHD1Z
ENSGALG00000014664	57880857	57984258	
ENSGALG00000014684	57003242	57017676	ERAP1
ENSGALG00000014736	77862437	77876315	KEL
ENSGALG00000014762	100238641	100256976	
ENSGALG00000014765	20588770	20606823	TRIM23
ENSGALG00000014799	101479110	101500299	METTL4
ENSGALG00000014848	60999895	61164573	TRDN
ENSGALG00000014865	13709871	13717629	

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ENSGALG00000014892	63018384	63155719	CEP85L
ENSGALG00000014923	24570223	24702341	ARHGEF28
ENSGALG00000014924	79422423	79478850	POLQ
ENSGALG00000014953	63973179	63984264	RWDD1
ENSGALG00000014982	103124812	103156745	RBBP8
ENSGALG00000014989	23387606	23392488	S100Z
ENSGALG00000015001	65864380	65965590	
ENSGALG00000015002	25266850	25313351	MRPS27
ENSGALG00000015029	79678051	79740966	EVC2
ENSGALG00000015056	103493136	103529171	
ENSGALG00000015086	103586107	103657016	OSBPL1A
ENSGALG00000015109	34585926	34650856	TJP2
ENSGALG00000015142	106423071	106443930	DSG2
ENSGALG00000015157	106612010	106661036	
ENSGALG00000015167	37397609	37448829	PRUNE2
ENSGALG00000015183	106851537	106876449	
ENSGALG00000015191	83409648	83412396	
ENSGALG00000015196	107248918	107350660	ASXL3
ENSGALG00000015204	83574965	83598582	ATG3
ENSGALG00000015218	83652332	83662208	SLC19A2
ENSGALG00000015230	83683837	83773394	NME7
ENSGALG00000015249	84135950	84154902	TTF2
ENSGALG00000015276	67163349	67182833	
ENSGALG00000015294	84937803	84959755	ADGRG7
ENSGALG00000015340	111439673	111462441	TGS1
ENSGALG00000015343	68272709	68292629	RTN4IP1
ENSGALG00000015348	86503359	86619306	ALCAM
ENSGALG00000015395	88706603	88713873	CD200L
ENSGALG00000015461	91922427	91932287	
ENSGALG00000015473	92237349	92247857	ADPRH
ENSGALG00000015474	92260427	92282945	CD80
ENSGALG00000015511	96489993	96603886	ROBO1
ENSGALG00000015513	72689670	72775816	MMS22L
ENSGALG00000015589	63936017	64052808	MSH3
ENSGALG00000015626	82573360	82637134	RGS12
ENSGALG00000015635	82710300	82783954	HTT
ENSGALG00000015652	82846661	82870981	MFSD10
ENSGALG00000015675	98044140	98077756	
ENSGALG00000015677	66156522	66193789	SUSD1
ENSGALG00000015709	84469256	84488069	TACC3
ENSGALG00000015802	103950360	103953450	N6AMT1
ENSGALG00000015810	76741929	76754201	
ENSGALG00000015836	77740723	77786312	CEP162
ENSGALG00000015854	78202202	78210827	PGM3
ENSGALG00000015878	79685822	79697524	LCA5
ENSGALG00000015887	104901269	104945059	URB1
ENSGALG00000015902	86469040	86474132	CD8B

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ENSGALG00000016062	107931746	107940716	PSMG1
ENSGALG00000016065	107943223	107993948	BRWD1
ENSGALG00000016105	91217010	91267485	DYSF
ENSGALG00000016142	108921073	108942022	MX1
ENSGALG00000016148	109107584	109141826	C2CD2
ENSGALG00000016157	109193368	109234694	UMODL1
ENSGALG00000016221	111056475	111115975	EFHC2
ENSGALG00000016224	111259525	111332024	MAOA
ENSGALG00000016254	112898627	112924531	OTC
ENSGALG00000016258	113045418	113063987	
ENSGALG00000016263	85768055	85882423	
ENSGALG00000016278	86965136	87048983	PRIM2
ENSGALG00000016279	87070833	87079598	RAB23
ENSGALG00000016281	114486908	115483002	DMD
ENSGALG00000016297	87914790	87948320	HCRTR2
ENSGALG00000016314	88598880	88636560	ELOVL5
ENSGALG00000016316	88656612	88663923	GCM1
ENSGALG00000016370	93135658	93174800	TPO
ENSGALG00000016392	94094085	94102761	RPS7
ENSGALG00000016400	95406461	95415464	RSAD2
ENSGALG00000016455	97786521	97842913	GREB1
ENSGALG00000016468	100637696	100646358	
ENSGALG00000016475	101790655	101806609	
ENSGALG00000016491	102659050	102693303	APOB
ENSGALG00000016492	102734234	102741569	TDRD15
ENSGALG00000016498	104544323	104575302	MFSD2B
ENSGALG00000016506	104782783	104798907	ZNF512
ENSGALG00000016536	105396910	105421148	HADHA
ENSGALG00000016556	105439100	105446401	
ENSGALG00000016557	121963490	121989828	BMX
ENSGALG00000016564	105498872	105511445	PTK2B
ENSGALG00000016569	122344605	122359048	FANCB
ENSGALG00000016620	106136554	106139941	PNOC
ENSGALG00000016639	106684652	106726136	
ENSGALG00000016664	107812743	107816159	NEIL2
ENSGALG00000016681	128680925	128885733	DHRSX
ENSGALG00000016684	109234225	109245385	RHAG
ENSGALG00000016692	109266889	109273908	CENPQ
ENSGALG00000016723	110542296	110545583	
ENSGALG00000016766	132634324	132687827	REV1
ENSGALG00000016785	133946557	133969773	IL1RL1
ENSGALG00000016788	134001612	134014941	IL18RAP
ENSGALG00000016809	136466224	136492266	EDAR
ENSGALG00000016813	136898933	136901779	CHAMP1
ENSGALG00000016815	136915096	136936956	UPF3A
ENSGALG00000016854	140176223	140179854	LIG4
ENSGALG00000016865	142848690	142895582	TPP2

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000016893	145871889	145950703	UGGT2
ENSGALG00000016902	147664506	148027057	GPC5
ENSGALG00000016911	153499603	153525605	RNF219
ENSGALG00000016920	154868242	154908783	LMO7
ENSGALG00000016943	165561980	165586181	OLFM4
ENSGALG00000016980	167776863	167806722	COG3
ENSGALG00000016988	168099691	168119251	RUBCNL
ENSGALG00000016994	168671611	168672512	NUDT15
ENSGALG00000017023	170371770	170391240	NEK5
ENSGALG00000017024	170393901	170406389	NEK3
ENSGALG00000017026	170416091	170435074	VPS36
ENSGALG00000017044	171798604	171935943	TRPC4
ENSGALG00000017073	174560560	174597292	BRCA2
ENSGALG00000017086	175631550	175648871	
ENSGALG00000017148	179310484	179327166	CENPJ
ENSGALG00000017185	182611334	182628423	TMEM123
ENSGALG00000017190	182813467	182848535	CEP126
ENSGALG00000017220	185871724	185874291	TAF1D
ENSGALG00000017234	187658853	187720624	FOLH1
ENSGALG00000017248	189111245	189150763	RAB30
ENSGALG00000017250	189208361	189209550	
ENSGALG00000017308	195912297	195938222	CHRDL2
ENSGALG00000017309	195882069	195901578	RNF169
ENSGALG00000017314	195778483	195812181	C2CD3
ENSGALG00000017326	195423605	195462321	
ENSGALG00000017378	22270053	22279635	CRTAC1
ENSGALG00000017414	5081253	5096768	JUP
ENSGALG00000017485	69963233	69968568	TLR1A
ENSGALG00000017493	194226590	194228925	
ENSGALG00000019003	49905486	49937351	PRAG1
ENSGALG00000019030	194659669	194660631	
ENSGALG00000019145	130465409	130466062	
ENSGALG00000019240	80801522	80803077	
ENSGALG00000019262	68393868	68394452	
ENSGALG00000019322	49510784	49512391	TNFRSF13C
ENSGALG00000019325	49197217	49205179	
ENSGALG00000019509	94402654	94510729	CCDC102B
ENSGALG00000019543	76489687	76496184	OTULIN
ENSGALG00000019768	10433382	10468658	ACSF2
ENSGALG00000019932	67118718	67150851	
ENSGALG00000020032	34909552	34914562	
ENSGALG00000020049	29168132	29175249	KCNK16
ENSGALG00000020084	7870260	7906818	CAPN13
ENSGALG00000020108	86646003	86652740	
ENSGALG00000020316	2848848	2864846	IL13RA2
ENSGALG00000020340	58155311	58158447	TMX1
ENSGALG00000020388	45685172	45688958	

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000020402	43659562	43715163	EFCAB11
ENSGALG00000020523	67114959	67119131	TOPORS
ENSGALG00000020561	16555609	16594096	
ENSGALG00000020703	20231963	20298979	GRB14
ENSGALG00000020737	18682039	18685720	KLHL23
ENSGALG00000020788	15144369	15196130	
ENSGALG00000020813	13705897	13741849	CCDC50
ENSGALG00000020836	12480858	12488246	FAM237A
ENSGALG00000020884	11667153	11694964	
ENSGALG00000020982	10511917	10517297	
ENSGALG00000021020	17836424	17838772	CGNRHRL
ENSGALG00000021135	13042626	13046863	HAPLN3
ENSGALG00000021171	12303445	12346719	
ENSGALG00000021198	3082764	3089843	
ENSGALG00000021301	13341134	13346015	
ENSGALG00000021304	11028678	11040410	
ENSGALG00000021355	9016408	9024018	
ENSGALG00000021395	7999197	8020520	
ENSGALG00000021442	1199475	1217413	CARMIL2
ENSGALG00000021525	2531907	2533175	
ENSGALG00000021647	1518381	1532850	NRTN
ENSGALG00000021656	3747288	3759758	PTPN22
ENSGALG00000021883	4347929	4350919	
ENSGALG00000022166	22682686	22692059	PNKD
ENSGALG00000022702	194820512	194824114	CHRNA10
ENSGALG00000022850	104926401	104932042	TMEM214
ENSGALG00000022875	98303218	98307540	
ENSGALG00000022882	91704833	91707742	ZADH2
ENSGALG00000022901	87198999	87201427	
ENSGALG00000023015	58158548	58178806	TMEM244
ENSGALG00000023338	9721862	9729512	CBX2
ENSGALG00000023497	23703644	23710582	MINDY4B
ENSGALG00000023506	16420760	16425137	
ENSGALG00000023683	4970847	4979332	TCTN2
ENSGALG00000023689	6346895	6367468	ASS1
ENSGALG00000023740	12156905	12158534	HBZ
ENSGALG00000023843	3476861	3485053	FRMD7
ENSGALG00000023847	5070342	5078795	
ENSGALG00000023886	1803327	1832501	ZNF804A
ENSGALG00000023898	1307477	1370931	PLEKHG4
ENSGALG00000023906	2669898	2671690	RNF223
ENSGALG00000023924	3190157	3190495	
ENSGALG00000023950	2657652	2663698	CR1L
ENSGALG00000023953	2634610	2641479	
ENSGALG00000024039	1632455	1636009	
ENSGALG00000024056	11977809	11983312	CHST3
ENSGALG00000024490	69891819	69904924	

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000025764	5102761	5107413	FKBP10
ENSGALG00000025971	105661748	105672793	KCNK3
ENSGALG00000025996	33407191	33426169	
ENSGALG00000026015	10715164	10719635	
ENSGALG00000026019	11469738	11497205	ASCC1
ENSGALG00000026038	14838941	14841124	
ENSGALG00000026151	1217950	1251928	CEP250
ENSGALG00000026152	2254875	2264684	GBP
ENSGALG00000026189	10204919	10208415	
ENSGALG00000026241	2909715	2914206	GRIN3B
ENSGALG00000026299	88660356	88667176	
ENSGALG00000026315	5799336	5801907	RAB34
ENSGALG00000026322	49045426	49051770	ARMT1
ENSGALG00000026328	4662820	4707653	MIEN1
ENSGALG00000026392	5925697	5928564	PIPOX
ENSGALG00000026395	52896075	52980564	
ENSGALG00000026422	28369889	28385093	
ENSGALG00000026431	5910507	5916770	SEZ6
ENSGALG00000026491	9118692	9123791	TMEM17
ENSGALG00000026850	4877060	4879564	TICAM1
ENSGALG00000026957	23090874	23099929	SEMA4G
ENSGALG00000027083	28871534	28873444	
ENSGALG00000027122	54262171	54293903	APPL2
ENSGALG00000027176	2795017	2803822	
ENSGALG00000027183	1251267	1255402	
ENSGALG00000027316	1168958	1170234	CRNN
ENSGALG00000027389	20155100	20189099	RGS7BP
ENSGALG00000027444	12591371	12598630	
ENSGALG00000027484	11480791	11484789	C20orf85
ENSGALG00000027506	22315127	22320358	DNAJB2
ENSGALG00000027526	4887092	4897385	COL9A2
ENSGALG00000027579	105648428	105695763	MRPS6
ENSGALG00000027635	13284132	13287411	NME3
ENSGALG00000027695	3131564	3134816	PCBP4
ENSGALG00000027702	5349153	5385670	SCN11A
ENSGALG00000027704	13862869	14132878	
ENSGALG00000027712	1331123	1334664	SLAMF8
ENSGALG00000027714	63371447	63454155	ATG10
ENSGALG00000027805	2279143	2280927	
ENSGALG00000027885	70320126	70322177	C4orf19
ENSGALG00000027922	10941215	10949135	ETAA1
ENSGALG00000027983	15004028	15017912	TNK2
ENSGALG00000028016	49189519	49197004	
ENSGALG00000028023	10114261	10120033	LRRC74B
ENSGALG00000028032	106882967	107143719	MSRA
ENSGALG00000028069	23246190	23256408	WNT16
ENSGALG00000028083	170470417	170471628	THSD1

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000028138	107205765	107228525	
ENSGALG00000028153	22043498	22045110	
ENSGALG00000028167	9220720	9231568	RBM18
ENSGALG00000028172	13160827	13181241	WDR90
ENSGALG00000028207	20762518	20774873	
ENSGALG00000028238	23565911	23569213	
ENSGALG00000028262	4970553	4972635	
ENSGALG00000028294	15906717	15914012	VWA5B2
ENSGALG00000028298	32755529	32886954	
ENSGALG00000028302	17160590	17161925	UQCRQ
ENSGALG00000028308	4872138	4879191	TNS4
ENSGALG00000028341	2684354	2687041	
ENSGALG00000028357	19456900	19489987	MMR1L2
ENSGALG00000028367	219651	222858	
ENSGALG00000028439	2684815	2703227	FAM35A
ENSGALG00000028457	30640415	30649263	MAP3K19
ENSGALG00000028473	8946359	8952613	
ENSGALG00000028506	1691893	1710105	NHSL2
ENSGALG00000028512	22415677	22485273	
ENSGALG00000028561	19787107	19841142	SZT2
ENSGALG00000028565	1828640	1876670	PCDHGC3
ENSGALG00000028620	9090918	9092123	
ENSGALG00000028622	1382998	1391936	PEAR1
ENSGALG00000028629	185798254	185812845	TM4SF1a
ENSGALG00000028666	54867978	54879976	
ENSGALG00000028759	35028709	35060292	LYPD6B
ENSGALG00000028815	6257931	6267229	
ENSGALG00000028830	9946953	9949387	
ENSGALG00000028849	30864013	30895009	SCAF11
ENSGALG00000028886	45498838	45519267	
ENSGALG00000028897	48678797	48722693	
ENSGALG00000028960	195852602	195857112	NEU3
ENSGALG00000028975	1976126	1980330	
ENSGALG00000029000	3231438	3234557	HYAL3
ENSGALG00000029015	3552405	3555683	TM6SF2
ENSGALG00000029118	81574893	81580647	TRMT10B
ENSGALG00000029151	2537062	2540128	ISLR2
ENSGALG00000029197	454235	690429	KIRREL3
ENSGALG00000029287	126413795	126551270	
ENSGALG00000029298	83605465	83640498	F5
ENSGALG00000029308	69135540	69146688	
ENSGALG00000029321	83586479	83614083	
ENSGALG00000029360	7756823	7779971	
ENSGALG00000029381	78333	81467	TAP2
ENSGALG00000029390	5097210	5099714	C15H12ORF65
ENSGALG00000029454	25432899	25445807	
ENSGALG00000029503	1234497	1237927	AES

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000029532	35249909	35251574	
ENSGALG00000029599	9635	25890	ACVR1B
ENSGALG00000029618	368166	371658	AGBL2
ENSGALG00000029621	3167398	3189955	SEMA3F
ENSGALG00000029635	4042828	4052619	
ENSGALG00000029652	503169	547399	OPHN1
ENSGALG00000029702	358398	367796	FNBP4
ENSGALG00000029714	20102968	20112060	UNC45A
ENSGALG00000029824	54863006	54871746	
ENSGALG00000030005	65206	68264	IGSF1L3
ENSGALG00000030012	5120164	5122823	EMILIN3
ENSGALG00000030024	32905460	32969236	USP15
ENSGALG00000030027	4208870	4217491	MCAM
ENSGALG00000030030	132121027	132231350	RSPO2
ENSGALG00000030055	1143254	1161618	RIPOR1
ENSGALG00000030084	43265788	43285281	EXOSC7
ENSGALG00000030097	2153100	2156682	RCC1
ENSGALG00000030139	5197792	5205005	
ENSGALG00000030160	555417	567680	DRC7
ENSGALG00000030169	6496192	6513565	
ENSGALG00000030270	14372	17201	CD1C
ENSGALG00000030316	5329605	5330854	
ENSGALG00000030324	7556518	7647412	KIAA1324L
ENSGALG00000030383	19227573	19298741	SPATA16
ENSGALG00000030405	2035813	2036205	
ENSGALG00000030506	77815472	77816407	
ENSGALG00000030511	6663741	6668938	SLC19A1
ENSGALG00000030552	41370014	41376467	
ENSGALG00000030587	30388737	30402788	
ENSGALG00000030602	90146901	90170368	ADAM33
ENSGALG00000030710	72501	90584	L3MBTL1
ENSGALG00000030718	13229154	13233433	
ENSGALG00000030719	45979330	45995515	CLMN
ENSGALG00000030789	10044964	10074000	
ENSGALG00000030802	125013467	125134159	SHROOM2
ENSGALG00000030844	7494480	7523025	DMTF1
ENSGALG00000030886	999174	1001420	PTGDS
ENSGALG00000030900	2551275	2558427	NCMAP
ENSGALG00000030925	32083864	32152185	LHPP
ENSGALG00000030930	35855432	35856382	
ENSGALG00000030941	1138597	1146644	KIAA1324
ENSGALG00000031021	91845292	91911288	ERICH1
ENSGALG00000031119	6099444	6113592	
ENSGALG00000031149	2653656	2657098	
ENSGALG00000031182	58868218	58927474	FANCM
ENSGALG00000031186	49551210	49586894	MEI1
ENSGALG00000031219	75794168	75800647	

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000031240	6251280	6259972	ACAD10
ENSGALG00000031276	240801	267480	
ENSGALG00000031281	105012037	105020075	GTF3C2
ENSGALG00000031393	10838850	10841240	
ENSGALG00000031416	13288569	13313056	UBN1
ENSGALG00000031511	5289267	5303607	HIP1R
ENSGALG00000031534	8297642	8403485	ARID5B
ENSGALG00000031560	79232533	79256355	USF3
ENSGALG00000031588	36056215	36063675	
ENSGALG00000031752	1397978	1403745	
ENSGALG00000031807	5095662	5099405	
ENSGALG00000031812	2863361	2867426	TDRKH
ENSGALG00000031814	71639774	71703468	
ENSGALG00000031820	4715737	4719058	
ENSGALG00000031841	12490400	12514687	SLX4
ENSGALG00000031866	884635	889464	
ENSGALG00000031895	9107305	9148769	SDK2
ENSGALG00000031906	1336572	1360690	FAM83C
ENSGALG00000032082	22722141	22725926	FAM133B
ENSGALG00000032092	98696183	98754996	PPP4R1
ENSGALG00000032143	17142610	17163354	CRISPLD2
ENSGALG00000032149	4232184	4238046	OSBPL7
ENSGALG00000032155	1543195	1557476	
ENSGALG00000032184	841145	846278	CSPG5
ENSGALG00000032231	58543	72898	C4
ENSGALG00000032372	7394751	7414352	CYB5R2
ENSGALG00000032386	33015814	33091642	DCLK2
ENSGALG00000032398	2613832	2645512	ASPM
ENSGALG00000032410	18767309	18788285	CBFA2T3
ENSGALG00000032588	4384127	4390002	ARPC1B
ENSGALG00000032599	77089837	77115522	ZNF384
ENSGALG00000032610	5381307	5386131	NAGLU
ENSGALG00000032718	128127251	128157395	NIPAL2
ENSGALG00000032732	138812399	138834988	WASHC5
ENSGALG00000032753	105390311	105396066	GAREM2
ENSGALG00000032780	40680767	40717054	TTC13
ENSGALG00000032916	7892569	7905427	
ENSGALG00000032957	29428817	29433345	NOCT
ENSGALG00000033001	4414437	4415527	ATP5J2
ENSGALG00000033002	2442374	2449919	SLC7A3
ENSGALG00000033060	23929924	23930989	
ENSGALG00000033068	391022	394724	TLR21
ENSGALG00000033106	42864751	42878912	
ENSGALG00000033138	6458891	6470750	ZMYND12
ENSGALG00000033162	4729921	4735633	PSMD3
ENSGALG00000033179	56104804	56137792	TGFBR1
ENSGALG00000033198	8830407	8858028	MYO5C

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000033199	105330816	105350209	
ENSGALG00000033212	49564706	49571912	HSP90AA1
ENSGALG00000033254	129000072	129034245	SPAG1
ENSGALG00000033277	2954266	2960956	PPM1M
ENSGALG00000033328	4097552	4162312	PACS2
ENSGALG00000033461	31378969	31387982	
ENSGALG00000033497	4844452	4882773	FOXP4
ENSGALG00000033553	9203782	9222107	
ENSGALG00000033557	19950725	19956592	CTSH
ENSGALG00000033562	11085271	11086071	
ENSGALG00000033671	171352433	171447282	FREM2
ENSGALG00000033759	28266953	28296420	RAVER2
ENSGALG00000033769	38032888	38034822	BBS10
ENSGALG00000033807	11501308	11503836	TYSND1
ENSGALG00000033953	1864533	1871303	SHROOM4
ENSGALG00000033956	10021724	10056809	SFXN1
ENSGALG00000033971	1214734	1216748	
ENSGALG00000033992	35784910	35786718	
ENSGALG00000034013	32198043	32203583	
ENSGALG00000034044	20052965	20087739	TBC1D12
ENSGALG00000034107	3220329	3225445	TRIM63
ENSGALG00000034119	55990571	56094186	COL15A1
ENSGALG00000034140	106123198	106130102	ZNF395
ENSGALG00000034225	500596	519834	DEAF1
ENSGALG00000034261	159555153	159555479	
ENSGALG00000034264	36155770	36201407	
ENSGALG00000034288	1141736	1142441	
ENSGALG00000034313	26292678	26293813	
ENSGALG00000034347	280212	292746	KIF21B
ENSGALG00000034374	57047012	57078983	STX7
ENSGALG00000034383	2116749	2123560	TRMT2B
ENSGALG00000034396	105312337	105323532	TMEM50B
ENSGALG00000034414	7821296	7832434	SLU7
ENSGALG00000034493	46064049	46088568	DCLK3
ENSGALG00000034504	50835752	50841816	
ENSGALG00000034518	51172152	51174975	
ENSGALG00000034675	117198086	117205612	XKR9
ENSGALG00000034761	4930777	4946186	FHAD1
ENSGALG00000034822	540362	550469	
ENSGALG00000034826	2407922	2408746	CXorf65
ENSGALG00000034932	108844363	108894770	BACE2
ENSGALG00000035017	2673198	2693403	
ENSGALG00000035047	4395017	4398275	
ENSGALG00000035075	81925	86753	TAP1
ENSGALG00000035115	12456914	12459658	
ENSGALG00000035136	66338169	66379299	C9orf84
ENSGALG00000035228	78962706	79001440	

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000035246	955760	959693	
ENSGALG00000035384	103261771	103315035	TMEM241
ENSGALG00000035397	142082573	142086949	NDRG1
ENSGALG00000035447	7336587	7340177	
ENSGALG00000035453	48198262	48204933	RP9
ENSGALG00000035465	19927084	19932226	WDR76
ENSGALG00000035492	46514678	46813840	ELMO1
ENSGALG00000035595	2279372	2289972	SLC14A1
ENSGALG00000035605	18632759	18667992	
ENSGALG00000035625	97142592	97198921	CEP192
ENSGALG00000035675	4940548	4957050	
ENSGALG00000035696	110033196	110055218	RRP1B
ENSGALG00000035721	1796430	1803097	C2
ENSGALG00000035743	16970803	16992524	ATP2C2
ENSGALG00000035761	22663994	22676382	
ENSGALG00000035762	2772675	2774216	PRSS57
ENSGALG00000035799	323770	336679	SHISA9
ENSGALG00000035814	1399403	1409506	
ENSGALG00000035827	13179584	13219022	
ENSGALG00000035856	1283095	1284656	CD48
ENSGALG00000035918	6912250	6917437	
ENSGALG00000035945	1257270	1260719	
ENSGALG00000035949	42421229	42481002	ACAD11
ENSGALG00000036067	56261726	56276820	RBFA
ENSGALG00000036086	2525471	2528124	TAGLN2
ENSGALG00000036093	357269	366141	PTPN7
ENSGALG00000036108	2080809	2096566	
ENSGALG00000036214	245686	252851	PARK7
ENSGALG00000036238	49145298	49176552	LUC7L2
ENSGALG00000036240	48974017	48992482	
ENSGALG00000036263	2405099	2411772	UBA7
ENSGALG00000036309	43050041	43132629	LARS2
ENSGALG00000036346	2018796	2022986	AMH
ENSGALG00000036484	3561216	3574042	NCAN
ENSGALG00000036516	108608380	108614937	
ENSGALG00000036583	11936299	11948564	
ENSGALG00000036629	1851537	1852461	
ENSGALG00000036689	32803127	32814128	
ENSGALG00000036771	785527	788793	
ENSGALG00000036783	4275996	4289784	
ENSGALG00000036789	17407355	17789217	ADGRL2
ENSGALG00000036805	311493	328512	SPTB
ENSGALG00000036840	3429551	3431477	
ENSGALG00000036892	558497	582785	BUB1B
ENSGALG00000036894	910977	933990	ABCA2
ENSGALG00000036965	5973062	5996551	PTPA
ENSGALG00000037018	9862750	9870989	USP36

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000037052	5170433	5172814	TMEM234
ENSGALG00000037076	105352798	105389904	GART
ENSGALG00000037163	6953116	6954713	
ENSGALG00000037241	656092	672722	KCNAB2
ENSGALG00000037256	3440629	3442213	GTPBP3
ENSGALG00000037301	36448667	36651282	ACVR1
ENSGALG00000037314	7009557	7026631	RPH3AL
ENSGALG00000037332	49474814	49502263	
ENSGALG00000037407	407251	416312	FAM118B
ENSGALG00000037410	284344	322060	HEPH
ENSGALG00000037414	105324804	105326122	DNAJC28
ENSGALG00000037435	9732868	9752834	
ENSGALG00000037439	134017093	134048686	SLC9A4
ENSGALG00000037453	118052590	118075361	TERF1
ENSGALG00000037464	41292667	41355829	WDR27
ENSGALG00000037526	3396001	3398518	
ENSGALG00000037625	259255	381102	
ENSGALG00000037644	123703762	123734221	CNGB3
ENSGALG00000037675	136894050	137014125	COL14A1
ENSGALG00000037781	34885417	34890567	GSR
ENSGALG00000037816	11250381	11266775	
ENSGALG00000037819	190601433	190603690	
ENSGALG00000037851	16816438	16818397	KK34
ENSGALG00000037860	2848252	2874073	TET3
ENSGALG00000037939	578267	583409	ADGRG1
ENSGALG00000037950	815996	845140	
ENSGALG00000037951	78465927	78476335	HSD3B1
ENSGALG00000038078	4273090	4285753	
ENSGALG00000038097	387616	395692	EI24
ENSGALG00000038109	4083525	4087730	MRPL45
ENSGALG00000038140	25162884	25180520	
ENSGALG00000038145	799227	818934	DPP7
ENSGALG00000038146	371053	377550	
ENSGALG00000038175	148983003	148988533	NAPRT
ENSGALG00000038209	169039	173420	TRIM39.1
ENSGALG00000038269	251816	252922	
ENSGALG00000038311	6633230	6662722	COL18A1
ENSGALG00000038426	937592	940719	CPLX4
ENSGALG00000038541	29471	33286	VPS37C
ENSGALG00000038584	1125790	1160045	
ENSGALG00000038612	9384943	9430089	COL4A3
ENSGALG00000038621	6325381	6354370	
ENSGALG00000038657	554078	559967	ZNF777
ENSGALG00000038710	71890196	71896378	MANSC1
ENSGALG00000038728	350677	356238	
ENSGALG00000038740	46121	50542	AMY2A
ENSGALG00000038771	49400755	49460118	TECRL

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000038801	1630552	1633524	ATP5B
ENSGALG00000038865	316485	332935	PRMT7
ENSGALG00000038954	11299573	11303669	LSM11
ENSGALG00000038972	4439972	4462470	
ENSGALG00000038984	5470595	5477143	
ENSGALG00000039001	80974887	81050425	FILIP1
ENSGALG00000039080	18956776	19014765	CD44
ENSGALG00000039139	55221387	55442502	TNS3
ENSGALG00000039155	5082235	5112652	ZHX3
ENSGALG00000039219	11545754	11563815	ADAMTS14
ENSGALG00000039224	141492463	141505508	HHLA1
ENSGALG00000039268	7994663	7995025	
ENSGALG00000039322	3813929	3819587	DDR2
ENSGALG00000039349	39594353	39768545	DISC1
ENSGALG00000039384	10048504	10057685	
ENSGALG00000039385	11621217	11622487	
ENSGALG00000039391	72832	80536	ZC3H12B
ENSGALG00000039479	53322790	53335591	
ENSGALG00000039499	123211702	123231013	LRRCC1
ENSGALG00000039509	141875709	142000765	TG
ENSGALG00000039535	4759613	4802966	D2HGDH
ENSGALG00000039554	405695	418007	
ENSGALG00000039590	138070329	138078402	
ENSGALG00000039611	2593226	2601741	
ENSGALG00000039643	25563	27209	TMEM79
ENSGALG00000039652	8425824	8435377	ARHGEF37
ENSGALG00000039659	9891183	9921006	
ENSGALG00000039707	4390621	4391652	
ENSGALG00000039716	5309931	5318833	RNF19B
ENSGALG00000039727	530264	535057	
ENSGALG00000039751	185732435	185751184	PANX1
ENSGALG00000039887	2504446	2506092	
ENSGALG00000039901	149440993	149468746	PUF60
ENSGALG00000039903	9938851	9946439	VSIG10
ENSGALG00000040041	963583	965332	SLC35A4
ENSGALG00000040070	12282289	12286205	PDIA2
ENSGALG00000040084	58055706	58065788	MRS2
ENSGALG00000040114	22901214	23034777	PTPRZ1
ENSGALG00000040156	44306591	44389396	CCDC88C
ENSGALG00000040279	2382455	2393033	RHCE
ENSGALG00000040321	170260135	170261034	
ENSGALG00000040395	6714135	6715477	SPATA22
ENSGALG00000040432	6835515	6861392	
ENSGALG00000040436	16272211	16303104	GAD2
ENSGALG00000040644	1003902	1006332	C8G
ENSGALG00000040663	6810990	6812834	RSC1A1
ENSGALG00000040709	132024486	132091229	VWA3B

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000040718	15609115	15610799	
ENSGALG00000040754	918081	919817	CYP1C1
ENSGALG00000040880	11004406	11017978	EDN3
ENSGALG00000040891	20027818	20125211	RSU1
ENSGALG00000040896	4968055	5062966	FASN
ENSGALG00000040908	328871	345898	HIP1
ENSGALG00000040923	7127033	7190412	AK8
ENSGALG00000040942	6162198	6186080	EFCAB5
ENSGALG00000040949	90715399	90844210	
ENSGALG00000040995	35383942	35421288	
ENSGALG00000041013	22734389	22773379	TNS1
ENSGALG00000041089	9474822	9588748	
ENSGALG00000041153	6153440	6155856	FAM109A
ENSGALG00000041179	128662474	128890608	VPS13B
ENSGALG00000041181	13910194	13915248	
ENSGALG00000041229	753930	754904	
ENSGALG00000041233	139401611	139404620	FAM84B
ENSGALG00000041249	246787	247800	
ENSGALG00000041251	20329726	20343807	HDAC10
ENSGALG00000041343	41475923	41504741	
ENSGALG00000041372	44156261	44201027	
ENSGALG00000041392	13180214	13211601	
ENSGALG00000041428	797572	814175	NEK4
ENSGALG00000041436	27623103	27657436	
ENSGALG00000041547	7012349	7015424	
ENSGALG00000041556	1679275	1709692	GPATCH8
ENSGALG00000041659	9810013	9813059	SLC2A4RG
ENSGALG00000041671	1204673	1205708	
ENSGALG00000041722	94035	139377	STX1A
ENSGALG00000041834	4713252	4725845	AEBP1
ENSGALG00000041854	76488439	76523293	FAM184B
ENSGALG00000041897	3463002	3466176	YJEFN3
ENSGALG00000041977	17396691	17432723	
ENSGALG00000042001	35288232	35306393	
ENSGALG00000042009	6718330	6730623	HMMR
ENSGALG00000042062	81985622	81988717	HMX1
ENSGALG00000042136	108086835	108304491	PKHD1
ENSGALG00000042153	3228730	3241731	APC2
ENSGALG00000042184	4544396	4552069	ALDH4A1
ENSGALG00000042199	10778501	10801878	SLC12A5
ENSGALG00000042275	1208698	1214238	
ENSGALG00000042388	58293669	58629545	LAMA2
ENSGALG00000042419	51527734	51536411	KCTD17
ENSGALG00000042460	5430750	5434416	FPGS
ENSGALG00000042469	108253971	108338935	PRKDC
ENSGALG00000042471	3482204	3498520	IL2RA
ENSGALG00000042481	65431282	65669969	FARS2

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000042485	2114444	2148315	PHACTR4
ENSGALG00000042597	8641682	8647707	
ENSGALG00000042647	510007	519341	CNGB1
ENSGALG00000042705	5476398	5479857	KCNK15
ENSGALG00000042761	4886188	4888849	MUL1
ENSGALG00000042769	1349102	1350281	
ENSGALG00000042801	4606606	4609137	
ENSGALG00000042839	8687069	8718924	FAM214A
ENSGALG00000042851	74475027	74593998	PPARGC1A
ENSGALG00000042871	22380435	22411706	SLIT1
ENSGALG00000042906	41879957	41881417	
ENSGALG00000042928	18941610	18947439	
ENSGALG00000043014	5548475	5552552	
ENSGALG00000043053	6661769	6666141	DAO
ENSGALG00000043088	245053	250144	
ENSGALG00000043223	3498587	3653964	COL26A1
ENSGALG00000043245	26430953	26433431	
ENSGALG00000043357	6939266	6946547	ANKRD13A
ENSGALG00000043379	41319152	41322432	
ENSGALG00000043389	8380486	8416166	PPARGC1B
ENSGALG00000043390	103416843	103491928	
ENSGALG00000043400	1411893	1416397	BCDIN3D
ENSGALG00000043401	25526958	25541830	
ENSGALG00000043570	115613450	115669550	SGK3
ENSGALG00000043584	83179142	83351003	COL19A1
ENSGALG00000043669	47198237	47232926	
ENSGALG00000043672	640217	687795	STAB1
ENSGALG00000043688	8592131	8600567	
ENSGALG00000043703	763219	769060	
ENSGALG00000043826	5164861	5184130	ANXA11
ENSGALG00000043828	1546320	1555575	HEXA
ENSGALG00000043852	68467127	68471014	
ENSGALG00000043904	17864463	17882839	SH3RF2
ENSGALG00000043909	17836546	17840466	
ENSGALG00000044007	8570011	8573489	
ENSGALG00000044019	17371299	17405300	
ENSGALG00000044053	4264395	4269225	NLRX1
ENSGALG00000044141	46639207	46643200	THAP9
ENSGALG00000044187	5793270	5946808	LMF1
ENSGALG00000044229	9816466	9817324	
ENSGALG00000044298	5790040	5791347	
ENSGALG00000044299	5210085	5219869	
ENSGALG00000044307	25393984	25411658	
ENSGALG00000044330	360973	378769	
ENSGALG00000044362	35975250	35980111	PP2D1
ENSGALG00000044406	4622928	4626326	PPP1R1B
ENSGALG00000044431	10037277	10037804	NPB

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000044433	4033907	4040176	MRPS15
ENSGALG00000044510	92226911	92240484	C18orf63
ENSGALG00000044567	2275195	2286110	
ENSGALG00000044573	167810540	167829768	
ENSGALG00000044576	8589162	8592265	
ENSGALG00000044606	106703338	106726193	MEP1B
ENSGALG00000044618	17798993	17805421	
ENSGALG00000044620	90177250	90228176	
ENSGALG00000044661	1271207	1272845	
ENSGALG00000044706	1217284	1222463	
ENSGALG00000044730	3709840	3744844	
ENSGALG00000044774	102133638	102134382	
ENSGALG00000044940	5342425	5343714	GCNT3
ENSGALG00000044979	15262989	15270491	
ENSGALG00000044997	6766480	6771143	SH2D5
ENSGALG00000045028	68528430	68534092	LRRC19
ENSGALG00000045029	21256994	21258283	
ENSGALG00000045035	931381	933117	
ENSGALG00000045067	6080671	6118332	
ENSGALG00000045092	78821219	78829951	CCDC112
ENSGALG00000045125	12927568	12929496	GP5
ENSGALG00000045155	25504621	25513779	
ENSGALG00000045168	59380189	59387463	
ENSGALG00000045173	83783694	83796470	
ENSGALG00000045179	2559893	2563120	
ENSGALG00000045204	154444261	154449459	FBXL3
ENSGALG00000045212	1507914	1513516	PLCD3
ENSGALG00000045218	7100719	7141338	MYO18B
ENSGALG00000045232	7026294	7051788	SYCP2
ENSGALG00000045286	23842908	23854232	
ENSGALG00000045310	1531397	1539853	
ENSGALG00000045350	16715725	16741025	
ENSGALG00000045365	194646692	194647502	OR51E1
ENSGALG00000045410	89236876	89239329	FASTKD5
ENSGALG00000045414	179330679	179371572	
ENSGALG00000045466	6816418	6817036	
ENSGALG00000045488	5633210	5642890	RGSL1
ENSGALG00000045584	11011877	11019401	
ENSGALG00000045605	171199227	171200360	
ENSGALG00000045611	28163	31040	GLMP
ENSGALG00000045671	13872559	13884307	
ENSGALG00000045706	778866	781827	
ENSGALG00000045776	12942659	12944948	CPN2
ENSGALG00000045792	28669035	28683746	WDR78
ENSGALG00000045816	250513	259541	ROBO3
ENSGALG00000045935	2672496	2676279	
ENSGALG00000045961	10166408	10170608	NRSN2

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000045983	22161538	22193169	
ENSGALG00000046062	11048079	11049623	
ENSGALG00000046069	2446126	2450103	
ENSGALG00000046130	3737835	3740420	
ENSGALG00000046180	27739027	27755635	TDRD1
ENSGALG00000046187	55786716	55800554	PARP12
ENSGALG00000046258	126387618	126404515	
ENSGALG00000046262	9719205	9743172	CCDC60
ENSGALG00000046263	10195351	10196257	MXD3
ENSGALG00000046282	49560738	49561602	
ENSGALG00000046384	4226296	4229044	LRRC46
ENSGALG00000046461	12939315	12941006	LRRC15
ENSGALG00000046580	29472036	29493604	
ENSGALG00000046598	39027631	39028922	
ENSGALG00000046616	16844159	16908817	
ENSGALG00000046637	88479684	88487279	
ENSGALG00000046646	1177769	1182943	
ENSGALG00000046649	5173725	5176544	DCDC2B

Table S 46. List of genes harbouring non-synonymous deleterious variants in 10 chicken populations

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000000123	134466	137899	
ENSGALG00000000243	1782741	1787570	RDM1
ENSGALG00000000365	1169897	1172573	NKX2-6
ENSGALG00000000430	551866	586908	SPPL2B
ENSGALG00000000498	2830975	2847223	ACE
ENSGALG00000000545	1715950	1719075	REN
ENSGALG00000000584	375289	387140	
ENSGALG00000000616	313618	317551	ELF3
ENSGALG00000001049	657606	667042	
ENSGALG00000001084	2286962	2297493	ATP8B3
ENSGALG00000001091	2605227	2608015	C1orf116
ENSGALG00000001378	3165104	3165577	C1orf74
ENSGALG00000001416	7992487	8008603	ADRA1B
ENSGALG00000001429	7946299	7979505	TTC1
ENSGALG00000001504	3284914	3291217	DDX20
ENSGALG00000001617	3300492	3382167	CAMKK1
ENSGALG00000001618	3560689	3587092	OGFOD3
ENSGALG00000001633	1636348	1640580	DUSP26
ENSGALG00000001653	3574708	3578036	MANEAL
ENSGALG00000001729	2176061	2184164	CD276
ENSGALG00000001800	1559956	1567028	
ENSGALG00000001828	4089023	4097513	SH2B2
ENSGALG00000001936	1309264	1343370	MYO7B
ENSGALG00000002008	4517732	4531542	RNF157
ENSGALG00000002111	13364535	13374948	
ENSGALG00000002222	2877635	2910779	NOC2L
ENSGALG00000002346	4239190	4252716	CLSPN

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000002417	22255213	22258170	
ENSGALG00000002549	3620501	3624059	RGS1
ENSGALG00000002744	6330204	6628545	PCDH15
ENSGALG00000002800	10271683	10289497	GRK7
ENSGALG00000002899	4478299	4515607	AACS
ENSGALG00000002922	4177695	4256719	NOTCH2
ENSGALG00000002968	2222383	2241992	ZNF341
ENSGALG00000003029	4315183	4317951	PLPP6
ENSGALG00000003146	4884285	4896278	CCDC92
ENSGALG00000003243	2636975	2674730	RAD54L2
ENSGALG00000003345	5282575	5292696	
ENSGALG00000003547	10979414	10990078	SKP2
ENSGALG00000003559	3889665	3899937	ACTR5
ENSGALG00000003863	5458325	5469803	P2RX7
ENSGALG00000004009	5880111	5882167	DHRS13
ENSGALG00000004017	6089879	6099342	TOR1AIP2
ENSGALG00000004028	5308806	5314214	
ENSGALG00000004134	12848118	12869490	GLRA1
ENSGALG00000004333	8021312	8048227	ABCA5
ENSGALG00000004365	5736958	5749931	WDR66
ENSGALG00000004393	1358530	1371111	
ENSGALG00000004496	13051554	13056671	TNIP1
ENSGALG00000004504	4030124	4041511	RADIL
ENSGALG00000004515	5949198	5981021	KNTC1
ENSGALG00000004545	8304412	8398284	WDR72
ENSGALG00000004711	4401977	4407450	
ENSGALG00000005028	5109957	5121859	TOP3A
ENSGALG00000005037	7068141	7090477	TEX14
ENSGALG00000005046	5132126	5136038	SHMT1
ENSGALG00000005077	2154809	2178532	F8
ENSGALG00000005083	5163796	5192508	SLC5A10
ENSGALG00000005162	11044213	11058808	RNPC3
ENSGALG00000005295	7659287	7972906	BCAS3
ENSGALG00000005535	13151075	13168747	TCOF1
ENSGALG00000005558	6182947	6193181	TBL3
ENSGALG00000005638	2403107	2407572	IL2RG
ENSGALG00000005644	4075462	4084282	MYO1G
ENSGALG00000005766	17521316	17535317	PKD2L1
ENSGALG00000005893	17763903	17784063	ZFAND4
ENSGALG00000005903	9533204	9542338	NRIP3
ENSGALG00000005999	9681793	9708956	ABTB1
ENSGALG00000006072	5408222	5438676	
ENSGALG00000006091	14585997	14605147	HFM1
ENSGALG00000006231	12312605	12454486	SERGEF
ENSGALG00000006270	7019086	7028500	SCNN1G
ENSGALG00000006388	12108394	12149216	IL16
ENSGALG00000006417	15802894	15826139	SEC24A
ENSGALG00000006469	2848179	2865777	ATP12A
ENSGALG00000006617	32571769	32577739	BCCIP
ENSGALG00000006631	12837819	12854365	TICRR
ENSGALG00000006679	10519797	10524406	BPIFB4
ENSGALG00000006714	3427461	3430996	CCDC61
ENSGALG00000006725	13047888	13091063	ACAN

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000006755	4178788	4187152	USP2
ENSGALG00000006776	11553069	11555613	KLHDC8B
ENSGALG00000006829	8372762	8430577	SMG1
ENSGALG00000006876	10729767	10733859	CTSA
ENSGALG00000006911	8539866	8565249	TMC5
ENSGALG00000006919	8696586	8712050	POF1B
ENSGALG00000007144	5115506	5186106	SIK3
ENSGALG00000007448	11080495	11081385	SPRY3
ENSGALG00000007466	11210631	11219813	EDNRB2
ENSGALG00000007476	11229010	11246791	VAMP7
ENSGALG00000007550	17116982	17174722	TPCN2
ENSGALG00000007559	16097994	16120120	PDSS1
ENSGALG00000007645	22530257	22534464	
ENSGALG00000007647	16304157	16397870	MYO3A
ENSGALG00000007676	10476723	10481875	EME1
ENSGALG00000007677	16726645	16729910	THNSL1
ENSGALG00000007700	17890386	17910730	CTTN
ENSGALG00000007837	23063011	23067024	KAZALD1
ENSGALG00000008155	11227663	11233652	KCTD18
ENSGALG00000008168	1044881	1060889	ANKRD16
ENSGALG00000008185	11249381	11285636	AOX1
ENSGALG00000008193	13046276	13318877	RELN
ENSGALG00000008218	23152839	23167347	DDB2
ENSGALG00000008479	12077100	12162229	PLEKHM3
ENSGALG00000008503	15914297	15916640	ALG3
ENSGALG00000008627	15903435	15979942	TTBK1
ENSGALG00000008784	16618438	16636096	SPATA1
ENSGALG00000008859	1957160	1961688	WDR31
ENSGALG00000008861	1948741	1954284	BSPRY
ENSGALG00000008881	1861276	1913128	RGS3
ENSGALG00000008946	27592399	27623494	NHLRC2
ENSGALG00000009032	19675023	19681422	PIF1
ENSGALG00000009224	15744817	15747320	TTC30B
ENSGALG00000009230	20091761	20162392	TMEM131L
ENSGALG00000009269	26068174	26082465	PTGR2
ENSGALG00000009315	26297611	26324915	PAPLN
ENSGALG00000009373	21053776	21061372	CTSO
ENSGALG00000009388	17813559	17842946	SUSD4
ENSGALG00000009415	27718429	27835276	SMOC1
ENSGALG00000009482	22957794	22975908	HEPACAM2
ENSGALG00000009494	28446182	28454715	THAP5
ENSGALG00000009621	4191291	4195531	ACTB
ENSGALG00000009689	23875666	23895602	PON2
ENSGALG00000009859	33794056	33841926	TBC1D30
ENSGALG00000009905	35112854	35137000	MDM1
ENSGALG00000009911	23119921	23148269	BICRAL
ENSGALG00000010078	29377291	29456632	GLP1R
ENSGALG00000010091	20435484	20440428	ATP6V0B
ENSGALG00000010130	34390208	34408877	INTS10
ENSGALG00000010218	22895278	22903708	
ENSGALG00000010316	35018318	35181390	FRAS1
ENSGALG00000010323	38322143	38331207	BATF
ENSGALG00000010326	38339289	38363624	FLVCR2

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000010391	35737241	35779227	MMRN1
ENSGALG00000010440	21871550	21892367	MKNK1
ENSGALG00000010507	2411319	2419611	FCRL4
ENSGALG00000010743	25193186	25198474	LRRC42
ENSGALG00000010863	29836832	29840103	TWISTNB
ENSGALG00000011068	20140771	20213740	COBLL1
ENSGALG00000011145	33598483	33600756	TRIL
ENSGALG00000011252	22249638	22253369	
ENSGALG00000011262	35587263	35752218	KCNH8
ENSGALG00000011289	37318200	37327078	NKIRAS1
ENSGALG00000011322	38560047	38575577	
ENSGALG00000011371	22575074	22586232	STK36
ENSGALG00000011570	1700996	1705561	ILF2
ENSGALG00000011593	25443913	25448325	TMEM177
ENSGALG00000011717	47884753	47909098	
ENSGALG00000012177	29971539	29999038	NCKAP5
ENSGALG00000012207	30610000	30632948	CCNT2
ENSGALG00000012211	58569546	58695921	PDLIM5
ENSGALG00000012259	30784867	30798568	UBXN4
ENSGALG00000012290	51089596	51098755	SOX10
ENSGALG00000012355	30835173	30873167	DARS
ENSGALG00000012857	56889138	56945866	DENND2A
ENSGALG00000012885	68102902	68190463	BCL2
ENSGALG00000012984	1185316	1196659	
ENSGALG00000013085	62813644	62962492	PTPRO
ENSGALG00000013149	85073411	85199421	MOCOS
ENSGALG00000013168	65318628	65322354	IAPP
ENSGALG00000013180	85992259	86016056	SLC6A18
ENSGALG00000013183	86021205	86050671	TERT
ENSGALG00000013247	190389807	190403692	CCDC83
ENSGALG00000013571	61766265	61782543	
ENSGALG00000013573	90006995	90008669	ALG2
ENSGALG00000013964	66571723	66587002	SPATA18
ENSGALG00000014041	67608354	67618608	
ENSGALG00000014115	66884633	66910624	SLAIN2
ENSGALG00000014126	68381261	68385975	
ENSGALG00000014643	2258114	2277397	
ENSGALG00000014918	63859412	63892453	RFX6
ENSGALG00000014924	79422423	79478850	POLQ
ENSGALG00000015030	103346605	103372094	NPC1
ENSGALG00000015097	32917400	32946020	
ENSGALG00000015259	110285815	110358845	RB1CC1
ENSGALG00000015307	84985337	85117095	ABI3BP
ENSGALG00000015374	53526993	53532383	RBP4
ENSGALG00000015630	62158975	62431421	EDIL3
ENSGALG00000015687	83332108	83333493	
ENSGALG00000015923	81803398	81811037	MTO1
ENSGALG00000016042	106660194	106677742	CHAF1B
ENSGALG00000016127	108027675	108053510	SH3BGR
ENSGALG00000016138	108236302	108412621	DSCAM
ENSGALG00000016174	83383540	83449168	LMBRD1
ENSGALG00000016358	118434845	118464479	PTCHD1
ENSGALG00000016509	104821709	104855287	IFT172

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000016556	105439100	105446401	
ENSGALG00000016576	122934649	122963767	OFD1
ENSGALG00000016639	106684652	106726136	
ENSGALG00000016648	128514145	128528599	
ENSGALG00000016692	109266889	109273908	CENPQ
ENSGALG00000016922	155063078	155069210	COMMD6
ENSGALG00000017015	169902418	169946212	RNASEH2B
ENSGALG00000017038	171237604	171257844	PROSER1
ENSGALG00000017148	179310484	179327166	CENPJ
ENSGALG00000017184	182581300	182585639	MMP7
ENSGALG00000017493	194226590	194228925	
ENSGALG00000019178	109072306	109103187	PRDM15
ENSGALG00000019211	91823350	91832861	MAEL
ENSGALG00000019543	76489687	76496184	OTULIN
ENSGALG00000019554	67906620	67915397	
ENSGALG00000019756	27814585	27819688	MLANA
ENSGALG00000020032	34909552	34914562	
ENSGALG00000020210	39752033	39762452	CENPU
ENSGALG00000020454	26192258	26194122	C5H14ORF169
ENSGALG00000020899	16538881	16556264	
ENSGALG00000020905	11280496	11328347	KSR2
ENSGALG00000021025	10210849	10215330	
ENSGALG00000021362	9226556	9229211	GPRC5C
ENSGALG00000021696	301097	305124	
ENSGALG00000022751	144542279	144543954	
ENSGALG00000022882	91704833	91707742	ZADH2
ENSGALG00000023120	52137022	52139535	SULT1B1
ENSGALG00000023708	4845916	4849134	UBXN10
ENSGALG00000023843	3476861	3485053	FRMD7
ENSGALG00000024051	2612501	2631106	SETDB1
ENSGALG00000024298	3256975	3261306	ADAMTSL5
ENSGALG00000026080	3414370	3416416	OMD
ENSGALG00000026152	2254875	2264684	GBP
ENSGALG00000026384	3250482	3255046	PCSK4
ENSGALG00000026431	5910507	5916770	SEZ6
ENSGALG00000026948	3524231	3543372	ADD2
ENSGALG00000027476	579684	584242	PLEKHG5
ENSGALG00000027700	1801816	1808119	FLAD1
ENSGALG00000027809	4053373	4054788	FAM196B
ENSGALG00000028262	4970553	4972635	
ENSGALG00000028302	17160590	17161925	UQCRQ
ENSGALG00000028367	219651	222858	
ENSGALG00000028457	30640415	30649263	MAP3K19
ENSGALG00000028520	15591701	15594391	CST3
ENSGALG00000028536	16906936	16909098	MPEG1
ENSGALG00000028620	9090918	9092123	
ENSGALG00000028675	81671863	81767102	
ENSGALG00000028849	30864013	30895009	SCAF11
ENSGALG00000028960	195852602	195857112	NEU3
ENSGALG00000029027	13113263	13120464	SEPT12
ENSGALG00000029040	194664785	194665750	
ENSGALG00000029440	7983437	8000891	
ENSGALG00000029896	16565634	16667942	

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000029935	84680635	84765600	EPB41L4B
ENSGALG00000030270	14372	17201	CD1C
ENSGALG00000030985	2722336	2748121	MYH7B
ENSGALG00000031119	6099444	6113592	
ENSGALG00000031142	985790	998134	ACAA2
ENSGALG00000031160	50410218	50412820	
ENSGALG00000031262	85886610	85913057	
ENSGALG00000031737	14760117	14805890	
ENSGALG00000031812	2863361	2867426	TDRKH
ENSGALG00000031906	1336572	1360690	FAM83C
ENSGALG00000031997	46310717	46320326	SFRP4
ENSGALG00000032156	20305696	20329063	TUBGCP6
ENSGALG00000032231	58543	72898	C4
ENSGALG00000032348	21405	22499	LTB4R
ENSGALG00000032372	7394751	7414352	CYB5R2
ENSGALG00000032419	559645	600269	STARD8
ENSGALG00000032642	770602	836615	SMARCC1
ENSGALG00000032943	293237	295905	ESAM
ENSGALG00000032999	30401258	30403162	
ENSGALG00000033089	126865549	126908440	
ENSGALG00000033199	105330816	105350209	
ENSGALG00000033203	104988818	104992131	TRIM54
ENSGALG00000033254	129000072	129034245	SPAG1
ENSGALG00000033497	4844452	4882773	FOXP4
ENSGALG00000033587	48193459	48195214	
ENSGALG00000033887	61679420	61699251	IL17RA
ENSGALG00000033953	1864533	1871303	SHROOM4
ENSGALG00000034094	18338330	18340228	SP5
ENSGALG00000034124	401009	426665	NLRPL
ENSGALG00000034347	280212	292746	KIF21B
ENSGALG00000034436	7248755	7254132	CEL
ENSGALG00000034493	46064049	46088568	DCLK3
ENSGALG00000034756	2588773	2595216	
ENSGALG00000034760	33379224	33417837	
ENSGALG00000034932	108844363	108894770	BACE2
ENSGALG00000035075	81925	86753	TAP1
ENSGALG00000035281	15342791	15398782	WAC
ENSGALG00000035625	97142592	97198921	CEP192
ENSGALG00000035774	17837266	17884273	PPFIA1
ENSGALG00000035814	1399403	1409506	
ENSGALG00000035918	6912250	6917437	
ENSGALG00000035945	1257270	1260719	
ENSGALG00000036171	41876496	41879009	
ENSGALG00000036240	48974017	48992482	
ENSGALG00000036356	2591447	2633020	YEATS2
ENSGALG00000036731	11210312	11216535	GAS2L1
ENSGALG00000036867	50804456	50812317	CBX6
ENSGALG00000037031	2952855	2958096	
ENSGALG00000037426	1086973	1234604	DYM
ENSGALG00000037526	3396001	3398518	
ENSGALG00000037625	259255	381102	
ENSGALG00000037642	2437835	2441728	SLC23A1
ENSGALG00000037735	56578	58190	CENPA

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000037819	190601433	190603690	
ENSGALG00000037852	3807434	3813304	HSD17B7
ENSGALG00000038041	26093813	26248608	PHF14
ENSGALG00000038393	90602	93633	DMB2
ENSGALG00000038748	2399479	2404284	
ENSGALG00000038884	12712422	12731398	SRL
ENSGALG00000039155	5082235	5112652	ZHX3
ENSGALG00000039193	2702980	2766080	AGRN
ENSGALG00000039212	3468756	3469830	
ENSGALG00000039322	3813929	3819587	DDR2
ENSGALG00000039349	39594353	39768545	DISC1
ENSGALG00000039708	899308	900931	
ENSGALG00000040157	6005683	6016988	CHTF18
ENSGALG00000040528	4009890	4027865	AP5Z1
ENSGALG00000040651	16697772	16838212	IGF1R
ENSGALG00000040864	3211486	3215691	WDR77
ENSGALG00000041013	22734389	22773379	TNS1
ENSGALG00000041179	128662474	128890608	VPS13B
ENSGALG00000041285	4510613	4536085	MAP2K3
ENSGALG00000041331	22344799	22356949	RRP12
ENSGALG00000041373	70658678	70767342	ARAP2
ENSGALG00000041437	1118722	1134255	FAM155B
ENSGALG00000041473	7069408	7109615	DDX31
ENSGALG00000041722	94035	139377	STX1A
ENSGALG00000041763	717732	720817	ADPRM
ENSGALG00000041808	17729748	17800632	ANO1
ENSGALG00000041845	230728	236886	ZNF692
ENSGALG00000042136	108086835	108304491	PKHD1
ENSGALG00000042624	222695	233308	CEP85
ENSGALG00000043198	22259564	22269563	
ENSGALG00000043265	148783909	148939588	ZC3H3
ENSGALG00000043363	11946755	11997989	KIAA0556
ENSGALG00000043379	41319152	41322432	
ENSGALG00000043390	103416843	103491928	
ENSGALG00000043416	2343395	2349349	TARS2
ENSGALG00000043448	81244337	81342994	ABLIM2
ENSGALG00000043476	456388	463442	ARF5
ENSGALG00000043831	31006925	31012835	LRRC73
ENSGALG00000043910	1350804	1351751	OR5AS1
ENSGALG00000043935	46064419	46096688	AFF1
ENSGALG00000044042	5085190	5087144	
ENSGALG00000044087	1292210	1304961	KCTD19
ENSGALG00000044298	5790040	5791347	
ENSGALG00000044343	345292	369940	
ENSGALG00000044425	194506121	194507731	
ENSGALG00000044478	41740334	41838759	LRRIQ1
ENSGALG00000044510	92226911	92240484	C18orf63
ENSGALG00000044606	106703338	106726193	MEP1B
ENSGALG00000044620	90177250	90228176	
ENSGALG00000045006	18546133	18549204	LCTL
ENSGALG00000045045	20073802	20074905	
ENSGALG00000045078	17445394	17453766	
ENSGALG00000045312	2658470	2664070	SEMA6C

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000045534	2551707	2558281	
ENSGALG00000045611	28163	31040	GLMP
ENSGALG00000046133	2696196	2701876	
ENSGALG00000046235	148970847	148980300	
ENSGALG00000046347	396088	398716	FOXRED1
ENSGALG00000046598	39027631	39028922	
ENSGALG00000046656	1781465	1784284	PMVK

Table S 47. Non-synonymous deleterious variants with allele frequency greater than 0.9 in 27 chicken populations.

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000000625	3126090	3162020	MAPT
ENSGALG00000000720	1432743	1440630	
ENSGALG00000001206	8366752	8370140	
ENSGALG00000001235	2618283	2624077	ANKRD24
ENSGALG00000001749	1642902	1659177	ACSBG2
ENSGALG00000001857	2472220	2486139	C1QTNF12
ENSGALG00000001895	4684399	4691245	
ENSGALG00000002098	3867936	3937207	GRIK3
ENSGALG00000002403	2638997	2708090	ULK1
ENSGALG00000002447	2590011	2698188	CTNNA1
ENSGALG00000002638	5116741	5157334	
ENSGALG00000002663	10472558	10508150	ATR
ENSGALG00000002679	3736274	3781857	GLT1D1
ENSGALG00000002849	5041127	5044158	DCXR
ENSGALG00000002945	3328395	3380261	TMEM266
ENSGALG00000003285	10365016	10375987	CDHR2
ENSGALG00000003572	4085166	4125847	
ENSGALG00000003589	5643262	5647788	VTN
ENSGALG00000003833	5721919	5794586	CACNA1E
ENSGALG00000004104	2565759	2592534	INTS1
ENSGALG00000004360	13024860	13028805	
ENSGALG00000004365	5736958	5749931	WDR66
ENSGALG00000004683	9736236	9752383	TPD52L2
ENSGALG00000004798	4691169	4749364	MPRIP
ENSGALG00000004921	4271288	4287004	SLC6A1
ENSGALG00000005014	2066138	2068061	AIPL1
ENSGALG00000005028	5109957	5121859	TOP3A
ENSGALG00000005118	8396685	8397791	FAM124B
ENSGALG00000005253	5617810	5620433	
ENSGALG00000005621	13192090	13212308	CAMK2A
ENSGALG00000005634	7229327	7230473	CRYBA4
ENSGALG00000005801	9071546	9090148	CHRNA4
ENSGALG00000006560	8824964	8995709	SEMA3A
ENSGALG00000006631	12837819	12854365	TICRR
ENSGALG00000007169	14127254	14169164	EPC1
ENSGALG00000007970	19107954	19156499	PIAS1
ENSGALG00000008077	19355200	19358789	PAQR5
ENSGALG00000008109	14151339	14182335	CDHR3
ENSGALG00000008120	19501916	19520583	TLE3
ENSGALG00000008180	19759094	19785369	SPG11

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000008537	16012725	16023253	EPHB3
ENSGALG00000008544	16328932	16398413	SLC8A1
ENSGALG00000008624	24855680	24884673	RPAP1
ENSGALG00000008645	16598334	16606619	NKRF
ENSGALG00000008692	25038945	25096118	
ENSGALG00000008725	5571728	5637205	KIF16B
ENSGALG00000008819	2026955	2051551	LRSAM1
ENSGALG00000008885	14004793	14133988	PDE1A
ENSGALG00000009205	14117925	14203370	
ENSGALG00000009844	32283463	32288278	ACTC1
ENSGALG00000010022	32220976	32236070	PRMT9
ENSGALG00000010108	34283512	34287993	C4orf33
ENSGALG00000010193	37713774	37731357	ZNF410
ENSGALG00000010276	21260097	21277121	GPBP1L1
ENSGALG00000010360	21671551	21675013	NSUN4
ENSGALG00000010572	40811286	40858950	TSHR
ENSGALG00000011149	21941750	21977517	PLA2R1
ENSGALG00000011235	34327646	34349885	GALNT15
ENSGALG00000011304	38055640	38075203	NGLY1
ENSGALG00000011687	51898823	51911235	
ENSGALG00000012005	54717088	54736656	LRRC9
ENSGALG00000012072	28389233	28403654	
ENSGALG00000012100	28481649	28499392	CFAP221
ENSGALG00000012155	58394125	58445817	EGF
ENSGALG00000012177	29971539	29999038	NCKAP5
ENSGALG00000012196	58526506	58553506	MCUB
ENSGALG00000012484	35331804	35359923	RIF1
ENSGALG00000012593	40166144	40179451	SLC28A3
ENSGALG00000013006	78498575	78505697	ROPN1L
ENSGALG00000013090	22249905	22254300	LOXL4
ENSGALG00000013268	89063802	89211727	
ENSGALG00000013548	16662049	16666243	GZMA
ENSGALG00000014664	57880857	57984258	
ENSGALG00000014765	20588770	20606823	TRIM23
ENSGALG00000014923	24570223	24702341	ARHGEF28
ENSGALG00000015002	25266850	25313351	MRPS27
ENSGALG00000015167	37397609	37448829	PRUNE2
ENSGALG00000015340	111439673	111462441	TGS1
ENSGALG00000016105	91217010	91267485	DYSF
ENSGALG00000016221	111056475	111115975	EFHC2
ENSGALG00000016279	87070833	87079598	RAB23
ENSGALG00000016314	88598880	88636560	ELOVL5
ENSGALG00000016815	136915096	136936956	UPF3A
ENSGALG00000016943	165561980	165586181	OLFM4
ENSGALG00000019030	194659669	194660631	
ENSGALG00000019768	10433382	10468658	ACSF2
ENSGALG00000021198	3082764	3089843	
ENSGALG00000023886	1803327	1832501	ZNF804A
ENSGALG00000025971	105661748	105672793	KCNK3
ENSGALG00000026015	10715164	10719635	
ENSGALG00000027704	13862869	14132878	
ENSGALG00000028238	23565911	23569213	
ENSGALG00000028298	32755529	32886954	

Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name
ENSGALG00000029000	3231438	3234557	HYAL3
ENSGALG00000029308	69135540	69146688	
ENSGALG00000029599	9635	25890	ACVR1B
ENSGALG00000030024	32905460	32969236	USP15
ENSGALG00000030169	6496192	6513565	
ENSGALG00000030844	7494480	7523025	DMTF1
ENSGALG00000031752	1397978	1403745	
ENSGALG00000031814	71639774	71703468	
ENSGALG00000032599	77089837	77115522	ZNF384
ENSGALG00000033068	391022	394724	TLR21
ENSGALG00000033199	105330816	105350209	
ENSGALG00000033328	4097552	4162312	PACS2
ENSGALG00000033497	4844452	4882773	FOXP4
ENSGALG00000033557	19950725	19956592	CTSH
ENSGALG00000033807	11501308	11503836	TYSND1
ENSGALG00000035384	103261771	103315035	TMEM241
ENSGALG00000035453	48198262	48204933	RP9
ENSGALG00000035625	97142592	97198921	CEP192
ENSGALG00000036516	108608380	108614937	
ENSGALG00000037163	6953116	6954713	
ENSGALG00000037301	36448667	36651282	ACVR1
ENSGALG00000037407	407251	416312	FAM118B
ENSGALG00000037410	284344	322060	HEPH
ENSGALG00000037414	105324804	105326122	DNAJC28
ENSGALG00000037644	123703762	123734221	CNGB3
ENSGALG00000038426	937592	940719	CPLX4
ENSGALG00000038972	4439972	4462470	
ENSGALG00000039322	3813929	3819587	DDR2
ENSGALG00000039707	4390621	4391652	
ENSGALG00000039716	5309931	5318833	RNF19B
ENSGALG00000039727	530264	535057	
ENSGALG00000039901	149440993	149468746	PUF60
ENSGALG00000041181	13910194	13915248	
ENSGALG00000041233	139401611	139404620	FAM84B
ENSGALG00000041977	17396691	17432723	
ENSGALG00000042001	35288232	35306393	
ENSGALG00000042485	2114444	2148315	PHACTR4
ENSGALG00000042705	5476398	5479857	KCNK15
ENSGALG00000043703	763219	769060	
ENSGALG00000044141	46639207	46643200	THAP9
ENSGALG00000045173	83783694	83796470	
ENSGALG00000045204	154444261	154449459	FBXL3
ENSGALG00000045218	7100719	7141338	MYO18B
ENSGALG00000045232	7026294	7051788	SYCP2
ENSGALG00000045350	16715725	16741025	
ENSGALG00000045365	194646692	194647502	OR51E1
ENSGALG00000045414	179330679	179371572	
ENSGALG00000045466	6816418	6817036	
ENSGALG00000045706	778866	781827	
ENSGALG00000045935	2672496	2676279	

Table S 48. Hp values within the threshold level (Hp ≤ -4) in Improved Horro (N=30).

Chr	Start	Stop	Hp	uZHp	µSNP
1	189490000	189510000	0.0000	-5.71	82
1	190890000	190910000	0.0000	-5.71	49
1	190900000	190920000	0.0000	-5.71	82
1	190910000	190930000	0.0000	-5.71	100
1	32500000	32520000	0.0005	-5.70	72
1	32490000	32510000	0.0006	-5.70	103
1	190920000	190940000	0.0009	-5.69	78
1	190880000	190900000	0.0015	-5.68	44
1	32450000	32470000	0.0026	-5.67	52
1	189480000	189500000	0.0029	-5.66	92
1	181220000	181240000	0.0030	-5.66	88
1	190980000	191000000	0.0032	-5.65	41
1	32560000	32580000	0.0045	-5.63	54
1	32480000	32500000	0.0067	-5.59	84
1	32550000	32570000	0.0069	-5.59	94
1	160960000	160980000	0.0087	-5.56	42
1	190960000	190980000	0.0090	-5.56	96
1	32530000	32550000	0.0109	-5.52	97
1	190990000	191010000	0.0120	-5.50	66
1	190950000	190970000	0.0127	-5.49	94
1	32520000	32540000	0.0132	-5.48	90
1	190870000	190890000	0.0136	-5.48	68
1	32510000	32530000	0.0139	-5.47	62
1	32540000	32560000	0.0147	-5.46	92
1	32460000	32480000	0.0150	-5.45	44
1	190930000	190950000	0.0172	-5.41	46
1	190970000	190990000	0.0191	-5.38	45
1	189470000	189490000	0.0212	-5.35	109
1	32470000	32490000	0.0220	-5.33	48
1	32630000	32650000	0.0259	-5.26	118
1	146760000	146780000	0.0261	-5.26	63
1	32790000	32810000	0.0265	-5.25	108
1	32800000	32820000	0.0265	-5.25	150
1	181850000	181870000	0.0268	-5.25	97
1	32660000	32680000	0.0271	-5.24	145
1	32810000	32830000	0.0273	-5.24	147
1	32620000	32640000	0.0275	-5.24	159
1	32670000	32690000	0.0280	-5.23	115
1	160950000	160970000	0.0284	-5.22	52
1	32640000	32660000	0.0296	-5.20	60
1	32650000	32670000	0.0319	-5.16	113
1	146810000	146830000	0.0320	-5.16	40
1	32610000	32630000	0.0324	-5.15	95

Chr	Start	Stop	Hp	uZHp	µSNP
1	181790000	181810000	0.0324	-5.15	95
1	146770000	146790000	0.0328	-5.15	33
1	146780000	146800000	0.0328	-5.15	42
1	181780000	181800000	0.0328	-5.15	60
1	181840000	181860000	0.0328	-5.15	109
1	174520000	174540000	0.0336	-5.13	155
1	32580000	32600000	0.0343	-5.12	21
1	55850000	55870000	0.0344	-5.12	175
1	190940000	190960000	0.0346	-5.12	55
1	32780000	32800000	0.0355	-5.10	108
1	142900000	142920000	0.0355	-5.10	186
1	146990000	147010000	0.0360	-5.09	30
1	146820000	146840000	0.0364	-5.08	81
1	55860000	55880000	0.0368	-5.08	97
1	181800000	181820000	0.0370	-5.07	122
1	43200000	43220000	0.0372	-5.07	66
1	32590000	32610000	0.0384	-5.05	23
1	189460000	189480000	0.0392	-5.04	120
1	161780000	161800000	0.0400	-5.02	62
1	181770000	181790000	0.0403	-5.02	85
1	146790000	146810000	0.0425	-4.98	69
1	55840000	55860000	0.0442	-4.95	171
1	146830000	146850000	0.0459	-4.92	83
1	146800000	146820000	0.0471	-4.90	47
1	160940000	160960000	0.0476	-4.89	28
1	181230000	181250000	0.0478	-4.89	85
1	32600000	32620000	0.0482	-4.88	27
1	179110000	179130000	0.0498	-4.85	144
1	129550000	129570000	0.0508	-4.84	159
1	76430000	76450000	0.0510	-4.83	79
1	162220000	162240000	0.0520	-4.82	96
1	179100000	179120000	0.0563	-4.74	185
1	146840000	146860000	0.0566	-4.74	48
1	76420000	76440000	0.0590	-4.70	98
1	162170000	162190000	0.0592	-4.69	24
1	111450000	111470000	0.0656	-4.58	54
1	103890000	103910000	0.0673	-4.55	206
1	55830000	55850000	0.0689	-4.53	189
1	162510000	162530000	0.0694	-4.52	144
1	111440000	111460000	0.0699	-4.51	63
1	32440000	32460000	0.0699	-4.51	74
1	111430000	111450000	0.0703	-4.50	79
1	174510000	174530000	0.0711	-4.49	219
1	76440000	76460000	0.0713	-4.48	27
1	67310000	67330000	0.0770	-4.39	91
1	190860000	190880000	0.0788	-4.36	80
1	181310000	181330000	0.0791	-4.35	66

Chr	Start	Stop	Hp	uZHp	µSNP
1	67160000	67180000	0.0795	-4.34	273
1	9400000	9420000	0.0795	-4.34	45
1	162500000	162520000	0.0800	-4.33	166
1	179090000	179110000	0.0804	-4.33	172
1	129560000	129580000	0.0808	-4.32	113
1	43210000	43230000	0.0810	-4.32	69
1	161770000	161790000	0.0822	-4.30	66
1	55530000	55550000	0.0828	-4.29	124
1	103880000	103900000	0.0829	-4.29	182
1	81720000	81740000	0.0838	-4.27	195
1	119500000	119520000	0.0843	-4.26	85
1	77090000	77110000	0.0844	-4.26	145
1	179070000	179090000	0.0849	-4.25	122
1	146980000	147000000	0.0852	-4.25	83
1	81710000	81730000	0.0856	-4.24	144
1	181240000	181260000	0.0857	-4.24	84
1	32680000	32700000	0.0868	-4.22	96
1	142910000	142930000	0.0882	-4.19	242
1	162520000	162540000	0.0884	-4.19	100
1	61360000	61380000	0.0892	-4.18	266
1	59230000	59250000	0.0896	-4.17	78
1	61370000	61390000	0.0899	-4.16	200
1	32820000	32840000	0.0923	-4.12	100
1	177150000	177170000	0.0932	-4.11	117
1	55520000	55540000	0.0934	-4.10	150
1	77080000	77100000	0.0948	-4.08	138
1	55510000	55530000	0.0954	-4.07	153
1	107330000	107350000	0.0960	-4.06	122
1	9390000	9410000	0.0961	-4.06	92
1	147040000	147060000	0.0971	-4.04	112
1	181250000	181270000	0.0974	-4.04	101
1	162490000	162510000	0.0976	-4.03	104
1	179080000	179100000	0.0977	-4.03	146
1	35320000	35340000	0.0987	-4.01	57
1	146920000	146940000	0.0993	-4.00	125
2	147310000	147330000	0.0004	-5.70	93
2	147300000	147320000	0.0033	-5.65	111
2	147290000	147310000	0.0048	-5.63	90
2	140520000	140540000	0.0077	-5.58	86
2	147280000	147300000	0.0126	-5.49	87
2	147270000	147290000	0.0131	-5.48	101
2	140510000	140530000	0.0273	-5.24	112
2	147260000	147280000	0.0285	-5.22	112
2	141430000	141450000	0.0382	-5.05	148
2	141410000	141430000	0.0413	-5.00	241
2	141420000	141440000	0.0435	-4.96	185
2	141400000	141420000	0.0460	-4.92	254

Chr	Start	Stop	Hp	uZHp	μSNP
2	8010000	8030000	0.0498	-4.85	188
2	141440000	141460000	0.0520	-4.82	154
2	140500000	140520000	0.0594	-4.69	187
2	21260000	21280000	0.0631	-4.63	186
2	8020000	8040000	0.0637	-4.62	198
2	60950000	60970000	0.0668	-4.56	93
2	147490000	147510000	0.0674	-4.55	202
2	140530000	140550000	0.0682	-4.54	155
2	147720000	147740000	0.0721	-4.47	183
2	140410000	140430000	0.0729	-4.46	150
2	147730000	147750000	0.0742	-4.43	175
2	147570000	147590000	0.0789	-4.35	167
2	147700000	147720000	0.0792	-4.35	165
2	142810000	142830000	0.0803	-4.33	39
2	147220000	147240000	0.0804	-4.33	162
2	147230000	147250000	0.0830	-4.28	154
2	147500000	147520000	0.0841	-4.26	210
2	147510000	147530000	0.0849	-4.25	246
2	147580000	147600000	0.0859	-4.23	109
2	111900000	111920000	0.0868	-4.22	192
2	147520000	147540000	0.0872	-4.21	242
2	142890000	142910000	0.0879	-4.20	47
2	147320000	147340000	0.0885	-4.19	93
2	8030000	8050000	0.0901	-4.16	221
2	73650000	73670000	0.0902	-4.16	69
2	147480000	147500000	0.0903	-4.16	193
2	11690000	11710000	0.0923	-4.12	118
2	73570000	73590000	0.0923	-4.12	180
2	111910000	111930000	0.0924	-4.12	165
2	147530000	147550000	0.0929	-4.11	186
2	73590000	73610000	0.0929	-4.11	130
2	140400000	140420000	0.0942	-4.09	142
2	147210000	147230000	0.0945	-4.09	115
2	73560000	73580000	0.0948	-4.08	134
2	21250000	21270000	0.0956	-4.07	194
2	111890000	111910000	0.0961	-4.06	188
2	4520000	4540000	0.0965	-4.05	81
2	111860000	111880000	0.0965	-4.05	119
2	111840000	111860000	0.0975	-4.03	157
2	82700000	82720000	0.0981	-4.02	68
2	73580000	73600000	0.0989	-4.01	161
3	36690000	36710000	0.0266	-5.25	73
3	36680000	36700000	0.0297	-5.20	74
3	78560000	78580000	0.0328	-5.15	108
3	57540000	57560000	0.0371	-5.07	38
3	20940000	20960000	0.0466	-4.91	286
3	51900000	51920000	0.0508	-4.84	207

Chr	Start	Stop	Hp	uZHp	µSNP
3	51890000	51910000	0.0512	-4.83	151
3	57530000	57550000	0.0512	-4.83	83
3	57560000	57580000	0.0634	-4.62	208
3	51910000	51930000	0.0640	-4.61	234
3	57520000	57540000	0.0647	-4.60	128
3	57550000	57570000	0.0682	-4.54	100
3	69840000	69860000	0.0765	-4.39	59
3	69060000	69080000	0.0767	-4.39	159
3	69820000	69840000	0.0770	-4.39	74
3	69850000	69870000	0.0790	-4.35	113
3	61520000	61540000	0.0847	-4.25	132
3	82470000	82490000	0.0886	-4.19	297
3	61510000	61530000	0.0923	-4.12	209
3	50290000	50310000	0.0933	-4.11	190
3	20970000	20990000	0.0963	-4.05	246
3	111060000	111080000	0.0992	-4.01	43
4	39500000	39520000	0.0023	-5.67	265
4	39490000	39510000	0.0032	-5.65	186
4	64960000	64980000	0.0108	-5.52	135
4	39410000	39430000	0.0122	-5.50	193
4	39400000	39420000	0.0122	-5.50	182
4	7970000	7990000	0.0215	-5.34	106
4	7960000	7980000	0.0295	-5.20	107
4	7980000	8000000	0.0328	-5.15	64
4	28840000	28860000	0.0335	-5.13	90
4	64950000	64970000	0.0342	-5.12	110
4	39420000	39440000	0.0368	-5.08	185
4	39440000	39460000	0.0380	-5.06	130
4	39480000	39500000	0.0383	-5.05	164
4	39720000	39740000	0.0391	-5.04	179
4	39730000	39750000	0.0400	-5.02	241
4	39430000	39450000	0.0410	-5.00	167
4	39690000	39710000	0.0422	-4.98	105
4	7990000	8010000	0.0476	-4.89	43
4	39390000	39410000	0.0488	-4.87	206
4	63140000	63160000	0.0511	-4.83	40
4	78120000	78140000	0.0526	-4.81	106
4	78110000	78130000	0.0528	-4.80	54
4	7950000	7970000	0.0557	-4.75	82
4	8000000	8020000	0.0624	-4.64	77
4	39450000	39470000	0.0659	-4.58	164
4	53740000	53760000	0.0667	-4.56	220
4	26340000	26360000	0.0679	-4.54	180
4	39470000	39490000	0.0707	-4.49	180
4	78100000	78120000	0.0726	-4.46	121
4	26350000	26370000	0.0738	-4.44	226
4	28470000	28490000	0.0748	-4.42	21

Chr	Start	Stop	Hp	uZHp	µSNP
4	38110000	38130000	0.0752	-4.42	118
4	39460000	39480000	0.0768	-4.39	192
4	27940000	27960000	0.0788	-4.35	45
4	39740000	39760000	0.0809	-4.32	195
4	8010000	8030000	0.0830	-4.28	96
4	39300000	39320000	0.0844	-4.26	183
4	28830000	28850000	0.0857	-4.24	84
4	78130000	78150000	0.0861	-4.23	136
4	37880000	37900000	0.0864	-4.23	255
4	27860000	27880000	0.0866	-4.22	97
4	39310000	39330000	0.0869	-4.22	119
4	78090000	78110000	0.0873	-4.21	177
4	26370000	26390000	0.0882	-4.19	89
4	39680000	39700000	0.0883	-4.19	225
4	37810000	37830000	0.0890	-4.18	110
4	39320000	39340000	0.0908	-4.15	135
4	26360000	26380000	0.0916	-4.14	167
4	27970000	27990000	0.0934	-4.10	38
4	27930000	27950000	0.0936	-4.10	85
4	26330000	26350000	0.0936	-4.10	171
4	27960000	27980000	0.0941	-4.09	32
4	7450000	7470000	0.0946	-4.08	149
4	71900000	71920000	0.0950	-4.08	132
4	7940000	7960000	0.0960	-4.06	86
4	78020000	78040000	0.0975	-4.03	244
4	53010000	53030000	0.0982	-4.02	227
5	40840000	40860000	0.0007	-5.70	152
5	2000000	2020000	0.0305	-5.19	98
5	2010000	2030000	0.0328	-5.15	50
5	2100000	2120000	0.0331	-5.14	101
5	2110000	2130000	0.0337	-5.13	73
5	2090000	2110000	0.0344	-5.12	100
5	40830000	40850000	0.0346	-5.12	163
5	2180000	2200000	0.0356	-5.10	46
5	2200000	2220000	0.0362	-5.09	57
5	2190000	2210000	0.0364	-5.08	71
5	2020000	2040000	0.0378	-5.06	147
5	2210000	2230000	0.0383	-5.05	41
5	2060000	2080000	0.0393	-5.03	99
5	2170000	2190000	0.0398	-5.03	23
5	2070000	2090000	0.0402	-5.02	100
5	2080000	2100000	0.0410	-5.01	94
5	2050000	2070000	0.0428	-4.97	99
5	2030000	2050000	0.0431	-4.97	158
5	22480000	22500000	0.0456	-4.93	30
5	2040000	2060000	0.0457	-4.92	94
5	2320000	2340000	0.0459	-4.92	61

Chr	Start	Stop	Hp	uZHp	µSNP
5	2120000	2140000	0.0481	-4.88	69
5	2280000	2300000	0.0482	-4.88	60
5	2160000	2180000	0.0521	-4.81	33
5	2290000	2310000	0.0522	-4.81	59
5	2270000	2290000	0.0530	-4.80	52
5	41880000	41900000	0.0538	-4.79	135
5	2150000	2170000	0.0545	-4.77	40
5	2130000	2150000	0.0563	-4.74	50
5	2240000	2260000	0.0571	-4.73	47
5	2140000	2160000	0.0581	-4.71	23
5	22490000	22510000	0.0590	-4.70	23
5	1990000	2010000	0.0591	-4.69	157
5	2260000	2280000	0.0594	-4.69	37
5	2250000	2270000	0.0596	-4.68	39
5	5390000	5410000	0.0600	-4.68	267
5	2300000	2320000	0.0612	-4.66	76
5	40850000	40870000	0.0616	-4.65	178
5	2310000	2330000	0.0620	-4.64	89
5	2220000	2240000	0.0625	-4.64	47
5	22400000	22420000	0.0671	-4.56	47
5	2230000	2250000	0.0679	-4.54	45
5	22370000	22390000	0.0683	-4.54	32
5	22690000	22710000	0.0686	-4.53	149
5	22410000	22430000	0.0717	-4.48	51
5	12700000	12720000	0.0789	-4.35	181
5	41890000	41910000	0.0803	-4.33	117
5	12690000	12710000	0.0805	-4.33	265
5	26440000	26460000	0.0827	-4.29	196
5	14950000	14970000	0.0878	-4.20	21
5	41870000	41890000	0.0911	-4.14	122
5	7480000	7500000	0.0969	-4.04	311
5	12680000	12700000	0.0991	-4.01	301
5	41710000	41730000	0.0994	-4.00	68
6	15650000	15670000	0.0364	-5.08	79
6	16000000	16020000	0.0418	-4.99	185
6	15670000	15690000	0.0450	-4.94	97
6	15660000	15680000	0.0483	-4.88	74
6	16010000	16030000	0.0581	-4.71	208
6	6680000	6700000	0.0826	-4.29	577
6	6670000	6690000	0.0876	-4.20	530
6	15990000	16010000	0.0934	-4.10	90
6	6650000	6670000	0.0963	-4.05	402
7	31490000	31510000	0.0776	-4.38	110
7	31240000	31260000	0.0796	-4.34	200
7	31480000	31500000	0.0834	-4.28	52
8	15250000	15270000	0.0184	-5.39	149
8	15260000	15280000	0.0187	-5.39	76

Chr	Start	Stop	Hp	uZHp	µSNP
8	15270000	15290000	0.0274	-5.24	36
8	15240000	15260000	0.0275	-5.24	202
8	15230000	15250000	0.0288	-5.21	197
8	15460000	15480000	0.0296	-5.20	103
8	15450000	15470000	0.0368	-5.08	128
8	15470000	15490000	0.0406	-5.01	99
8	15440000	15460000	0.0419	-4.99	165
8	15490000	15510000	0.0451	-4.93	132
8	15500000	15520000	0.0461	-4.92	118
8	15430000	15450000	0.0478	-4.89	177
8	15480000	15500000	0.0481	-4.88	127
8	8830000	8850000	0.0481	-4.88	229
8	8820000	8840000	0.0583	-4.71	209
8	8990000	9010000	0.0602	-4.68	44
8	9160000	9180000	0.0639	-4.61	123
8	9730000	9750000	0.0684	-4.53	71
8	8810000	8830000	0.0738	-4.44	126
8	13100000	13120000	0.0742	-4.43	57
8	8800000	8820000	0.0748	-4.42	27
8	9680000	9700000	0.0776	-4.38	47
8	16200000	16220000	0.0783	-4.36	305
8	9720000	9740000	0.0810	-4.32	67
8	15510000	15530000	0.0815	-4.31	112
8	9170000	9190000	0.0828	-4.29	87
8	9800000	9820000	0.0836	-4.27	69
8	19380000	19400000	0.0838	-4.27	119
8	230000	250000	0.0855	-4.24	35
8	16210000	16230000	0.0890	-4.18	216
8	9200000	9220000	0.0901	-4.16	92
8	9000000	9020000	0.0907	-4.15	28
8	8980000	9000000	0.0910	-4.15	164
8	9520000	9540000	0.0913	-4.14	89
8	9740000	9760000	0.0918	-4.13	74
8	9790000	9810000	0.0930	-4.11	59
8	15980000	16000000	0.0934	-4.10	150
8	9130000	9150000	0.0942	-4.09	75
8	9150000	9170000	0.0982	-4.02	113
8	16220000	16240000	0.0982	-4.02	205
8	15220000	15240000	0.0992	-4.00	192
9	10180000	10200000	0.0005	-5.70	61
9	10150000	10170000	0.0033	-5.65	71
9	10190000	10210000	0.0104	-5.53	54
9	10170000	10190000	0.0169	-5.42	84
9	10160000	10180000	0.0184	-5.39	88
9	12400000	12420000	0.0252	-5.28	30
9	14250000	14270000	0.0380	-5.06	116
9	14260000	14280000	0.0492	-4.86	128

Chr	Start	Stop	Hp	uZHp	µSNP
9	10200000	10220000	0.0907	-4.15	126
9	12410000	12430000	0.0914	-4.14	133
9	10410000	10430000	0.0981	-4.02	87
11	1610000	1630000	0.0249	-5.28	196
11	13520000	13540000	0.0691	-4.52	60
11	13530000	13550000	0.0905	-4.15	77
12	7730000	7750000	0.0000	-5.71	61
12	7740000	7760000	0.0162	-5.43	45
12	7720000	7740000	0.0666	-4.57	116
12	7750000	7770000	0.0812	-4.31	114
13	1650000	1670000	0.0773	-4.38	29
13	1660000	1680000	0.0808	-4.32	32
14	5300000	5320000	0.0148	-5.46	76
14	14780000	14800000	0.0287	-5.22	71
14	8380000	8400000	0.0530	-4.80	184
14	14770000	14790000	0.0636	-4.62	75
18	90000	110000	0.0659	-4.58	25
18	10290000	10310000	0.0702	-4.50	76
18	10280000	10300000	0.0761	-4.40	157
18	10270000	10290000	0.0802	-4.33	169
18	80000	100000	0.0932	-4.11	28
21	60000	80000	0.0413	-5.00	30
21	70000	90000	0.0415	-5.00	33
21	80000	100000	0.0451	-4.93	26
21	10000	30000	0.0506	-4.84	25
21	130000	150000	0.0697	-4.51	41
21	120000	140000	0.0722	-4.47	36
21	90000	110000	0.0759	-4.41	27
21	1590000	1610000	0.0795	-4.34	141
21	180000	200000	0.0799	-4.34	36
21	1600000	1620000	0.0844	-4.26	143
22	1670000	1690000	0.0888	-4.18	44
23	4930000	4950000	0.0731	-4.45	189
23	4980000	5000000	0.0852	-4.25	188
23	5290000	5310000	0.0875	-4.21	156
23	60000	80000	0.0883	-4.19	63
23	50000	70000	0.0907	-4.15	63
23	40000	60000	0.0918	-4.13	75
23	130000	150000	0.0962	-4.06	52
23	110000	130000	0.0986	-4.02	25
27	5460000	5480000	0.0404	-5.01	21
27	5470000	5490000	0.0682	-4.54	25
27	5620000	5640000	0.0683	-4.54	25
27	5480000	5500000	0.0805	-4.33	25
27	5540000	5560000	0.0905	-4.15	27

Table S 49. List of genes for Improved Horro based on Hp methods.

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
1	ENSGALG00000044624	59245579	59246586		protein coding
1	ENSGALG00000026901	76447763	76447872	gga-mir-6606	miRNA
1	ENSGALG00000027781	103899869	103900014	RF02271	Misc RNA
1	ENSGALG00000038995	181192418	181414573	GRIA4	protein coding
1	ENSGALG00000012791	55806774	56041222	TBXAS1	protein coding
1	ENSGALG00000013273	67167377	67170581	SPX	protein coding
1	ENSGALG00000032599	77089837	77115522	ZNF384	protein coding
1	ENSGALG00000012760	55504144	55518514		protein coding
1	ENSGALG00000012761	55547853	55561586	DRAM1	protein coding
1	ENSGALG00000009945	35315781	35347355	CPM	protein coding
1	ENSGALG00000014457	77069090	77083835	ING4	protein coding
1	ENSGALG00000017139	179051034	179094239		protein coding
1	ENSGALG00000045031	59237872	59238879		protein coding
1	ENSGALG00000011930	76345584	76430119	OVST	protein coding
1	ENSGALG00000044524	59241726	59242732		protein coding
1	ENSGALG00000016900	146527090	147094328	GPC6	protein coding
1	ENSGALG00000016936	162193513	162295112	TDRD3	protein coding
1	ENSGALG00000044959	59249433	59250440		protein coding
1	ENSGALG00000017071	174502627	174526844		protein coding
1	ENSGALG00000027868	177160927	177162801	AMER2	protein coding
1	ENSGALG00000016937	162382843	162527048	DIAPH3	protein coding
1	ENSGALG00000043421	179104456	179142555		protein coding
1	ENSGALG00000045907	160634644	161043700		lincRNA
1	ENSGALG00000033721	160954713	161173427		lincRNA
1	ENSGALG00000030557	161681381	161818838		lincRNA
1	ENSGALG00000042343	177157394	177159079		lincRNA
1	ENSGALG00000033716	181770866	181805885		lincRNA
1	ENSGALG00000038179	32268154	32452343		lincRNA
1	ENSGALG00000042870	32603425	32604254		lincRNA
1	ENSGALG00000040898	76458738	76463188		lincRNA
2	ENSGALG00000012941	73245203	73614065	CDH12	protein coding
2	ENSGALG00000005710	4515467	4582669	CTDSPL	protein coding
2	ENSGALG00000006372	8000159	8085723	RBM33	protein coding
2	ENSGALG00000039533	141406000	141466443	EFR3A	protein coding
2	ENSGALG00000037014	147222471	147418330	TSNARE1	protein coding
3	ENSGALG00000029012	111042233	111235595		protein coding
3	ENSGALG00000015864	78537400	78582981	IBTK	protein coding
3	ENSGALG00000015410	69051906	69078558	BVES	protein coding
3	ENSGALG00000013710	51880188	51917321	SNX9	protein coding
3	ENSGALG00000015944	82215093	82512310	RIMS1	protein coding
3	ENSGALG00000010778	36525270	36778774	CHRM3	protein coding
3	ENSGALG00000031196	57534342	57538397		lincRNA
3	ENSGALG00000041356	61528901	61657319		lincRNA

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
4	ENSGALG00000013715	64904550	64998990	DLC1	protein coding
4	ENSGALG00000014931	78013279	78074717	RAB28	protein coding
4	ENSGALG00000020210	39752033	39762452	CENPU	protein coding
4	ENSGALG00000010596	39448857	39482459	TACR3	protein coding
4	ENSGALG00000039411	37840437	37922607	COL25A1	protein coding
4	ENSGALG00000010628	39713691	39752253	ACSL1	protein coding
4	ENSGALG00000037073	39299620	39301401		lincRNA
5	ENSGALG00000009345	26454626	26467002		protein coding
5	ENSGALG00000005353	7450883	7488646	FAR1	protein coding
5	ENSGALG00000038950	14921862	14996500		protein coding
5	ENSGALG00000003908	2161580	2188356	SLC6A5	protein coding
5	ENSGALG00000010576	40868271	40894704	GTF2A1	protein coding
5	ENSGALG00000003999	1910717	1996488	NAV2	protein coding
5	ENSGALG00000003777	2201059	2481132	NELL1	protein coding
5	ENSGALG00000003965	2002977	2006676	DBX1	protein coding
5	ENSGALG00000003958	2086559	2141355	PRMT3	protein coding
5	ENSGALG00000006368	12685002	12717134	PTPN5	protein coding
5	ENSGALG00000010572	40811286	40858950	TSHR	protein coding
5	ENSGALG00000009338	26425311	26448293	ZFYVE1	protein coding
5	ENSGALG00000008053	22282853	22433771		protein coding
6	ENSGALG00000002769	6666081	6675111	DNAJC12	protein coding
6	ENSGALG00000005207	15971180	16002247	SYNPO2L	protein coding
6	ENSGALG00000002845	6694536	7131100	CTNNA3	protein coding
6	ENSGALG00000005226	16010360	16025442	MYOZ1	protein coding
6	ENSGALG00000005088	15570960	15678544	CAMK2G	protein coding
6	ENSGALG00000002761	6640858	6662304	SIRT1	protein coding
7	ENSGALG00000012362	31073812	31346787	THSD7B	protein coding
8	ENSGALG00000006261	15967856	15987226	SELENOF	protein coding
8	ENSGALG00000008658	16222861	16250213	ZNHIT6	protein coding
8	ENSGALG00000006284	15997170	16014128	SH3GLB1	protein coding
8	ENSGALG00000005065	9797493	9862645	PLA2G4A	protein coding
8	ENSGALG00000006864	16125706	16215909	COL24A1	protein coding
8	ENSGALG00000006237	15219523	15269342	PKN2	protein coding
8	ENSGALG00000033708	9019159	9019789		lincRNA
8	ENSGALG00000043258	9537043	9545093		lincRNA
9	ENSGALG00000002897	10142631	10150156	SLC16A14	protein coding
9	ENSGALG00000036543	10205227	10208808	ZBTB38	protein coding
9	ENSGALG00000038512	12398415	12430615	AGTR1	protein coding
9	ENSGALG00000002850	10213881	10256070	RASA2	protein coding
9	ENSGALG00000002729	10392753	10431361	GK5	protein coding
9	ENSGALG00000034946	10189098	10190468		lincRNA
11	ENSGALG00000002407	1604963	1708650	HYDIN	protein coding
12	ENSGALG00000005400	7323310	7733469		protein coding
13	ENSGALG00000040453	1649170	1650955	SRA1	protein coding
13	ENSGALG00000001132	1651000	1654407		protein coding

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
13	ENSGALG00000001099	1544222	1650955	ANKHD1	protein coding
14	ENSGALG00000002119	14717931	14809857	VPS35L	protein coding
14	ENSGALG00000005215	5264613	5339317	CACNA1H	protein coding
14	ENSGALG00000006829	8372762	8430577	SMG1	protein coding
18	ENSGALG00000034134	79958	84622	ZNF302	protein coding
18	ENSGALG00000007522	10231908	10275081	ABCC3	protein coding
18	ENSGALG00000007623	10279329	10388753	CACNA1G	protein coding
21	ENSGALG00000043128	117333	138142	ARHGEF10L	protein coding
21	ENSGALG00000029212	174319	183170	PADI2	protein coding
21	ENSGALG00000031684	141487	148632	RCC2	protein coding
21	ENSGALG00000041401	183587	196195	MRPS16	protein coding
21	ENSGALG00000037479	23092	65640	IGSF21	protein coding
21	ENSGALG00000033340	197834	205169	SLC45A1	protein coding
21	ENSGALG00000042772	66618	76987		lincRNA
23	ENSGALG00000018302	4947355	4947443	gga-mir-30c-1	miRNA
23	ENSGALG00000039716	5309931	5318833	RNF19B	protein coding
23	ENSGALG00000018301	4946132	4946227	gga-mir-30e	miRNA
23	ENSGALG00000040519	4980932	4982596	PEF1	protein coding
23	ENSGALG00000026836	4983358	4985730		protein coding
23	ENSGALG00000037136	117566	147202	RPS6KA1L	protein coding
23	ENSGALG00000003189	4927211	4955061	NFYC	protein coding
23	ENSGALG00000029316	33777	89058		protein coding
23	ENSGALG00000003567	5294114	5304982	FNDC5	protein coding
23	ENSGALG00000036040	149854	155064		lincRNA
23	ENSGALG00000031251	5305277	5306769		lincRNA
27	ENSGALG00000002804	5549486	5564038	RND2	protein coding
27	ENSGALG00000034345	5473594	5474209	COA3	protein coding
27	ENSGALG00000046412	5494647	5500006		protein coding
27	ENSGALG00000043285	5473787	5477716	CNTD1	protein coding
27	ENSGALG00000033522	5499722	5504356		protein coding
27	ENSGALG00000002973	5478574	5483356	BECN1	protein coding
27	ENSGALG00000002937	5483514	5490234	PSME3	protein coding
27	ENSGALG00000035580	5615996	5621784	MPP2	protein coding
27	ENSGALG00000032191	5462100	5472837	WNK4	protein coding
27	ENSGALG00000002818	5538068	5543804	VAT1	protein coding
27	ENSGALG00000034991	5627940	5629042		lincRNA
27	ENSGALG00000041872	5628317	5635317		lincRNA

lincRNA = Long intergenic noncoding RNAs

Table S 50. Hp values within the threshold level (Hp ≤ -4) in Local Horro (N = 6).

Chr	Window Start	Window End	Hp	SNP Count	ZHp
1	111090000	111110000	0.002	270	-5.76
1	111080000	111100000	0.003	249	-5.75
1	111100000	111120000	0.003	239	-5.74
1	119510000	119530000	0.005	101	-5.72
1	111110000	111130000	0.008	205	-5.66
1	119500000	119520000	0.010	67	-5.63
1	127510000	127530000	0.010	33	-5.63
1	190950000	190970000	0.011	102	-5.60
1	127540000	127560000	0.013	62	-5.57
1	111200000	111220000	0.016	21	-5.53
1	127530000	127550000	0.016	41	-5.52
1	127550000	127570000	0.019	52	-5.47
1	190940000	190960000	0.023	51	-5.41
1	111120000	111140000	0.024	184	-5.38
1	127520000	127540000	0.024	27	-5.38
1	83890000	83910000	0.034	43	-5.21
1	32530000	32550000	0.040	103	-5.11
1	190930000	190950000	0.042	43	-5.08
1	32620000	32640000	0.045	141	-5.01
1	111130000	111150000	0.048	101	-4.96
1	119520000	119540000	0.049	117	-4.96
1	32520000	32540000	0.050	97	-4.93
1	32630000	32650000	0.053	110	-4.88
1	127150000	127170000	0.053	67	-4.88
1	67240000	67260000	0.054	147	-4.86
1	111260000	111280000	0.056	141	-4.82
1	127160000	127180000	0.064	40	-4.68
1	127170000	127190000	0.066	39	-4.65
1	127340000	127360000	0.067	65	-4.64
1	85120000	85140000	0.067	191	-4.63
1	127820000	127840000	0.070	48	-4.58
1	32610000	32630000	0.072	81	-4.55
1	32640000	32660000	0.076	57	-4.48
1	127810000	127830000	0.076	84	-4.48
1	32540000	32560000	0.077	102	-4.47
1	127330000	127350000	0.077	58	-4.46
1	127180000	127200000	0.080	44	-4.41
1	111250000	111270000	0.081	158	-4.40
1	91680000	91700000	0.081	169	-4.39
1	111180000	111200000	0.081	102	-4.39
1	127190000	127210000	0.083	52	-4.36
1	32480000	32500000	0.083	88	-4.35
1	111210000	111230000	0.084	68	-4.34
1	32510000	32530000	0.086	67	-4.32
1	127560000	127580000	0.086	48	-4.30

Chr	Window Start	Window End	Hp	SNP Count	ZHp
1	90920000	90940000	0.087	200	-4.30
1	32470000	32490000	0.087	77	-4.29
1	32450000	32470000	0.087	66	-4.29
1	90930000	90950000	0.088	207	-4.28
1	103840000	103860000	0.088	200	-4.27
1	25510000	25530000	0.089	71	-4.25
1	127350000	127370000	0.090	69	-4.24
1	127320000	127340000	0.090	51	-4.23
1	55520000	55540000	0.091	126	-4.23
1	83900000	83920000	0.091	127	-4.22
1	190960000	190980000	0.092	123	-4.21
1	55220000	55240000	0.092	117	-4.20
1	127310000	127330000	0.092	48	-4.20
1	127390000	127410000	0.094	89	-4.16
1	111070000	111090000	0.096	258	-4.14
1	111190000	111210000	0.096	33	-4.14
1	67200000	67220000	0.096	102	-4.13
1	85820000	85840000	0.098	225	-4.09
1	103880000	103900000	0.099	159	-4.08
1	119470000	119490000	0.101	142	-4.05
1	83880000	83900000	0.101	106	-4.04
1	32440000	32460000	0.102	88	-4.03
1	83870000	83890000	0.102	179	-4.03
1	116130000	116150000	0.102	120	-4.02
1	111220000	111240000	0.103	187	-4.02
1	55860000	55880000	0.104	73	-4.00
2	116370000	116390000	0.000	162	-5.80
2	116360000	116380000	0.000	145	-5.80
2	140530000	140550000	0.004	80	-5.73
2	140500000	140520000	0.005	133	-5.71
2	140520000	140540000	0.006	83	-5.70
2	140510000	140530000	0.007	99	-5.68
2	116380000	116400000	0.015	111	-5.54
2	147260000	147280000	0.020	101	-5.46
2	140490000	140510000	0.021	139	-5.43
2	140460000	140480000	0.035	94	-5.20
2	4520000	4540000	0.038	26	-5.15
2	140480000	140500000	0.062	119	-4.72
2	116100000	116120000	0.064	99	-4.70
2	60600000	60620000	0.068	109	-4.62
2	147250000	147270000	0.068	118	-4.62
2	140470000	140490000	0.070	87	-4.58
2	116070000	116090000	0.076	148	-4.49
2	116350000	116370000	0.078	148	-4.45
2	74040000	74060000	0.078	51	-4.44
2	9160000	9180000	0.078	108	-4.44
2	116260000	116280000	0.080	52	-4.41

Chr	Window Start	Window End	Hp	SNP Count	ZHp
2	26380000	26400000	0.081	149	-4.40
2	30300000	30320000	0.082	187	-4.38
2	9150000	9170000	0.083	69	-4.36
2	4480000	4500000	0.085	168	-4.32
2	141580000	141600000	0.088	115	-4.27
2	116080000	116100000	0.092	164	-4.21
2	4530000	4550000	0.095	124	-4.16
2	9170000	9190000	0.095	102	-4.16
2	74030000	74050000	0.095	30	-4.15
2	73980000	74000000	0.095	25	-4.15
2	4380000	4400000	0.097	211	-4.12
2	73970000	73990000	0.097	26	-4.11
2	32780000	32800000	0.098	223	-4.09
2	40240000	40260000	0.099	215	-4.08
2	122420000	122440000	0.100	264	-4.07
2	31730000	31750000	0.100	237	-4.07
2	122430000	122450000	0.102	279	-4.03
2	26410000	26430000	0.102	137	-4.02
2	60650000	60670000	0.103	136	-4.01
3	77950000	77970000	0.000	96	-5.80
3	103610000	103630000	0.000	72	-5.80
3	103570000	103590000	0.000	52	-5.80
3	103020000	103040000	0.000	51	-5.80
3	103160000	103180000	0.000	51	-5.80
3	103460000	103480000	0.000	27	-5.80
3	77940000	77960000	0.002	106	-5.77
3	103600000	103620000	0.002	74	-5.76
3	103070000	103090000	0.003	63	-5.76
3	103470000	103490000	0.003	58	-5.75
3	77990000	78010000	0.003	107	-5.75
3	77930000	77950000	0.003	97	-5.74
3	103150000	103170000	0.004	95	-5.74
3	103490000	103510000	0.004	95	-5.74
3	103480000	103500000	0.004	87	-5.73
3	103050000	103070000	0.004	85	-5.73
3	77960000	77980000	0.004	84	-5.73
3	103510000	103530000	0.004	41	-5.73
3	103120000	103140000	0.005	72	-5.72
3	103060000	103080000	0.005	71	-5.72
3	103560000	103580000	0.006	60	-5.71
3	103520000	103540000	0.006	83	-5.70
3	103500000	103520000	0.006	54	-5.69
3	103040000	103060000	0.006	128	-5.69
3	103030000	103050000	0.007	102	-5.69
3	103100000	103120000	0.007	67	-5.67
3	103110000	103130000	0.008	84	-5.66
3	103550000	103570000	0.009	70	-5.64

Chr	Window Start	Window End	Hp	SNP Count	ZHp
3	103010000	103030000	0.009	35	-5.64
3	77980000	78000000	0.010	99	-5.63
3	103080000	103100000	0.010	66	-5.63
3	103140000	103160000	0.010	98	-5.62
3	103090000	103110000	0.010	65	-5.62
3	103580000	103600000	0.011	31	-5.62
3	103450000	103470000	0.012	28	-5.60
3	103130000	103150000	0.013	65	-5.58
3	103540000	103560000	0.013	65	-5.58
3	103530000	103550000	0.014	72	-5.56
3	103590000	103610000	0.014	35	-5.55
3	77970000	77990000	0.016	85	-5.53
3	103170000	103190000	0.019	26	-5.47
3	103620000	103640000	0.027	43	-5.34
3	103630000	103650000	0.037	48	-5.15
3	103650000	103670000	0.056	66	-4.82
3	103640000	103660000	0.057	40	-4.82
3	74030000	74050000	0.064	111	-4.69
3	74000000	74020000	0.073	115	-4.54
3	74020000	74040000	0.075	118	-4.50
3	72820000	72840000	0.075	247	-4.50
3	74010000	74030000	0.077	121	-4.47
3	103440000	103460000	0.079	73	-4.43
3	102690000	102710000	0.079	168	-4.43
3	59780000	59800000	0.080	28	-4.41
3	72810000	72830000	0.084	213	-4.35
3	50640000	50660000	0.084	100	-4.34
3	103430000	103450000	0.087	148	-4.29
3	102760000	102780000	0.088	119	-4.27
3	102700000	102720000	0.089	173	-4.25
3	91600000	91620000	0.089	103	-4.25
3	90940000	90960000	0.090	46	-4.24
3	84960000	84980000	0.092	93	-4.20
3	102670000	102690000	0.093	118	-4.19
3	102750000	102770000	0.095	174	-4.16
3	83350000	83370000	0.095	197	-4.15
3	73490000	73510000	0.095	148	-4.15
3	102680000	102700000	0.095	113	-4.15
3	50650000	50670000	0.096	168	-4.13
3	51660000	51680000	0.098	92	-4.10
3	77770000	77790000	0.098	166	-4.10
3	78100000	78120000	0.100	242	-4.07
3	77760000	77780000	0.100	253	-4.07
3	102640000	102660000	0.100	154	-4.07
3	55040000	55060000	0.101	191	-4.05
3	103420000	103440000	0.101	133	-4.05
3	91610000	91630000	0.101	161	-4.05

Chr	Window Start	Window End	Hp	SNP Count	ZHp
3	73990000	74010000	0.104	105	-4.00
4	78120000	78140000	0.005	92	-5.71
4	7970000	7990000	0.010	69	-5.63
4	7980000	8000000	0.011	45	-5.61
4	39420000	39440000	0.020	157	-5.45
4	78110000	78130000	0.038	52	-5.15
4	7960000	7980000	0.040	66	-5.11
4	78130000	78150000	0.056	142	-4.83
4	39410000	39430000	0.064	190	-4.68
4	39430000	39450000	0.067	179	-4.63
4	39380000	39400000	0.069	222	-4.60
4	78160000	78180000	0.087	90	-4.30
4	78090000	78110000	0.089	181	-4.26
4	39490000	39510000	0.090	236	-4.23
4	78100000	78120000	0.092	134	-4.20
4	39480000	39500000	0.092	180	-4.20
4	78150000	78170000	0.093	142	-4.19
4	76850000	76870000	0.093	192	-4.18
4	78020000	78040000	0.094	181	-4.17
4	78170000	78190000	0.096	74	-4.13
4	39500000	39520000	0.097	344	-4.11
4	78140000	78160000	0.098	181	-4.10
5	27220000	27240000	0.000	214	-5.80
5	27240000	27260000	0.000	202	-5.80
5	27230000	27250000	0.000	194	-5.80
5	40840000	40860000	0.001	165	-5.78
5	27270000	27290000	0.001	135	-5.78
5	17790000	17810000	0.002	78	-5.76
5	27250000	27270000	0.004	129	-5.73
5	27260000	27280000	0.004	119	-5.73
5	40850000	40870000	0.004	156	-5.73
5	27210000	27230000	0.005	220	-5.71
5	22530000	22550000	0.009	39	-5.65
5	22540000	22560000	0.009	36	-5.64
5	17780000	17800000	0.010	100	-5.63
5	27200000	27220000	0.015	178	-5.54
5	40860000	40880000	0.021	112	-5.44
5	40830000	40850000	0.024	177	-5.38
5	22480000	22500000	0.037	22	-5.16
5	11380000	11400000	0.040	62	-5.12
5	11370000	11390000	0.043	80	-5.06
5	27850000	27870000	0.043	217	-5.06
5	27280000	27300000	0.057	107	-4.80
5	27840000	27860000	0.058	139	-4.79
5	25050000	25070000	0.058	199	-4.79
5	47670000	47690000	0.062	193	-4.73
5	11420000	11440000	0.069	72	-4.60

Chr	Window Start	Window End	Hp	SNP Count	ZHp
5	35730000	35750000	0.076	150	-4.49
5	22520000	22540000	0.076	21	-4.48
5	41020000	41040000	0.077	158	-4.46
5	11410000	11430000	0.079	61	-4.44
5	22470000	22490000	0.080	28	-4.41
5	22490000	22510000	0.080	22	-4.41
5	26750000	26770000	0.081	262	-4.39
5	41880000	41900000	0.084	123	-4.35
5	41050000	41070000	0.085	133	-4.32
5	26770000	26790000	0.087	278	-4.29
5	25080000	25100000	0.092	153	-4.20
5	27820000	27840000	0.095	93	-4.15
5	26760000	26780000	0.098	249	-4.10
5	7940000	7960000	0.099	197	-4.09
5	26780000	26800000	0.100	289	-4.07
5	27810000	27830000	0.100	132	-4.06
5	18420000	18440000	0.101	273	-4.05
5	47680000	47700000	0.104	193	-4.00
6	14980000	15000000	0.041	79	-5.08
6	14990000	15010000	0.063	94	-4.70
6	15000000	15020000	0.075	124	-4.50
6	14970000	14990000	0.095	95	-4.15
7	19920000	19940000	0.060	57	-4.77
7	20480000	20500000	0.070	126	-4.58
7	20490000	20510000	0.071	114	-4.57
7	17040000	17060000	0.073	263	-4.53
7	19910000	19930000	0.079	71	-4.42
7	8590000	8610000	0.097	60	-4.11
7	20510000	20530000	0.098	122	-4.09
7	20500000	20520000	0.100	99	-4.06
7	8580000	8600000	0.104	76	-4.00
8	13100000	13120000	0.042	47	-5.08
8	8830000	8850000	0.044	221	-5.05
8	8820000	8840000	0.046	201	-5.00
8	9160000	9180000	0.048	119	-4.97
8	8810000	8830000	0.058	114	-4.79
8	8990000	9010000	0.062	44	-4.72
8	9150000	9170000	0.064	106	-4.69
8	9140000	9160000	0.070	92	-4.59
8	9520000	9540000	0.077	79	-4.46
8	9170000	9190000	0.079	81	-4.43
8	9200000	9220000	0.080	86	-4.41
8	9130000	9150000	0.081	71	-4.40
8	9000000	9020000	0.083	23	-4.36
8	9190000	9210000	0.088	63	-4.27
8	12910000	12930000	0.088	97	-4.26
8	1770000	1790000	0.097	187	-4.11

Chr	Window Start	Window End	Hp	SNP Count	ZHp
9	12410000	12430000	0.005	102	-5.72
9	12400000	12420000	0.006	28	-5.70
9	10160000	10180000	0.012	68	-5.59
9	12380000	12400000	0.013	117	-5.58
9	10270000	10290000	0.016	128	-5.53
9	10170000	10190000	0.020	67	-5.46
9	10280000	10300000	0.020	108	-5.46
9	10150000	10170000	0.028	71	-5.32
9	12390000	12410000	0.033	40	-5.23
9	10260000	10280000	0.049	187	-4.95
9	10180000	10200000	0.056	66	-4.82
9	11160000	11180000	0.077	155	-4.46
9	5510000	5530000	0.080	102	-4.41
9	10220000	10240000	0.084	180	-4.34
9	10250000	10270000	0.087	173	-4.28
9	10410000	10430000	0.093	58	-4.19
9	12370000	12390000	0.098	152	-4.10
9	10230000	10250000	0.100	229	-4.07
10	18100000	18120000	0.103	157	-4.01
11	1610000	1630000	0.009	143	-5.64
12	10520000	10540000	0.054	184	-4.87
13	1650000	1670000	0.080	24	-4.41
13	16720000	16740000	0.090	67	-4.24
14	5300000	5320000	0.027	85	-5.33
14	14780000	14800000	0.092	68	-4.20
15	6770000	6790000	0.097	112	-4.11
17	950000	970000	0.094	95	-4.17
20	8170000	8190000	0.093	121	-4.19
20	8080000	8100000	0.093	209	-4.18
24	6110000	6130000	0.053	168	-4.88
24	6120000	6140000	0.103	137	-4.02

Chr = Chromosome

Table S 51. List of candidate genes in Local Horro (N=6).

Chr.	Gene stable ID	Gene end (bp)	Gene start (bp)	Gene name	Gene type
1	ENSGALG00000027781	103900014	103899869	RF02271	misc_RNA
1	ENSGALG00000014030	67232162	67216258		protein coding
1	ENSGALG00000042479	67209545	67209491	gga-mir-7451	miRNA
1	ENSGALG00000032836	111277522	111228641	MAOB	protein coding
1	ENSGALG00000014031	67242703	67235341	ETFRF1	protein coding
1	ENSGALG00000016224	111332024	111259525	MAOA	protein coding
1	ENSGALG00000012791	56041222	55806774	TBXAS1	protein coding
1	ENSGALG00000014011	67215800	67203135	LRMP	protein coding
1	ENSGALG00000016221.	111115975	111056475	EFHC2	protein coding
1	ENSGALG00000015446	91748448	91662967	POU2F1	protein coding
1	ENSGALG00000030943	67263388	67241669	KRAS	protein coding
1	ENSGALG00000039376	83934219	83908116	DPT	protein coding
1	ENSGALG00000016288	116671490	116055337	IL1RAPL1	protein coding
1	ENSGALG00000016222	111204533	111184729	NDP	protein coding
1	ENSGALG00000038090	25570813	25413945		lincRNA
1	ENSGALG00000038179	32452343	32268154		lincRNA
1	ENSGALG00000030019	127858054	127725469		lincRNA
1	ENSGALG00000029967	127826062	127825392		lincRNA
2	ENSGALG00000005710	4582669	4515467	CTDSPL	protein coding
2	ENSGALG00000034561	116395434	116286317		protein coding
2	ENSGALG00000012689	60709367	60597695	KIF13A	protein coding
2	ENSGALG00000037626	141705820	141521126	KCNQ3	protein coding
2	ENSGALG00000010718	26546888	26317033	THSD7A	protein coding
2	ENSGALG00000030054	9397176	8821485	PTPRN2	protein coding
2	ENSGALG00000037014	147418330	147222471	TSNARE1	protein coding
2	ENSGALG00000011007	31771000	31704354	OSBPL3	protein coding
2	ENSGALG00000042354	116131725	116026798	PREX2	protein coding
2	ENSGALG00000005694	4396355	4374027	GARS	protein coding
3	ENSGALG00000015846	77987344	77916880	SNAP91	protein coding
3	ENSGALG00000026500	103172181	103172072	gga-mir-6678	miRNA
3	ENSGALG00000016491	102693303	102659050	APOB	protein coding
3	ENSGALG00000036005	50738444	50653163	TIAM2	protein coding
3	ENSGALG00000013869	55055817	55035015	IL20RA	protein coding
3	ENSGALG00000043584	83351003	83179142	COL19A1	protein coding
3	ENSGALG00000015836	77786312	77740723	CEP162	protein coding
3	ENSGALG00000013689	51700024	51679654	TMEM242	protein coding
3	ENSGALG00000015847	78001876	78000086	PRSS35	protein coding
3	ENSGALG00000015517	72823589	72784599		protein coding
3	ENSGALG00000029200	72871521	72819230		protein coding
3	ENSGALG00000015849	78198472	78041071	ME1	protein coding
3	ENSGALG00000037938	90940562	90939896		lincRNA
4	ENSGALG00000014931	78074717	78013279	RAB28	protein coding
4	ENSGALG00000010596	39482459	39448857	TACR3	protein coding
4	ENSGALG00000014485	76951561	76744861	LDB2	protein coding
5	ENSGALG00000005438	7948685	7919891	PARVA	protein coding
5	ENSGALG00000008692	25096118	25038945		protein coding
5	ENSGALG00000009415	27835276	27718429	SMOC1	protein coding
5	ENSGALG00000000296	27283175	27201732	PCNX1	protein coding
5	ENSGALG00000009368	26906126	26680031	RGS6	protein coding
5	ENSGALG00000010576	40894704	40868271	GTF2A1	protein coding
5	ENSGALG00000041808	17800632	17729748	ANO1	protein coding

Chr.	Gene stable ID	Gene end (bp)	Gene start (bp)	Gene name	Gene type
5	ENSGALG00000010572	40858950	40811286	TSHR	protein coding
5	ENSGALG00000010001	35767270	35742881	EGLN3	protein coding
6	ENSGALG00000005035	15068657	14982062	KAT6B	protein coding
6	ENSGALG00000005019	14975346	14955839	DUPD1	protein coding
7	ENSGALG00000011009	19968241	19912741	SCN2A	protein coding
7	ENSGALG00000010971	19910444	19815163	CSRNP3	protein coding
7	ENSGALG00000009325	17116055	17030281	OLA1	protein coding
8	ENSGALG00000033708	9019789	9019159		lincRNA
8	ENSGALG00000043258	9545093	9537043		lincRNA
9	ENSGALG00000002897	10150156	10142631	SLC16A14	protein coding
9	ENSGALG00000038512	12430615	12398415	AGTR1	protein coding
9	ENSGALG00000002850	10256070	10213881	RASA2	protein coding
9	ENSGALG00000002729	10431361	10392753	GK5	protein coding
9	ENSGALG00000021117	10269197	10262779	RNF7	protein coding
9	ENSGALG00000002800	10289497	10271683	GRK7	protein coding
9	ENSGALG00000005521	5526782	5502475	PER2	protein coding
9	ENSGALG00000034946	10190468	10189098		lincRNA
10	ENSGALG00000007495	18109320	18094354	SLC24A1	protein coding
10	ENSGALG00000041403	18150025	18113901	DENND4A	protein coding
11	ENSGALG00000002407	1708650	1604963	HYDIN	protein coding
12	ENSGALG00000034289	10520263	10499369	SLC41A3	protein coding
13	ENSGALG00000017462	16736631	16678225	FNIP1	protein coding
13	ENSGALG00000040453	1650955	1649170	SRA1	protein coding
13	ENSGALG00000001132	1654407	1651000		protein coding
13	ENSGALG00000001099	1650955	1544222	ANKHD1	protein coding
13	ENSGALG00000044678	16746031	16739994		protein coding
14	ENSGALG00000002119	14809857	14717931	VPS35L	protein coding
14	ENSGALG00000005215	5339317	5264613	CACNA1H	protein coding
15	ENSGALG00000005122	6789221	6773611	MYO1H	protein coding
17	ENSGALG00000031482	953061	950257	Pou5f3	protein coding
17	ENSGALG00000042635	971844	953350	NPDC1	protein coding
24	ENSGALG00000007868	6130965	6110301	BCO2	protein coding

Chr = Chromosome

Table S 52. Hp values for threshold windows in Jarso chicken populations.

Chr	Window Start	Window end	Hp	SNP(N)	Genomic Position	ZHp
1	103000000	1.03E+08	0.039	112	103000000	-4.06
2	66020000	66040000	0.026	185	262000000	-4.26
2	78570000	78590000	0.034	69	275000000	-4.14
2	147000000	1.47E+08	0.039	105	343000000	-4.06
3	61490000	61510000	0.027	138	407000000	-4.25
4	39450000	39470000	0.004	98	497000000	-4.63
4	39460000	39480000	0.006	90	497000000	-4.6
5	40840000	40860000	0.002	169	589000000	-4.65
5	40850000	40870000	0.003	159	589000000	-4.64
5	40860000	40880000	0.008	112	589000000	-4.56
5	47580000	47600000	0.009	45	596000000	-4.53
5	40830000	40850000	0.01	177	589000000	-4.52
5	41880000	41900000	0.022	129	590000000	-4.32
5	41870000	41890000	0.027	117	590000000	-4.25
6	18320000	18340000	0.04	155	627000000	-4.05
7	8370000	8390000	0.014	96	652000000	-4.46
7	8400000	8420000	0.021	48	652000000	-4.35
7	8580000	8600000	0.037	68	652000000	-4.09
7	8360000	8380000	0.037	60	652000000	-4.08
8	9160000	9180000	0.032	127	690000000	-4.17
8	8830000	8850000	0.032	231	689000000	-4.16
9	10340000	10360000	0.002	145	721000000	-4.65
9	10410000	10430000	0.004	36	721000000	-4.62
9	10350000	10370000	0.006	140	721000000	-4.59
9	10360000	10380000	0.008	101	721000000	-4.55
9	10370000	10390000	0.015	141	721000000	-4.44
9	10380000	10400000	0.035	135	721000000	-4.11
9	10330000	10350000	0.042	126	721000000	-4.01
13	520000	540000	0	36	796000000	-4.68
13	530000	550000	0	36	796000000	-4.68
13	1650000	1670000	0.041	26	797000000	-4.02

Chr = Chromosome

Table S 53. List of candidate genes in Jarso chicken

Gene stable ID	Gene start (bp)	Gene end (bp)	Chr	Gene name	Gene type
ENSGALG00000015770	102609866	102809834	1	APP	protein coding
ENSGALG00000040453	1649170	1650955	13	SRA1	protein coding
ENSGALG00000001132	1651000	1654407	13		protein coding
ENSGALG00000001099	1544222	1650955	13	ANKHD1	protein coding
ENSGALG00000035925	78567875	78573368	2		protein coding
ENSGALG00000037014	147222471	147418330	2	TSNARE1	protein coding
ENSGALG00000038420	61487557	61508738	3	HSF2	protein coding
ENSGALG00000010596	39448857	39482459	4	TACR3	protein coding
ENSGALG00000010576	40868271	40894704	5	GTF2A1	protein coding
ENSGALG00000010572	40811286	40858950	5	TSHR	protein coding
ENSGALG00000002729	10392753	10431361	9	GK5	protein coding
ENSGALG00000025759	10338213	10382351	9	TFDP2	protein coding
ENSGALG00000030000	10355033	10369237	9		lincRNA

Chr = Chromosome

Table S 54. Hp values within the threshold level (Hp ≤ -4) in Jarso (N=14).

Chr	Window start	Window end	Hp	SNP(N)	Genomic Position	ZHp
1	81690000	81710000	0.011	64	81710000	-4.95
1	175400000	175420000	0.011	160	175420000	-4.94
1	77480000	77500000	0.014	130	77500000	-4.90
1	77470000	77490000	0.016	140	77490000	-4.87
1	81700000	81720000	0.020	99	81720000	-4.80
1	81710000	81730000	0.028	101	81730000	-4.67
1	168990000	169010000	0.038	82	169010000	-4.52
1	175080000	175100000	0.042	106	175100000	-4.45
1	175390000	175410000	0.045	158	175410000	-4.41
1	76430000	76450000	0.046	76	76450000	-4.39
1	66940000	66960000	0.053	150	66960000	-4.28
1	58790000	58810000	0.057	179	58810000	-4.23
1	66950000	66970000	0.058	147	66970000	-4.21
1	80270000	80290000	0.062	67	80290000	-4.14
1	31890000	31910000	0.062	59	31910000	-4.14
1	119520000	119540000	0.066	158	119540000	-4.08
1	58780000	58800000	0.067	170	58800000	-4.07
1	109570000	109590000	0.067	252	109590000	-4.06
1	119530000	119550000	0.071	79	119550000	-4.01
2	122490000	122510000	0.004	214	318712544	-5.06
2	122480000	122500000	0.004	220	318702544	-5.05
2	122470000	122490000	0.005	150	318692544	-5.05
2	119160000	119180000	0.005	39	315382544	-5.04
2	132740000	132760000	0.008	47	328962544	-4.99
2	122460000	122480000	0.017	161	318682544	-4.85
2	119170000	119190000	0.019	64	315392544	-4.83
2	119180000	119200000	0.019	73	315402544	-4.82
2	68440000	68460000	0.027	44	264662544	-4.70

Chr	Window start	Window end	Hp	SNP(N)	Genomic Position	ZHp
2	122450000	122470000	0.031	177	318672544	-4.64
2	119190000	119210000	0.032	79	315412544	-4.61
2	147260000	147280000	0.035	116	343482544	-4.57
2	61630000	61650000	0.036	138	257852544	-4.56
2	120590000	120610000	0.036	35	316812544	-4.55
2	68430000	68450000	0.040	132	264652544	-4.49
2	120580000	120600000	0.050	55	316802544	-4.34
2	120650000	120670000	0.050	146	316872544	-4.33
2	120660000	120680000	0.051	132	316882544	-4.32
2	21820000	21840000	0.061	260	218042544	-4.16
2	132730000	132750000	0.063	60	328952544	-4.13
2	86680000	86700000	0.064	77	282902544	-4.11
2	86690000	86710000	0.067	107	282912544	-4.07
2	21210000	21230000	0.067	171	217432544	-4.06
2	63590000	63610000	0.069	111	259812544	-4.03
2	58680000	58700000	0.071	160	254902544	-4.00
2	120640000	120660000	0.071	123	316862544	-4.00
3	50630000	50650000	0.000	43	396413279	-5.12
3	50650000	50670000	0.002	131	396433279	-5.09
3	50640000	50660000	0.002	80	396423279	-5.08
3	26390000	26410000	0.003	159	372173279	-5.07
3	26400000	26420000	0.017	156	372183279	-4.85
3	60660000	60680000	0.048	130	406443279	-4.37
3	85790000	85810000	0.053	42	431573279	-4.28
3	85800000	85820000	0.057	80	431583279	-4.22
3	26310000	26330000	0.057	95	372093279	-4.22
3	103430000	103450000	0.057	156	449213279	-4.22
3	26410000	26430000	0.058	158	372193279	-4.21
3	26230000	26250000	0.061	256	372013279	-4.16
3	26300000	26320000	0.062	105	372083279	-4.15
3	26240000	26260000	0.063	191	372023279	-4.13
3	85760000	85780000	0.063	52	431543279	-4.13
3	85780000	85800000	0.064	35	431563279	-4.12
3	26470000	26490000	0.064	81	372253279	-4.11
3	103420000	103440000	0.066	141	449203279	-4.09
3	26290000	26310000	0.067	88	372073279	-4.07
3	85810000	85830000	0.067	98	431593279	-4.07
3	89550000	89570000	0.069	49	435333279	-4.04
3	60880000	60900000	0.071	95	406663279	-4.01
4	7020000	7040000	0.000	79	464105401	-5.12
4	7930000	7950000	0.000	29	465015401	-5.12
4	7940000	7960000	0.000	56	465025401	-5.12
4	7980000	8000000	0.000	42	465065401	-5.12
4	76360000	76380000	0.002	94	533445401	-5.09
4	78490000	78510000	0.003	79	535575401	-5.08
4	76370000	76390000	0.006	67	533455401	-5.03
4	7970000	7990000	0.008	66	465055401	-5.00

Chr	Window start	Window end	Hp	SNP(N)	Genomic Position	ZHp
4	7950000	7970000	0.008	51	465035401	-5.00
4	78480000	78500000	0.011	61	535565401	-4.94
4	78470000	78490000	0.012	101	535555401	-4.93
4	19930000	19950000	0.013	132	477015401	-4.92
4	76350000	76370000	0.014	120	533435401	-4.90
4	7960000	7980000	0.016	55	465045401	-4.86
4	7030000	7050000	0.018	113	464115401	-4.83
4	28650000	28670000	0.019	107	485735401	-4.81
4	28640000	28660000	0.020	119	485725401	-4.81
4	28630000	28650000	0.023	128	485715401	-4.76
4	19940000	19960000	0.024	62	477025401	-4.74
4	28620000	28640000	0.031	132	485705401	-4.63
4	28470000	28490000	0.036	22	485555401	-4.56
4	78460000	78480000	0.036	95	535545401	-4.55
4	78370000	78390000	0.038	60	535455401	-4.53
4	6620000	6640000	0.041	67	463705401	-4.48
4	78360000	78380000	0.042	51	535445401	-4.46
4	78390000	78410000	0.043	90	535475401	-4.44
4	78400000	78420000	0.043	63	535485401	-4.44
4	78380000	78400000	0.044	88	535465401	-4.42
4	78110000	78130000	0.045	57	535195401	-4.42
4	27840000	27860000	0.047	65	484925401	-4.39
4	6690000	6710000	0.047	138	463775401	-4.39
4	11360000	11380000	0.051	134	468445401	-4.32
4	78500000	78520000	0.051	145	535585401	-4.32
4	78120000	78140000	0.052	114	535205401	-4.30
4	78180000	78200000	0.053	81	535265401	-4.29
4	28610000	28630000	0.055	96	485695401	-4.26
4	19960000	19980000	0.057	34	477045401	-4.22
4	7260000	7280000	0.058	108	464345401	-4.22
4	6700000	6720000	0.058	154	463785401	-4.21
4	27800000	27820000	0.058	40	484885401	-4.21
4	28460000	28480000	0.058	35	485545401	-4.21
4	19920000	19940000	0.062	100	477005401	-4.15
4	19880000	19900000	0.063	23	476965401	-4.13
4	78170000	78190000	0.064	82	535255401	-4.12
4	29870000	29890000	0.065	154	486955401	-4.10
4	45960000	45980000	0.065	200	503045401	-4.10
4	27790000	27810000	0.067	45	484875401	-4.08
4	21600000	21620000	0.067	197	478685401	-4.07
4	27810000	27830000	0.067	42	484895401	-4.07
4	39450000	39470000	0.067	170	496535401	-4.06
4	21670000	21690000	0.069	159	478755401	-4.04
4	28660000	28680000	0.069	94	485745401	-4.04
5	18930000	18950000	0.000	67	567298057	-5.12
5	40840000	40860000	0.001	169	589208057	-5.11
5	40850000	40870000	0.004	159	589218057	-5.06

Chr	Window start	Window end	Hp	SNP(N)	Genomic Position	ZHp
5	21380000	21400000	0.008	72	569748057	-4.99
5	40830000	40850000	0.009	179	589198057	-4.98
5	40860000	40880000	0.011	113	589228057	-4.95
5	18810000	18830000	0.015	94	567178057	-4.89
5	55440000	55460000	0.020	218	603808057	-4.80
5	41880000	41900000	0.047	134	590248057	-4.38
5	18820000	18840000	0.049	130	567188057	-4.35
5	41020000	41040000	0.050	185	589388057	-4.33
5	41660000	41680000	0.051	127	590028057	-4.32
5	27450000	27470000	0.054	163	575818057	-4.28
5	41870000	41890000	0.057	119	590238057	-4.22
5	41650000	41670000	0.058	203	590018057	-4.20
5	27460000	27480000	0.060	183	575828057	-4.17
5	37400000	37420000	0.061	216	585768057	-4.16
5	55430000	55450000	0.067	196	603798057	-4.08
5	21510000	21530000	0.067	59	569878057	-4.07
5	41050000	41070000	0.067	138	589418057	-4.07
5	41030000	41050000	0.067	173	589398057	-4.06
5	27150000	27170000	0.069	215	575518057	-4.04
6	34450000	34470000	0.026	177	642643359	-4.71
6	14980000	15000000	0.053	90	623173359	-4.29
6	18320000	18340000	0.068	235	626513359	-4.06
6	18340000	18360000	0.071	65	626533359	-4.00
7	34990000	35010000	0.005	127	678650375	-5.04
7	34980000	35000000	0.034	154	678640375	-4.58
7	35000000	35020000	0.056	135	678660375	-4.24
7	28200000	28220000	0.058	118	671860375	-4.20
7	25840000	25860000	0.066	116	669500375	-4.09
8	15230000	15250000	0.002	128	695837311	-5.08
8	23110000	23130000	0.003	110	703717311	-5.08
8	23120000	23140000	0.003	138	703727311	-5.07
8	15240000	15260000	0.005	148	695847311	-5.04
8	23130000	23150000	0.005	95	703737311	-5.04
8	23140000	23160000	0.008	76	703747311	-5.00
8	0	20000	0.011	26	680607311	-4.94
8	10000	30000	0.016	32	680617311	-4.88
8	8830000	8850000	0.017	213	689437311	-4.85
8	9160000	9180000	0.023	116	689767311	-4.76
8	280000	300000	0.024	21	680887311	-4.75
8	8820000	8840000	0.025	199	689427311	-4.72
8	9190000	9210000	0.026	56	689797311	-4.70
8	9050000	9070000	0.029	131	689657311	-4.66
8	9170000	9190000	0.030	80	689777311	-4.65
8	9520000	9540000	0.031	87	690127311	-4.64
8	9060000	9080000	0.031	128	689667311	-4.64
8	8800000	8820000	0.032	28	689407311	-4.62
8	9200000	9220000	0.032	92	689807311	-4.62

Chr	Window start	Window end	Hp	SNP(N)	Genomic Position	ZHp
8	15250000	15270000	0.035	146	695857311	-4.57
8	9720000	9740000	0.035	56	690327311	-4.57
8	8810000	8830000	0.035	123	689417311	-4.57
8	9070000	9090000	0.035	92	689677311	-4.57
8	9510000	9530000	0.036	139	690117311	-4.55
8	9140000	9160000	0.037	96	689747311	-4.54
8	9150000	9170000	0.039	106	689757311	-4.51
8	9680000	9700000	0.039	35	690287311	-4.50
8	9730000	9750000	0.042	63	690337311	-4.46
8	23010000	23030000	0.042	105	703617311	-4.46
8	8990000	9010000	0.042	44	689597311	-4.46
8	9500000	9520000	0.044	130	690107311	-4.43
8	9130000	9150000	0.046	76	689737311	-4.39
8	9000000	9020000	0.047	29	689607311	-4.38
8	9690000	9710000	0.051	44	690297311	-4.32
8	9120000	9140000	0.051	93	689727311	-4.31
8	9420000	9440000	0.053	77	690027311	-4.29
8	9110000	9130000	0.055	130	689717311	-4.26
8	9670000	9690000	0.056	35	690277311	-4.25
8	9180000	9200000	0.057	41	689787311	-4.23
8	8890000	8910000	0.058	264	689497311	-4.22
8	9410000	9430000	0.058	113	690017311	-4.20
8	8900000	8920000	0.061	253	689507311	-4.16
8	11670000	11690000	0.062	84	692277311	-4.14
8	15220000	15240000	0.062	127	695827311	-4.14
8	9040000	9060000	0.064	123	689647311	-4.12
8	8840000	8860000	0.065	194	689447311	-4.10
8	8860000	8880000	0.065	228	689467311	-4.10
8	9710000	9730000	0.067	52	690317311	-4.07
8	9080000	9100000	0.067	88	689687311	-4.07
8	8960000	8980000	0.067	209	689567311	-4.07
8	9430000	9450000	0.068	88	690037311	-4.05
8	8850000	8870000	0.069	208	689457311	-4.04
8	8910000	8930000	0.069	284	689517311	-4.03
8	9340000	9360000	0.069	135	689947311	-4.03
8	15270000	15290000	0.070	37	695877311	-4.02
8	15290000	15310000	0.071	112	695897311	-4.01
8	230000	250000	0.071	34	680837311	-4.01
9	10230000	10250000	0.006	155	720800324	-5.03
9	10240000	10260000	0.007	124	720810324	-5.00
9	10280000	10300000	0.008	104	720850324	-5.00
9	10270000	10290000	0.027	134	720840324	-4.70
9	10290000	10310000	0.033	100	720860324	-4.59
9	10220000	10240000	0.036	170	720790324	-4.56
9	10250000	10270000	0.037	124	720820324	-4.53
9	10260000	10280000	0.042	181	720830324	-4.46
9	10410000	10430000	0.056	63	720980324	-4.25

Chr	Window start	Window end	Hp	SNP(N)	Genomic Position	ZHp
9	12040000	12060000	0.058	166	722610324	-4.21
9	10210000	10230000	0.060	220	720780324	-4.17
9	16460000	16480000	0.064	199	727030324	-4.12
9	16450000	16470000	0.065	208	727020324	-4.10
9	16440000	16460000	0.066	205	727010324	-4.09
9	7870000	7890000	0.070	77	718440324	-4.02
10	12450000	12470000	0.029	123	747111890	-4.67
10	14600000	14620000	0.041	151	749261890	-4.48
10	13740000	13760000	0.061	158	748401890	-4.16
10	12460000	12480000	0.063	116	747121890	-4.14
11	5880000	5900000	0.065	77	760977232	-4.09
11	4680000	4700000	0.069	128	759777232	-4.03
12	4400000	4420000	0.014	97	779716025	-4.89
12	7730000	7750000	0.016	64	783046025	-4.88
12	3410000	3430000	0.045	261	778726025	-4.41
12	3420000	3440000	0.046	192	778736025	-4.40
12	7520000	7540000	0.051	114	782836025	-4.31
12	7530000	7550000	0.060	99	782846025	-4.18
13	4470000	4490000	0.005	103	799734179	-5.04
13	1660000	1680000	0.022	22	796924179	-4.77
13	1650000	1670000	0.039	25	796914179	-4.50
13	4460000	4480000	0.058	153	799724179	-4.21
23	5560000	5580000	0.063	23	905933666	-4.13
23	5600000	5620000	0.067	26	905973666	-4.07
23	5720000	5740000	0.070	29	906093666	-4.02
24	960000	980000	0.065	148	907120194	-4.10

Chr = Chromosomes

Table S 55. Hp values within the threshold level (P ≤ -4) Hugub (N=10).

Chr	Window start	Window end	Hp	SNP (N)	Genomic Position	ZHp
1	81690000	81710000	0.010878	64	81710000	-4.95
1	175400000	175420000	0.011187	160	175420000	-4.94
1	77480000	77500000	0.01375	130	77500000	-4.9
1	77470000	77490000	0.015591	140	77490000	-4.87
1	81700000	81720000	0.019998	99	81720000	-4.8
1	81710000	81730000	0.028301	101	81730000	-4.67
1	168990000	169010000	0.038263	82	169010000	-4.52
1	175080000	175100000	0.042455	106	175100000	-4.45
1	175390000	175410000	0.045135	158	175410000	-4.41
1	76430000	76450000	0.046247	76	76450000	-4.39
1	66940000	66960000	0.053172	150	66960000	-4.28
1	58790000	58810000	0.056939	179	58810000	-4.23
1	66950000	66970000	0.058072	147	66970000	-4.21
1	80270000	80290000	0.06212	67	80290000	-4.14
1	31890000	31910000	0.062333	59	31910000	-4.14
1	119520000	119540000	0.066018	158	119540000	-4.08
1	58780000	58800000	0.067003	170	58800000	-4.07
1	109570000	109590000	0.067402	252	109590000	-4.06
1	119530000	119550000	0.070723	79	119550000	-4.01
2	122490000	122510000	0.003731	214	318712544	-5.06
2	122480000	122500000	0.004083	220	318702544	-5.05
2	122470000	122490000	0.004656	150	318692544	-5.05
2	119160000	119180000	0.005115	39	315382544	-5.04
2	132740000	132760000	0.008474	47	328962544	-4.99
2	122460000	122480000	0.01724	161	318682544	-4.85
2	119170000	119190000	0.018574	64	315392544	-4.83
2	119180000	119200000	0.018994	73	315402544	-4.82
2	68440000	68460000	0.026901	44	264662544	-4.7
2	122450000	122470000	0.030591	177	318672544	-4.64
2	119190000	119210000	0.03237	79	315412544	-4.61
2	147260000	147280000	0.03472	116	343482544	-4.57
2	61630000	61650000	0.035576	138	257852544	-4.56
2	120590000	120610000	0.036453	35	316812544	-4.55
2	68430000	68450000	0.040072	132	264652544	-4.49
2	120580000	120600000	0.049613	55	316802544	-4.34
2	120650000	120670000	0.05005	146	316872544	-4.33
2	120660000	120680000	0.050907	132	316882544	-4.32
2	21820000	21840000	0.061068	260	218042544	-4.16
2	132730000	132750000	0.062888	60	328952544	-4.13
2	86680000	86700000	0.06404	77	282902544	-4.11
2	86690000	86710000	0.066767	107	282912544	-4.07
2	21210000	21230000	0.067169	171	217432544	-4.06
2	63590000	63610000	0.069475	111	259812544	-4.03
2	58680000	58700000	0.071031	160	254902544	-4

Chr	Window start	Window end	Hp	SNP (N)	Genomic Position	ZHp
2	120640000	120660000	0.071247	123	316862544	-4
3	50630000	50650000	0	43	396413279	-5.12
3	50650000	50670000	0.001526	131	396433279	-5.09
3	50640000	50660000	0.002497	80	396423279	-5.08
3	26390000	26410000	0.00314	159	372173279	-5.07
3	26400000	26420000	0.017158	156	372183279	-4.85
3	60660000	60680000	0.048019	130	406443279	-4.37
3	85790000	85810000	0.053263	42	431573279	-4.28
3	85800000	85820000	0.057024	80	431583279	-4.22
3	26310000	26330000	0.05721	95	372093279	-4.22
3	103430000	103450000	0.057235	156	449213279	-4.22
3	26410000	26430000	0.057724	158	372193279	-4.21
3	26230000	26250000	0.061279	256	372013279	-4.16
3	26300000	26320000	0.061774	105	372083279	-4.15
3	26240000	26260000	0.062814	191	372023279	-4.13
3	85760000	85780000	0.063247	52	431543279	-4.13
3	85780000	85800000	0.063555	35	431563279	-4.12
3	26470000	26490000	0.064444	81	372253279	-4.11
3	103420000	103440000	0.065767	141	449203279	-4.09
3	26290000	26310000	0.066916	88	372073279	-4.07
3	85810000	85830000	0.06698	98	431593279	-4.07
3	89550000	89570000	0.068878	49	435333279	-4.04
3	60880000	60900000	0.07097	95	406663279	-4.01
4	7020000	7040000	0	79	464105401	-5.12
4	7930000	7950000	0	29	465015401	-5.12
4	7940000	7960000	0	56	465025401	-5.12
4	7980000	8000000	0	42	465065401	-5.12
4	76360000	76380000	0.002125	94	533445401	-5.09
4	78490000	78510000	0.002528	79	535575401	-5.08
4	76370000	76390000	0.005952	67	533455401	-5.03
4	7970000	7990000	0.007547	66	465055401	-5
4	7950000	7970000	0.007812	51	465035401	-5
4	78480000	78500000	0.01141	61	535565401	-4.94
4	78470000	78490000	0.011811	101	535555401	-4.93
4	19930000	19950000	0.012796	132	477015401	-4.92
4	76350000	76370000	0.014066	120	533435401	-4.9
4	7960000	7980000	0.01623	55	465045401	-4.86
4	7030000	7050000	0.018411	113	464115401	-4.83
4	28650000	28670000	0.019434	107	485735401	-4.81
4	28640000	28660000	0.019965	119	485725401	-4.81
4	28630000	28650000	0.023163	128	485715401	-4.76
4	19940000	19960000	0.023901	62	477025401	-4.74
4	28620000	28640000	0.031312	132	485705401	-4.63
4	28470000	28490000	0.035703	22	485555401	-4.56
4	78460000	78480000	0.036163	95	535545401	-4.55

Chr	Window start	Window end	Hp	SNP (N)	Genomic Position	ZHp
4	78370000	78390000	0.037599	60	535455401	-4.53
4	6620000	6640000	0.040918	67	463705401	-4.48
4	78360000	78380000	0.042207	51	535445401	-4.46
4	78390000	78410000	0.043457	90	535475401	-4.44
4	78400000	78420000	0.043457	63	535485401	-4.44
4	78380000	78400000	0.044422	88	535465401	-4.42
4	78110000	78130000	0.044574	57	535195401	-4.42
4	27840000	27860000	0.046555	65	484925401	-4.39
4	6690000	6710000	0.046682	138	463775401	-4.39
4	11360000	11380000	0.050874	134	468445401	-4.32
4	78500000	78520000	0.05104	145	535585401	-4.32
4	78120000	78140000	0.052077	114	535205401	-4.3
4	78180000	78200000	0.052846	81	535265401	-4.29
4	28610000	28630000	0.054668	96	485695401	-4.26
4	19960000	19980000	0.057093	34	477045401	-4.22
4	7260000	7280000	0.057503	108	464345401	-4.22
4	6700000	6720000	0.057956	154	463785401	-4.21
4	27800000	27820000	0.0582	40	484885401	-4.21
4	28460000	28480000	0.0582	35	485545401	-4.21
4	19920000	19940000	0.061952	100	477005401	-4.15
4	19880000	19900000	0.063091	23	476965401	-4.13
4	78170000	78190000	0.063685	82	535255401	-4.12
4	29870000	29890000	0.064646	154	486955401	-4.1
4	45960000	45980000	0.065222	200	503045401	-4.1
4	27790000	27810000	0.066516	45	484875401	-4.07
4	21600000	21620000	0.066653	197	478685401	-4.07
4	27810000	27830000	0.066664	42	484895401	-4.07
4	39450000	39470000	0.067204	170	496535401	-4.06
4	21670000	21690000	0.068544	159	478755401	-4.04
4	28660000	28680000	0.068736	94	485745401	-4.04
5	18930000	18950000	0	67	567298057	-5.12
5	40840000	40860000	0.000592	169	589208057	-5.11
5	40850000	40870000	0.003766	159	589218057	-5.06
5	21380000	21400000	0.008299	72	569748057	-4.99
5	40830000	40850000	0.008899	179	589198057	-4.98
5	40860000	40880000	0.010563	113	589228057	-4.95
5	18810000	18830000	0.014783	94	567178057	-4.89
5	55440000	55460000	0.020429	218	603808057	-4.8
5	41880000	41900000	0.047331	134	590248057	-4.38
5	18820000	18840000	0.04875	130	567188057	-4.35
5	41020000	41040000	0.050033	185	589388057	-4.33
5	41660000	41680000	0.050618	127	590028057	-4.32
5	27450000	27470000	0.05369	163	575818057	-4.28
5	41870000	41890000	0.057093	119	590238057	-4.22
5	41650000	41670000	0.058293	203	590018057	-4.2

Chr	Window start	Window end	Hp	SNP (N)	Genomic Position	ZHp
5	27460000	27480000	0.060355	183	575828057	-4.17
5	37400000	37420000	0.061415	216	585768057	-4.16
5	55430000	55450000	0.066506	196	603798057	-4.08
5	21510000	21530000	0.067077	59	569878057	-4.07
5	41050000	41070000	0.067146	138	589418057	-4.07
5	41030000	41050000	0.067496	173	589398057	-4.06
5	27150000	27170000	0.068631	215	575518057	-4.04
6	34450000	34470000	0.026201	177	642643359	-4.71
6	14980000	15000000	0.052962	90	623173359	-4.29
6	18320000	18340000	0.067748	235	626513359	-4.06
6	18340000	18360000	0.07112	65	626533359	-4
7	34990000	35010000	0.004713	127	678650375	-5.04
7	34980000	35000000	0.03445	154	678640375	-4.58
7	35000000	35020000	0.056109	135	678660375	-4.24
7	28200000	28220000	0.058359	118	671860375	-4.2
7	25840000	25860000	0.065784	116	669500375	-4.09
8	15230000	15250000	0.002341	128	695837311	-5.08
8	23110000	23130000	0.002724	110	703717311	-5.08
8	23120000	23140000	0.002894	138	703727311	-5.07
8	15240000	15260000	0.004719	148	695847311	-5.04
8	23130000	23150000	0.005249	95	703737311	-5.04
8	23140000	23160000	0.007864	76	703747311	-5
8	0	20000	0.011472	26	680607311	-4.94
8	10000	30000	0.015503	32	680617311	-4.88
8	8830000	8850000	0.01722	213	689437311	-4.85
8	9160000	9180000	0.023005	116	689767311	-4.76
8	280000	300000	0.023526	21	680887311	-4.75
8	8820000	8840000	0.0253	199	689427311	-4.72
8	9190000	9210000	0.026427	56	689797311	-4.7
8	9050000	9070000	0.029328	131	689657311	-4.66
8	9170000	9190000	0.02955	80	689777311	-4.65
8	9520000	9540000	0.030553	87	690127311	-4.64
8	9060000	9080000	0.030762	128	689667311	-4.64
8	8800000	8820000	0.031626	28	689407311	-4.62
8	9200000	9220000	0.032077	92	689807311	-4.62
8	15250000	15270000	0.034982	146	695857311	-4.57
8	9720000	9740000	0.035077	56	690327311	-4.57
8	8810000	8830000	0.035133	123	689417311	-4.57
8	9070000	9090000	0.035226	92	689677311	-4.57
8	9510000	9530000	0.036018	139	690117311	-4.55
8	9140000	9160000	0.036797	96	689747311	-4.54
8	9150000	9170000	0.038838	106	689757311	-4.51
8	9680000	9700000	0.0392	35	690287311	-4.5
8	9730000	9750000	0.041939	63	690337311	-4.46
8	23010000	23030000	0.041939	105	703617311	-4.46

Chr	Window start	Window end	Hp	SNP (N)	Genomic Position	ZHp
8	8990000	9010000	0.04225	44	689597311	-4.46
8	9500000	9520000	0.04362	130	690107311	-4.43
8	9130000	9150000	0.046247	76	689737311	-4.39
8	9000000	9020000	0.047111	29	689607311	-4.38
8	9690000	9710000	0.050907	44	690297311	-4.32
8	9120000	9140000	0.0513	93	689727311	-4.31
8	9420000	9440000	0.053058	77	690027311	-4.29
8	9110000	9130000	0.054577	130	689717311	-4.26
8	9670000	9690000	0.05551	35	690277311	-4.25
8	9180000	9200000	0.056823	41	689787311	-4.23
8	8890000	8910000	0.057575	264	689497311	-4.22
8	9410000	9430000	0.058366	113	690017311	-4.2
8	8900000	8920000	0.061274	253	689507311	-4.16
8	11670000	11690000	0.062219	84	692277311	-4.14
8	15220000	15240000	0.062483	127	695827311	-4.14
8	9040000	9060000	0.063685	123	689647311	-4.12
8	8840000	8860000	0.064765	194	689447311	-4.1
8	8860000	8880000	0.064854	228	689467311	-4.1
8	9710000	9730000	0.066834	52	690317311	-4.07
8	9080000	9100000	0.066916	88	689687311	-4.07
8	8960000	8980000	0.066971	209	689567311	-4.07
8	9430000	9450000	0.067973	88	690037311	-4.05
8	8850000	8870000	0.068622	208	689457311	-4.04
8	8910000	8930000	0.069251	284	689517311	-4.03
8	9340000	9360000	0.069271	135	689947311	-4.03
8	15270000	15290000	0.07031	37	695877311	-4.02
8	15290000	15310000	0.070534	112	695897311	-4.01
8	230000	250000	0.070826	34	680837311	-4.01
9	10230000	10250000	0.00579	155	720800324	-5.03
9	10240000	10260000	0.007243	124	720810324	-5
9	10280000	10300000	0.007663	104	720850324	-5
9	10270000	10290000	0.026505	134	720840324	-4.7
9	10290000	10310000	0.033422	100	720860324	-4.59
9	10220000	10240000	0.035806	170	720790324	-4.56
9	10250000	10270000	0.037244	124	720820324	-4.53
9	10260000	10280000	0.042165	181	720830324	-4.46
9	10410000	10430000	0.05551	63	720980324	-4.25
9	12040000	12060000	0.05786	166	722610324	-4.21
9	10210000	10230000	0.060334	220	720780324	-4.17
9	16460000	16480000	0.063786	199	727030324	-4.12
9	16450000	16470000	0.064714	208	727020324	-4.1
9	16440000	16460000	0.065506	205	727010324	-4.09
9	7870000	7890000	0.070083	77	718440324	-4.02
10	12450000	12470000	0.02884	123	747111890	-4.67
10	14600000	14620000	0.040852	151	749261890	-4.48

Chr	Window start	Window end	Hp	SNP (N)	Genomic Position	ZHp
10	13740000	13760000	0.061288	158	748401890	-4.16
10	12460000	12480000	0.062565	116	747121890	-4.14
11	5880000	5900000	0.065252	77	760977232	-4.09
11	4680000	4700000	0.069292	128	759777232	-4.03
12	4400000	4420000	0.014329	97	779716025	-4.89
12	7730000	7750000	0.015503	64	783046025	-4.88
12	3410000	3430000	0.045286	261	778726025	-4.41
12	3420000	3440000	0.045776	192	778736025	-4.4
12	7520000	7540000	0.051247	114	782836025	-4.31
12	7530000	7550000	0.059718	99	782846025	-4.18
13	4470000	4490000	0.004843	103	799734179	-5.04
13	1660000	1680000	0.022469	22	796924179	-4.77
13	1650000	1670000	0.0392	25	796914179	-4.5
13	4460000	4480000	0.057708	153	799724179	-4.21
23	5560000	5580000	0.063091	23	905933666	-4.13
23	5600000	5620000	0.066834	26	905973666	-4.07
23	5720000	5740000	0.069792	29	906093666	-4.02
24	960000	980000	0.064655	148	907120194	-4.1

N=Count

Table S 56. List of candidate genes in Hugub (N=10).

Chre	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene	Gene type
1	ENSGALG00000026901	76447763	76447872	gga-mir-	miRNA
1	ENSGALG00000016187	109577831	109599269	WDR4	protein coding
1	ENSGALG00000013244	66927420	66999781	ABCC9	protein coding
1	ENSGALG00000011930	76345584	76430119	OVST	protein coding
1	ENSGALG00000014685	77485688	77486689		protein coding
1	ENSGALG00000014687	77496575	77530024	EPHA1	protein coding
1	ENSGALG00000026781	175088272	175096275	ALOX5AP	protein coding
1	ENSGALG00000017002	168999957	169111965	FNDC3A	protein coding
1	ENSGALG00000017084	175340869	175397791	UBL3	protein coding
2	ENSGALG00000012889	68401769	68441726	ZCCHC2	protein coding
2	ENSGALG00000037014	147222471	147418330	TSNARE1	protein coding
2	ENSGALG00000042621	119132532	119162556	HNF4G	protein coding
2	ENSGALG00000033849	63594678	63599141		lincRNA
3	ENSGALG00000034313	26292678	26293813		protein coding
3	ENSGALG00000016263	85768055	85882423		protein coding
3	ENSGALG00000036005	50653163	50738444	TIAM2	protein coding
3	ENSGALG00000010000	26395277	26573746	PRKCE	protein coding
3	ENSGALG00000009990	26149684	26271666	SRBD1	protein coding
4	ENSGALG00000014421	76375272	76448502	LCORL	protein coding
4	ENSGALG00000009826	29873452	29888948	CLGN	protein coding
4	ENSGALG00000007530	11353982	11360783		protein coding
4	ENSGALG00000025899	11370765	11378924		protein coding
4	ENSGALG00000010921	45959958	45974346	PKD2	protein coding
4	ENSGALG00000006851	6599257	7006957		protein coding
4	ENSGALG00000010596	39448857	39482459	TACR3	protein coding
4	ENSGALG00000010926	45974555	45977750	SPP1	protein coding

Chre	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene	Gene type
4	ENSGALG00000009813	29867280	29870882	SCOC	protein coding
4	ENSGALG00000009405	21570620	21658066	GRIA2	protein coding
4	ENSGALG00000035886	27788185	27825157		lincRNA
5	ENSGALG00000010576	40868271	40894704	GTF2A1	protein coding
5	ENSGALG00000012085	55426088	55436007		protein coding
5	ENSGALG00000046577	18799853	18820890		protein coding
5	ENSGALG00000035537	27443274	27450430	SYNJ2BP	protein coding
5	ENSGALG00000012089	55450095	55492082	C14orf37	protein coding
5	ENSGALG00000010572	40811286	40858950	TSHR	protein coding
5	ENSGALG00000009387	27443194	27531009		protein coding
5	ENSGALG00000043759	37413460	37415830		lincRNA
6	ENSGALG00000005035	14982062	15068657	KAT6B	protein coding
7	ENSGALG00000012049	28191739	28205266	ZNF148	protein coding
7	ENSGALG00000012462	34961029	35028577	KIF5C	protein coding
8	ENSGALG00000044067	9703686	9705755		protein coding
8	ENSGALG00000036909	22774073	23612126	AGBL4	protein coding
8	ENSGALG00000020884	11667153	11694964		protein coding
8	ENSGALG00000010505	23084517	23113939	BEND5	protein coding
8	ENSGALG00000006237	15219523	15269342	PKN2	protein coding
8	ENSGALG00000033708	9019159	9019789		lincRNA
8	ENSGALG00000043258	9537043	9545093		lincRNA
9	ENSGALG00000002764	10307410	10329985	ATP1B3	protein coding
9	ENSGALG00000002850	10213881	10256070	RASA2	protein coding
9	ENSGALG00000008785	16440040	16455955	MCCC1	protein coding
9	ENSGALG00000002729	10392753	10431361	GK5	protein coding
9	ENSGALG00000021117	10262779	10269197	RNF7	protein coding
9	ENSGALG00000002800	10271683	10289497	GRK7	protein coding
9	ENSGALG00000030944	7888137	7948484	PAX3	protein coding
9	ENSGALG00000008807	16461899	16479137	DCUN1D1	protein coding
10	ENSGALG00000006445	12413427	12483133	ARNT2	protein coding
10	ENSGALG00000006819	13624751	13893408	AGBL1	protein coding
10	ENSGALG00000006949	14615742	14681032	CHD2	protein coding
12	ENSGALG00000004932	4379082	4468625	ATG7	protein coding
12	ENSGALG00000026080	3414370	3416416	OMD	protein coding
12	ENSGALG00000026736	3424659	3435067	OGN	protein coding
12	ENSGALG00000005400	7323310	7733469		protein coding
12	ENSGALG00000004687	3334370	3451194	CENPP	protein coding
13	ENSGALG00000040453	1649170	1650955	SRA1	protein coding
13	ENSGALG00000001132	1651000	1654407		protein coding
13	ENSGALG00000001099	1544222	1650955	ANKHD1	protein coding
13	ENSGALG00000001916	4204850	4675881	SLIT3	protein coding
23	ENSGALG00000003986	5598141	5600060	PITHD1	protein coding
23	ENSGALG00000004112	5614065	5618727	FUCA1	protein coding
23	ENSGALG00000004002	5602159	5605993	LYPLA2	protein coding
23	ENSGALG00000004057	5610015	5613638	HMGCL	protein coding
23	ENSGALG00000036294	5563597	5574294	CAP1	protein coding
23	ENSGALG00000004047	5607021	5609856	GALE	protein coding
23	ENSGALG00000004120	5619783	5620838	CNR2	protein coding
23	ENSGALG00000003879	5554873	5562608	MFSD2A	protein coding
23	ENSGALG00000003936	5575818	5580472	PPT1	protein coding
23	ENSGALG00000004249	5719948	5741312	GRHL3	protein coding
24	ENSGALG00000038377	975734	983980		lincRNA

Table S 57. Hp values within the threshold level (Hp ≤ -4) in Arabo chicken (N=10).

Chr	Window start	Window end	Hp	N	Genomic Position	ZHp
1	162410000	162430000	0.03737	168	162430000	-4.32188
1	162400000	162420000	0.040291	134	162420000	-4.27448
1	162220000	162240000	0.041219	76	162240000	-4.25942
1	101630000	101650000	0.041329	213	101650000	-4.25763
1	101640000	101660000	0.042484	172	101660000	-4.23888
1	32520000	32540000	0.05016	101	32540000	-4.11433
1	32530000	32550000	0.050264	107	32550000	-4.11264
1	162420000	162440000	0.054595	162	162440000	-4.04235
1	162430000	162450000	0.056946	150	162450000	-4.00421
2	61240000	61260000	0.020616	72	257462544	-4.59374
2	48510000	48530000	0.039636	141	244732544	-4.2851
2	61230000	61250000	0.052137	56	257452544	-4.08225
3	82480000	82500000	0.002008	199	428263279	-4.89571
3	82470000	82490000	0.003072	195	428253279	-4.87844
3	82490000	82510000	0.004393	159	428273279	-4.85701
3	23770000	23790000	0.017788	117	369553279	-4.63965
3	82460000	82480000	0.034854	186	428243279	-4.3627
3	23760000	23780000	0.047645	129	369543279	-4.15514
4	39500000	39520000	0.004007	274	496585401	-4.86328
4	39490000	39510000	0.006012	199	496575401	-4.83074
4	28650000	28670000	0.026427	112	485735401	-4.49945
4	27850000	27870000	0.027608	50	484935401	-4.48029
4	28640000	28660000	0.02805	123	485725401	-4.47311
4	28630000	28650000	0.030527	129	485715401	-4.43292
4	28620000	28640000	0.031518	128	485705401	-4.41683
4	27860000	27880000	0.036541	94	484945401	-4.33533
4	64960000	64980000	0.041636	167	522045401	-4.25265
4	27840000	27860000	0.042793	64	484925401	-4.23387
4	75200000	75220000	0.047442	109	532285401	-4.15843
4	27800000	27820000	0.051714	32	484885401	-4.08911
4	28610000	28630000	0.052973	101	485695401	-4.06868
4	27810000	27830000	0.053058	33	484895401	-4.0673
4	78130000	78150000	0.053058	165	535215401	-4.0673
4	27870000	27890000	0.05551	126	484955401	-4.0275
5	40840000	40860000	0.002323	172	589208057	-4.8906
5	21380000	21400000	0.00944	74	569748057	-4.77511
5	22540000	22560000	0.014888	40	570908057	-4.68671
5	11480000	11500000	0.024406	61	559848057	-4.53224
5	40830000	40850000	0.038263	205	589198057	-4.30738
5	22530000	22550000	0.038529	46	570898057	-4.30306
5	22480000	22500000	0.047216	31	570848057	-4.16209
5	41880000	41900000	0.049805	135	590248057	-4.12009
5	22490000	22510000	0.056632	24	570858057	-4.0093

Chr	Window start	Window end	Hp	N	Genomic Position	ZHp
6	7440000	7460000	0.017721	151	615633359	-4.64073
7	21020000	21040000	0.003221	93	664680375	-4.87603
7	21030000	21050000	0.019965	119	664690375	-4.60432
7	21010000	21030000	0.031448	97	664670375	-4.41797
7	21070000	21090000	0.0409	79	664730375	-4.26459
7	11870000	11890000	0.051039	121	655530375	-4.10006
13	1650000	1670000	0.042293	35	796914179	-4.24198

Chr = Chromosome; N= count

Table S 58. List of candidate genes in Arabo chicken (N=10).

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
1	ENSGALG00000016936	1.62E+08	1.62E+08	TDRD3	protein coding
1	ENSGALG00000016937	1.62E+08	1.63E+08	DIAPH3	protein coding
2	ENSGALG00000039935	48353052	48628045	PDE1C	protein coding
3	ENSGALG00000009915	23653116	23805917	EML4	protein coding
3	ENSGALG00000015944	82215093	82512310	RIMS1	protein coding
4	ENSGALG00000035886	27788185	27825157		lincRNA
4	ENSGALG00000013715	64904550	64998990	DLC1	protein coding
5	ENSGALG00000040491	11466672	11559343		lincRNA
5	ENSGALG00000010572	40811286	40858950	TSHR	protein coding
7	ENSGALG00000008459	11874180	11969327	BMPR2	protein coding
7	ENSGALG00000038543	21044195	21149299		protein coding
13	ENSGALG00000001099	1544222	1650955	ANKHD1	protein coding
13	ENSGALG00000040453	1649170	1650955	SRA1	protein coding
13	ENSGALG00000001132	1651000	1654407		protein coding

Chr = Chromosome

Table S 59. Top Fst values (1%) in Improved with local Horro chicken.

Chr	Window start	Window end	SNP(N)	Weighted Fst	Mean Fst	ZFst
1	117420001	117440000	94	0.18	0.14	8.39
1	116210001	116230000	127	0.17	0.11	7.91
1	116220001	116240000	42	0.16	0.08	7.35
1	116710001	116730000	214	0.15	0.11	7.16

Chr	Window start	Window end	SNP(N)	Weighted Fst	Mean Fst	ZFst
1	117930001	117950000	206	0.15	0.09	6.86
1	115450001	115470000	244	0.15	0.07	6.86
1	116200001	116220000	217	0.15	0.06	6.85
1	117920001	117940000	266	0.15	0.09	6.81
1	116250001	116270000	181	0.15	0.10	6.79
1	116720001	116740000	190	0.14	0.09	6.69
1	115460001	115480000	167	0.14	0.08	6.62
1	105540001	105560000	201	0.14	0.10	6.48
1	70450001	70470000	328	0.14	0.08	6.41
1	118080001	118100000	307	0.13	0.07	6.28
1	70460001	70480000	428	0.13	0.08	6.22
1	70440001	70460000	133	0.13	0.07	6.17
1	105550001	105570000	215	0.13	0.08	6.12
1	118120001	118140000	403	0.13	0.09	6.08
1	116150001	116170000	123	0.13	0.06	6.06
1	116700001	116720000	213	0.13	0.10	6.06
1	116260001	116280000	141	0.13	0.08	6.05
1	70520001	70540000	396	0.13	0.06	6.05
1	117410001	117430000	213	0.12	0.09	5.89
1	70470001	70490000	513	0.12	0.07	5.89
1	116240001	116260000	209	0.12	0.05	5.88
1	96900001	96920000	118	0.12	0.08	5.87
1	114560001	114580000	234	0.12	0.07	5.84
1	117650001	117670000	328	0.12	0.06	5.61
1	105560001	105580000	228	0.12	0.06	5.57
1	117610001	117630000	280	0.11	0.06	5.56
1	70510001	70530000	465	0.11	0.04	5.55
1	115440001	115460000	274	0.11	0.04	5.51
1	70500001	70520000	463	0.11	0.05	5.49
1	117640001	117660000	319	0.11	0.05	5.46
1	96890001	96910000	75	0.11	0.06	5.45
1	117620001	117640000	282	0.11	0.06	5.36
1	77960001	77980000	263	0.11	0.06	5.29
1	70490001	70510000	468	0.11	0.04	5.28
1	116690001	116710000	187	0.11	0.08	5.26
1	108330001	108350000	244	0.11	0.06	5.26
1	105530001	105550000	271	0.11	0.07	5.21
1	108320001	108340000	354	0.11	0.04	5.21
1	116190001	116210000	254	0.11	0.03	5.20
1	70480001	70500000	535	0.11	0.05	5.20
1	105460001	105480000	342	0.11	0.06	5.17
1	105490001	105510000	308	0.11	0.07	5.17
1	84710001	84730000	208	0.10	0.06	5.13
1	118090001	118110000	380	0.10	0.05	5.12
1	117630001	117650000	308	0.10	0.05	5.11

Chr	Window start	Window end	SNP(N)	Weighted Fst	Mean Fst	ZFst
1	78260001	78280000	184	0.10	0.05	5.11
1	118640001	118660000	205	0.10	0.06	5.10
1	107060001	107080000	203	0.10	0.05	5.09
1	109580001	109600000	290	0.10	0.08	5.09
1	77950001	77970000	247	0.10	0.06	5.07
1	108190001	108210000	400	0.10	0.05	5.07
1	107050001	107070000	249	0.10	0.06	5.05
1	116280001	116300000	157	0.10	0.05	5.05
1	77970001	77990000	182	0.10	0.06	5.04
1	116120001	116140000	132	0.10	0.07	5.03
1	118110001	118130000	400	0.10	0.06	4.99
1	116270001	116290000	156	0.10	0.04	4.98
1	116660001	116680000	153	0.10	0.06	4.98
1	114550001	114570000	256	0.10	0.06	4.96
1	108960001	108980000	264	0.10	0.06	4.92
1	113430001	113450000	354	0.10	0.01	4.91
1	77570001	77590000	226	0.10	0.05	4.91
1	113500001	113520000	271	0.10	0.01	4.91
1	108200001	108220000	403	0.10	0.05	4.90
1	115830001	115850000	54	0.10	0.07	4.89
1	109590001	109610000	282	0.10	0.06	4.89
1	108180001	108200000	332	0.10	0.05	4.87
1	117030001	117050000	111	0.10	0.09	4.86
1	77580001	77600000	177	0.10	0.06	4.85
1	105450001	105470000	373	0.10	0.06	4.85
1	105480001	105500000	392	0.10	0.06	4.85
1	70610001	70630000	209	0.10	0.04	4.83
1	108210001	108230000	384	0.10	0.05	4.81
1	117020001	117040000	121	0.10	0.09	4.81
1	113410001	113430000	442	0.10	0.02	4.79
1	116290001	116310000	169	0.10	0.06	4.77
1	105500001	105520000	341	0.10	0.06	4.75
1	108160001	108180000	326	0.10	0.05	4.75
1	116180001	116200000	197	0.09	0.03	4.73
1	118650001	118670000	268	0.09	0.06	4.71
1	108170001	108190000	305	0.09	0.05	4.71
1	113440001	113460000	411	0.09	0.01	4.71
1	116140001	116160000	156	0.09	0.04	4.70
1	117040001	117060000	42	0.09	0.08	4.64
1	117850001	117870000	219	0.09	0.07	4.64
1	105470001	105490000	368	0.09	0.06	4.64
1	114590001	114610000	260	0.09	0.05	4.63
1	117600001	117620000	280	0.09	0.05	4.63
1	113400001	113420000	497	0.09	0.04	4.63
1	118070001	118090000	232	0.09	0.05	4.62

Chr	Window start	Window end	SNP(N)	Weighted Fst	Mean Fst	ZFst
1	70530001	70550000	304	0.09	0.06	4.61
1	78270001	78290000	129	0.09	0.03	4.59
1	77920001	77940000	174	0.09	0.03	4.57
1	114400001	114420000	289	0.09	0.05	4.56
1	118240001	118260000	298	0.09	0.06	4.55
1	115820001	115840000	188	0.09	0.07	4.54
1	108220001	108240000	313	0.09	0.05	4.54
1	108290001	108310000	281	0.09	0.03	4.54
1	78250001	78270000	217	0.09	0.04	4.53
1	107580001	107600000	107	0.09	0.05	4.53
1	116580001	116600000	130	0.09	0.05	4.52
1	115470001	115490000	195	0.09	0.06	4.52
1	108790001	108810000	240	0.09	0.03	4.52
1	78290001	78310000	294	0.09	0.05	4.50
1	113950001	113970000	233	0.09	0.06	4.49
1	69880001	69900000	111	0.09	0.06	4.47
1	108870001	108890000	221	0.09	0.04	4.46
1	112470001	112490000	173	0.09	0.05	4.45
1	114670001	114690000	306	0.09	0.05	4.45
1	108970001	108990000	264	0.09	0.05	4.45
1	115920001	115940000	156	0.09	0.05	4.44
1	115770001	115790000	262	0.09	0.05	4.44
1	89960001	89980000	188	0.09	0.06	4.43
1	117500001	117520000	81	0.09	0.07	4.43
1	108880001	108900000	178	0.09	0.04	4.42
1	77910001	77930000	204	0.09	0.03	4.40
1	116160001	116180000	151	0.09	0.03	4.40
1	116130001	116150000	190	0.09	0.05	4.38
1	116570001	116590000	123	0.09	0.05	4.37
1	108340001	108360000	202	0.09	0.06	4.37
1	77990001	78010000	190	0.09	0.05	4.37
1	105430001	105450000	237	0.09	0.06	4.37
1	105510001	105530000	400	0.09	0.05	4.36
1	108310001	108330000	332	0.09	0.03	4.35
1	114410001	114430000	274	0.09	0.04	4.34
1	113460001	113480000	237	0.08	0.01	4.33
1	113490001	113510000	223	0.08	0.01	4.33
1	113250001	113270000	290	0.08	0.06	4.33
1	78280001	78300000	227	0.08	0.03	4.32
1	96910001	96930000	144	0.08	0.05	4.31
1	105440001	105460000	340	0.08	0.06	4.31
1	118250001	118270000	336	0.08	0.05	4.31
1	77890001	77910000	279	0.08	0.04	4.30
1	96880001	96900000	34	0.08	0.04	4.30
1	77980001	78000000	135	0.08	0.04	4.29

Chr	Window start	Window end	SNP(N)	Weighted Fst	Mean Fst	ZFst
1	100980001	101000000	124	0.08	0.06	4.29
1	113420001	113440000	364	0.08	0.00	4.27
1	113940001	113960000	214	0.08	0.06	4.27
1	105370001	105390000	308	0.08	0.04	4.26
1	117820001	117840000	230	0.08	0.04	4.25
1	77940001	77960000	216	0.08	0.04	4.25
1	113390001	113410000	454	0.08	0.03	4.25
1	87430001	87450000	217	0.08	0.06	4.24
1	117660001	117680000	342	0.08	0.04	4.23
1	70340001	70360000	335	0.08	0.06	4.22
1	108990001	109010000	262	0.08	0.04	4.22
1	113510001	113530000	273	0.08	0.00	4.22
1	114580001	114600000	254	0.08	0.05	4.21
1	84700001	84720000	171	0.08	0.04	4.21
1	114390001	114410000	323	0.08	0.05	4.20
1	115780001	115800000	328	0.08	0.05	4.20
1	77900001	77920000	224	0.08	0.03	4.20
1	113610001	113630000	303	0.08	0.01	4.19
1	96950001	96970000	166	0.08	0.06	4.19
1	108540001	108560000	161	0.08	0.04	4.18
1	113600001	113620000	220	0.08	0.01	4.18
1	105360001	105380000	309	0.08	0.04	4.18
1	108530001	108550000	226	0.08	0.03	4.17
1	106430001	106450000	142	0.08	0.06	4.16
1	700001	720000	253	0.08	0.04	4.15
1	84450001	84470000	233	0.08	0.06	4.15
1	114660001	114680000	318	0.08	0.04	4.13
1	113620001	113640000	326	0.08	0.01	4.11
1	70200001	70220000	287	0.08	0.05	4.11
1	1210001	1230000	184	0.08	0.04	4.11
1	77560001	77580000	244	0.08	0.04	4.11
1	77880001	77900000	250	0.08	0.04	4.11
1	115790001	115810000	264	0.08	0.05	4.09
1	114570001	114590000	215	0.08	0.05	4.09
1	108950001	108970000	274	0.08	0.04	4.08
1	108860001	108880000	254	0.08	0.04	4.08
1	108780001	108800000	242	0.08	0.02	4.08
1	69820001	69840000	212	0.08	0.04	4.07
1	115430001	115450000	283	0.08	0.04	4.07
1	118130001	118150000	352	0.08	0.05	4.06
1	107830001	107850000	71	0.08	0.08	4.06
1	115810001	115830000	291	0.08	0.06	4.05
1	105520001	105540000	332	0.08	0.05	4.04
1	89930001	89950000	229	0.08	0.04	4.04
1	87290001	87310000	220	0.08	0.06	4.04

Chr	Window start	Window end	SNP(N)	Weighted Fst	Mean Fst	ZFst
1	109500001	109520000	350	0.08	0.05	4.02
1	107570001	107590000	114	0.08	0.02	4.01
1	117830001	117850000	235	0.08	0.04	4.01
1	107040001	107060000	200	0.08	0.04	3.99
1	107590001	107610000	79	0.08	0.03	3.99
1	55860001	55880000	76	0.08	0.06	3.98
1	113380001	113400000	329	0.08	0.02	3.98
1	108520001	108540000	229	0.08	0.04	3.98
1	116070001	116090000	155	0.08	0.06	3.98
1	69930001	69950000	304	0.08	0.04	3.98
1	116730001	116750000	127	0.08	0.04	3.97
1	70210001	70230000	229	0.08	0.04	3.96
1	105330001	105350000	282	0.08	0.04	3.96
1	113960001	113980000	161	0.08	0.05	3.95
1	108510001	108530000	188	0.08	0.03	3.95
1	118630001	118650000	163	0.08	0.04	3.95
1	87440001	87460000	222	0.08	0.05	3.95
1	113680001	113700000	307	0.08	0.01	3.94
1	116680001	116700000	191	0.08	0.04	3.94
1	114430001	114450000	301	0.08	0.04	3.93
1	116300001	116320000	173	0.08	0.04	3.93
1	69920001	69940000	288	0.07	0.05	3.93
1	117840001	117860000	191	0.07	0.05	3.93
1	86870001	86890000	228	0.07	0.05	3.92
1	107070001	107090000	86	0.07	0.04	3.92
1	108980001	109000000	277	0.07	0.04	3.92
1	115930001	115950000	158	0.07	0.04	3.89
1	112660001	112680000	241	0.07	0.04	3.89
1	84460001	84480000	222	0.07	0.05	3.89
1	70410001	70430000	374	0.07	0.03	3.89
1	107490001	107510000	141	0.07	0.07	3.88
1	113450001	113470000	345	0.07	0.00	3.88
1	116670001	116690000	179	0.07	0.03	3.87
1	86880001	86900000	213	0.07	0.05	3.86
1	89530001	89550000	42	0.07	0.05	3.86
1	70350001	70370000	324	0.07	0.05	3.84
1	70190001	70210000	299	0.07	0.04	3.84
1	77800001	77820000	292	0.07	0.04	3.84
1	107530001	107550000	170	0.07	0.04	3.83
1	112840001	112860000	235	0.07	0.03	3.83
1	930001	950000	234	0.07	0.05	3.83
1	84530001	84550000	174	0.07	0.07	3.82
1	114420001	114440000	271	0.07	0.04	3.81
1	107620001	107640000	207	0.07	0.03	3.81
1	77930001	77950000	183	0.07	0.02	3.80

Chr	Window start	Window end	SNP(N)	Weighted Fst	Mean Fst	ZFst
1	116080001	116100000	154	0.07	0.06	3.79
1	113470001	113490000	236	0.07	0.01	3.79
1	114380001	114400000	372	0.07	0.04	3.78
1	89950001	89970000	165	0.07	0.04	3.78
1	114980001	115000000	406	0.07	0.05	3.77
1	117910001	117930000	295	0.07	0.05	3.77
1	70680001	70700000	183	0.07	0.05	3.76
1	78220001	78240000	103	0.07	0.04	3.75
1	118280001	118300000	411	0.07	0.04	3.75
1	112480001	112500000	250	0.07	0.04	3.75
1	2140001	2160000	129	0.07	0.06	3.75
1	114360001	114380000	400	0.07	0.03	3.75
1	118660001	118680000	310	0.07	0.05	3.74
1	117070001	117090000	53	0.07	0.06	3.74
1	105380001	105400000	266	0.07	0.03	3.74
1	107540001	107560000	206	0.07	0.03	3.74
1	108800001	108820000	221	0.07	0.03	3.73
1	116430001	116450000	161	0.07	0.05	3.71
1	104840001	104860000	282	0.07	0.03	3.70
1	115760001	115780000	217	0.07	0.04	3.69
1	84520001	84540000	213	0.07	0.06	3.69
1	78300001	78320000	293	0.07	0.03	3.68
1	113310001	113330000	309	0.07	0.01	3.68
1	77590001	77610000	185	0.07	0.04	3.68
1	78000001	78020000	190	0.07	0.04	3.67
1	107500001	107520000	101	0.07	0.06	3.67
1	77550001	77570000	319	0.07	0.04	3.67
1	112150001	112170000	354	0.07	0.04	3.67
1	84720001	84740000	235	0.07	0.04	3.66
1	115890001	115910000	229	0.07	0.04	3.66
1	114370001	114390000	374	0.07	0.04	3.66
1	108300001	108320000	255	0.07	0.03	3.65
1	115800001	115820000	256	0.07	0.05	3.65
1	107820001	107840000	165	0.07	0.05	3.64
1	86970001	86990000	173	0.07	0.03	3.64
1	113370001	113390000	223	0.07	0.02	3.63
1	107630001	107650000	188	0.07	0.02	3.62
1	116510001	116530000	233	0.07	0.04	3.62
1	107610001	107630000	250	0.07	0.03	3.61
1	117860001	117880000	238	0.07	0.05	3.61
1	169430001	169450000	222	0.07	0.03	3.60
1	176980001	177000000	114	0.07	0.04	3.60
1	118290001	118310000	394	0.07	0.04	3.59
1	116540001	116560000	137	0.07	0.04	3.59
1	106200001	106220000	158	0.07	0.03	3.59

Chr	Window start	Window end	SNP(N)	Weighted Fst	Mean Fst	ZFst
1	89920001	89940000	208	0.07	0.04	3.59
1	55850001	55870000	138	0.07	0.05	3.58
1	116230001	116250000	98	0.07	0.01	3.57
1	70420001	70440000	355	0.07	0.03	3.57
1	89940001	89960000	208	0.07	0.03	3.56
1	107090001	107110000	223	0.07	0.04	3.56
1	107550001	107570000	161	0.07	0.02	3.56
1	112830001	112850000	274	0.07	0.02	3.55
1	115100001	115120000	173	0.07	0.05	3.54
1	113630001	113650000	232	0.07	-0.01	3.53
1	115840001	115860000	116	0.07	0.04	3.53
1	112670001	112690000	223	0.07	0.04	3.53
1	116170001	116190000	151	0.07	0.02	3.53
1	116520001	116540000	182	0.07	0.04	3.52
1	113670001	113690000	273	0.07	0.01	3.52
1	113260001	113280000	348	0.07	0.05	3.52
1	107600001	107620000	181	0.06	0.02	3.51
1	108380001	108400000	261	0.06	0.04	3.51
1	118270001	118290000	430	0.06	0.04	3.51
1	115480001	115500000	257	0.06	0.05	3.51
1	105420001	105440000	216	0.06	0.04	3.51
1	117590001	117610000	252	0.06	0.03	3.50
1	92860001	92880000	217	0.06	0.06	3.50
1	70220001	70240000	206	0.06	0.04	3.50
1	109490001	109510000	325	0.06	0.05	3.49
1	101030001	101050000	31	0.06	0.06	3.49
1	82880001	82900000	110	0.06	0.05	3.49
1	108370001	108390000	236	0.06	0.04	3.48
1	107480001	107500000	171	0.06	0.06	3.48
1	78080001	78100000	127	0.06	0.01	3.47
1	77450001	77470000	264	0.06	0.04	3.47
1	70600001	70620000	199	0.06	0.04	3.47
2	129250001	129270000	261	0.14	0.08	6.56
2	129240001	129260000	267	0.14	0.09	6.49
2	144690001	144710000	180	0.13	0.12	6.31
2	132390001	132410000	139	0.13	0.13	6.26
2	130020001	130040000	293	0.13	0.08	6.08
2	129180001	129200000	388	0.12	0.08	5.96
2	132400001	132420000	147	0.12	0.11	5.92
2	130380001	130400000	149	0.12	0.08	5.68
2	144700001	144720000	245	0.12	0.09	5.63
2	145380001	145400000	231	0.12	0.07	5.60
2	144670001	144690000	165	0.12	0.10	5.60
2	135910001	135930000	215	0.11	0.09	5.49
2	130390001	130410000	187	0.11	0.08	5.45

Chr	Window start	Window end	SNP(N)	Weighted Fst	Mean Fst	ZFst
2	134130001	134150000	102	0.11	0.07	5.38
2	144680001	144700000	151	0.11	0.10	5.31
2	145390001	145410000	234	0.11	0.06	5.29
2	129730001	129750000	278	0.11	0.06	5.25
2	42340001	42360000	233	0.11	0.08	5.24
2	129710001	129730000	276	0.11	0.06	5.21
2	144230001	144250000	86	0.11	0.08	5.16
2	129280001	129300000	304	0.10	0.06	5.15
2	144210001	144230000	112	0.10	0.06	5.12
2	147500001	147520000	169	0.10	0.09	5.12
2	131090001	131110000	236	0.10	0.07	5.07
2	144660001	144680000	191	0.10	0.08	5.06
2	132230001	132250000	172	0.10	0.10	5.05
2	132440001	132460000	205	0.10	0.07	5.04
2	129170001	129190000	410	0.10	0.05	5.03
2	130230001	130250000	286	0.10	0.07	5.02
2	23780001	23800000	204	0.10	0.07	5.00
2	147070001	147090000	97	0.10	0.10	4.99
2	147020001	147040000	114	0.10	0.10	4.99
2	134120001	134140000	112	0.10	0.06	4.99
2	147010001	147030000	135	0.10	0.10	4.98
2	147000001	147020000	121	0.10	0.10	4.97
2	144220001	144240000	78	0.10	0.05	4.96
2	147050001	147070000	114	0.10	0.10	4.96
2	144170001	144190000	63	0.10	0.08	4.96
2	147060001	147080000	94	0.10	0.10	4.95
2	146990001	147010000	80	0.10	0.10	4.95
2	132380001	132400000	183	0.10	0.09	4.93
2	146980001	147000000	67	0.10	0.10	4.93
2	42350001	42370000	268	0.10	0.07	4.92
2	147080001	147100000	81	0.10	0.10	4.92
2	134150001	134170000	101	0.10	0.06	4.91
2	129720001	129740000	301	0.10	0.06	4.90
2	144200001	144220000	132	0.10	0.06	4.90
2	129190001	129210000	328	0.10	0.07	4.90
2	144180001	144200000	120	0.10	0.07	4.90
2	130010001	130030000	266	0.10	0.05	4.90
2	147040001	147060000	107	0.10	0.10	4.89
2	147030001	147050000	85	0.10	0.10	4.86
2	147510001	147530000	205	0.10	0.08	4.84
2	129290001	129310000	351	0.10	0.06	4.84
2	144160001	144180000	25	0.10	0.04	4.82
2	144190001	144210000	129	0.10	0.07	4.79
2	144240001	144260000	102	0.10	0.08	4.79
2	132480001	132500000	350	0.10	0.07	4.79

Chr	Window start	Window end	SNP(N)	Weighted Fst	Mean Fst	ZFst
2	129230001	129250000	306	0.10	0.06	4.78
2	131490001	131510000	321	0.09	0.09	4.71
2	134200001	134220000	110	0.09	0.07	4.71
2	132120001	132140000	219	0.09	0.04	4.70
2	130060001	130080000	214	0.09	0.06	4.67
2	134140001	134160000	87	0.09	0.05	4.66
2	129480001	129500000	265	0.09	0.06	4.66
2	132430001	132450000	194	0.09	0.08	4.62
2	130240001	130260000	149	0.09	0.05	4.62
2	130030001	130050000	351	0.09	0.06	4.62
2	132450001	132470000	279	0.09	0.06	4.59
2	129260001	129280000	357	0.09	0.04	4.59
2	145370001	145390000	179	0.09	0.05	4.59
2	146970001	146990000	88	0.09	0.09	4.56
2	129150001	129170000	191	0.09	0.06	4.55
2	23770001	23790000	199	0.09	0.06	4.55
2	147490001	147510000	152	0.09	0.07	4.54
2	20120001	20140000	174	0.09	0.08	4.53
2	129310001	129330000	123	0.09	0.05	4.51
2	20110001	20130000	160	0.09	0.07	4.50
2	146190001	146210000	272	0.09	0.06	4.49
2	132220001	132240000	198	0.09	0.08	4.49
2	129700001	129720000	223	0.09	0.04	4.48
2	129210001	129230000	305	0.09	0.05	4.47
2	144150001	144170000	58	0.09	0.03	4.44
2	132410001	132430000	175	0.09	0.07	4.44
2	131980001	132000000	333	0.09	0.06	4.43
2	129220001	129240000	357	0.09	0.05	4.42
2	131600001	131620000	449	0.09	0.06	4.39
2	144340001	144360000	95	0.09	0.03	4.38
2	129470001	129490000	220	0.09	0.04	4.38
2	42330001	42350000	172	0.09	0.06	4.37
2	129300001	129320000	306	0.09	0.05	4.34
2	130050001	130070000	255	0.09	0.05	4.34
2	130200001	130220000	300	0.08	0.06	4.33
2	128920001	128940000	191	0.08	0.05	4.33
2	129110001	129130000	244	0.08	0.05	4.32
2	130860001	130880000	223	0.08	0.04	4.31
2	132590001	132610000	502	0.08	0.06	4.30
2	132130001	132150000	250	0.08	0.05	4.27
2	135920001	135940000	213	0.08	0.08	4.27
2	132470001	132490000	300	0.08	0.05	4.27
2	134210001	134230000	106	0.08	0.06	4.26
2	130210001	130230000	337	0.08	0.06	4.25
2	129550001	129570000	228	0.08	0.06	4.23

Chr	Window start	Window end	SNP(N)	Weighted Fst	Mean Fst	ZFst
2	141470001	141490000	209	0.08	0.05	4.22
2	146960001	146980000	82	0.08	0.08	4.22
2	129270001	129290000	377	0.08	0.04	4.21
2	144350001	144370000	105	0.08	0.05	4.21
2	129740001	129760000	275	0.08	0.05	4.19
2	132290001	132310000	290	0.08	0.06	4.19
2	132490001	132510000	317	0.08	0.06	4.18
2	129040001	129060000	339	0.08	0.04	4.18
2	132210001	132230000	149	0.08	0.07	4.16
2	143150001	143170000	84	0.08	0.06	4.15
2	147590001	147610000	82	0.08	0.06	4.13
2	133920001	133940000	110	0.08	0.05	4.12
2	141460001	141480000	107	0.08	0.06	4.12
2	134190001	134210000	123	0.08	0.05	4.10
2	132000001	132020000	347	0.08	0.06	4.10
2	146200001	146220000	248	0.08	0.05	4.09
2	132600001	132620000	467	0.08	0.06	4.09
2	130180001	130200000	324	0.08	0.05	4.08
2	130220001	130240000	311	0.08	0.06	4.08
2	131080001	131100000	228	0.08	0.06	4.08
2	128930001	128950000	234	0.08	0.05	4.08
2	132460001	132480000	276	0.08	0.04	4.08
2	129440001	129460000	315	0.08	0.05	4.07
2	144090001	144110000	110	0.08	0.03	4.06
2	129200001	129220000	283	0.08	0.05	4.06
2	131210001	131230000	199	0.08	0.04	4.06
2	129430001	129450000	349	0.08	0.04	4.04
2	131200001	131220000	199	0.08	0.03	4.03
2	133790001	133810000	120	0.08	0.06	4.02
2	132300001	132320000	334	0.08	0.05	4.01
2	132370001	132390000	221	0.08	0.07	4.00
2	130590001	130610000	311	0.08	0.05	4.00
2	131910001	131930000	253	0.08	0.07	4.00
2	130980001	131000000	199	0.08	0.04	3.98
2	134500001	134520000	155	0.08	0.07	3.98
2	132060001	132080000	270	0.08	0.05	3.96
2	129160001	129180000	375	0.08	0.04	3.96
2	129380001	129400000	309	0.08	0.04	3.95
2	131970001	131990000	300	0.08	0.04	3.95
2	130570001	130590000	321	0.08	0.06	3.94
2	132070001	132090000	317	0.08	0.05	3.94
2	23790001	23810000	238	0.08	0.02	3.93
2	144100001	144120000	119	0.07	0.02	3.92
2	129030001	129050000	368	0.07	0.05	3.92
2	132010001	132030000	347	0.07	0.05	3.92

Chr	Window start	Window end	SNP(N)	Weighted Fst	Mean Fst	ZFst
2	131900001	131920000	281	0.07	0.06	3.88
2	131840001	131860000	224	0.07	0.04	3.88
2	130190001	130210000	255	0.07	0.04	3.88
2	130340001	130360000	222	0.07	0.03	3.86
2	131220001	131240000	260	0.07	0.05	3.85
2	130450001	130470000	237	0.07	0.06	3.85
2	129510001	129530000	329	0.07	0.05	3.84
2	129100001	129120000	231	0.07	0.04	3.84
2	131280001	131300000	190	0.07	0.05	3.84
2	131990001	132010000	334	0.07	0.05	3.83
2	145400001	145420000	305	0.07	0.03	3.82
2	134160001	134180000	75	0.07	0.05	3.80
2	147520001	147540000	218	0.07	0.05	3.80
2	132780001	132800000	223	0.07	0.05	3.80
2	129330001	129350000	152	0.07	0.03	3.79
2	134490001	134510000	134	0.07	0.06	3.78
2	20100001	20120000	150	0.07	0.05	3.78
2	22660001	22680000	266	0.07	0.03	3.78
2	132420001	132440000	215	0.07	0.06	3.78
2	129140001	129160000	140	0.07	0.04	3.78
2	129890001	129910000	369	0.07	0.05	3.77
2	130640001	130660000	278	0.07	0.05	3.77
2	131930001	131950000	236	0.07	0.05	3.77
2	133530001	133550000	86	0.07	0.05	3.76
2	131500001	131520000	294	0.07	0.06	3.76
2	129660001	129680000	358	0.07	0.05	3.75
2	71900001	71920000	77	0.07	0.05	3.75
2	133800001	133820000	148	0.07	0.05	3.75
2	130460001	130480000	257	0.07	0.05	3.75
2	134220001	134240000	93	0.07	0.05	3.74
2	129560001	129580000	289	0.07	0.05	3.73
2	130840001	130860000	239	0.07	0.04	3.73
2	132140001	132160000	273	0.07	0.06	3.73
2	130600001	130620000	380	0.07	0.05	3.73
2	132110001	132130000	134	0.07	0.02	3.73
2	131540001	131560000	420	0.07	0.05	3.73
2	129880001	129900000	309	0.07	0.05	3.72
2	144270001	144290000	114	0.07	0.06	3.72
2	132150001	132170000	250	0.07	0.06	3.72
2	131530001	131550000	382	0.07	0.05	3.72
2	133540001	133560000	84	0.07	0.05	3.72
2	144000001	144020000	150	0.07	0.07	3.71
2	134250001	134270000	95	0.07	0.03	3.71
2	130250001	130270000	143	0.07	0.04	3.71
2	127440001	127460000	209	0.07	0.06	3.71

Chr	Window start	Window end	SNP(N)	Weighted Fst	Mean Fst	ZFst
2	127450001	127470000	239	0.07	0.07	3.70
2	130630001	130650000	335	0.07	0.05	3.70
2	131140001	131160000	212	0.07	0.03	3.70
2	128960001	128980000	247	0.07	0.04	3.69
2	129420001	129440000	340	0.07	0.04	3.68
2	133930001	133950000	98	0.07	0.04	3.68
2	146950001	146970000	88	0.07	0.06	3.67
2	146490001	146510000	226	0.07	0.08	3.67
2	131590001	131610000	464	0.07	0.05	3.66
2	132090001	132110000	68	0.07	0.02	3.66
2	130580001	130600000	288	0.07	0.05	3.65
2	131130001	131150000	224	0.07	0.03	3.64
2	146180001	146200000	272	0.07	0.05	3.64
2	129490001	129510000	249	0.07	0.04	3.64
2	129500001	129520000	279	0.07	0.04	3.64
2	144060001	144080000	170	0.07	0.03	3.64
2	131460001	131480000	291	0.07	0.06	3.63
2	144010001	144030000	108	0.07	0.06	3.63
2	132160001	132180000	210	0.07	0.04	3.62
2	130930001	130950000	250	0.07	0.02	3.62
2	135900001	135920000	260	0.07	0.05	3.62
2	129670001	129690000	341	0.07	0.04	3.61
2	129390001	129410000	352	0.07	0.03	3.61
2	129450001	129470000	340	0.07	0.04	3.61
2	132080001	132100000	217	0.07	0.03	3.60
2	129910001	129930000	473	0.07	0.05	3.60
2	143140001	143160000	116	0.07	0.04	3.60
2	144040001	144060000	115	0.07	0.05	3.59
2	144050001	144070000	169	0.07	0.04	3.59
2	136090001	136110000	245	0.07	0.05	3.59
2	129120001	129140000	318	0.07	0.04	3.59
2	131960001	131980000	293	0.07	0.04	3.58
2	132750001	132770000	209	0.07	0.05	3.57
2	131870001	131890000	320	0.07	0.04	3.57
2	131830001	131850000	273	0.07	0.04	3.56
2	143990001	144010000	81	0.07	0.06	3.55
2	132280001	132300000	292	0.07	0.05	3.54
2	131480001	131500000	362	0.07	0.06	3.54
2	132310001	132330000	329	0.07	0.04	3.54
2	130370001	130390000	166	0.07	0.02	3.53
2	124030001	124050000	183	0.07	0.05	3.53
2	137440001	137460000	199	0.06	0.05	3.52
2	144070001	144090000	108	0.06	0.02	3.52
2	134650001	134670000	83	0.06	0.05	3.52
2	129620001	129640000	277	0.06	0.05	3.51

Chr	Window start	Window end	SNP(N)	Weighted Fst	Mean Fst	ZFst
2	131880001	131900000	236	0.06	0.04	3.51
2	131520001	131540000	352	0.06	0.04	3.49
2	133910001	133930000	120	0.06	0.04	3.48
2	129130001	129150000	304	0.06	0.03	3.48
2	142520001	142540000	275	0.06	0.03	3.47
2	134730001	134750000	58	0.06	0.06	3.47
2	129540001	129560000	186	0.06	0.04	3.47
2	130870001	130890000	263	0.06	0.02	3.47
2	129070001	129090000	253	0.06	0.05	3.47
2	71790001	71810000	121	0.06	0.05	3.47
3	49430001	49450000	183	0.15	0.15	7.12
3	49440001	49460000	144	0.15	0.15	7.10
3	49420001	49440000	169	0.14	0.13	6.40
3	31350001	31370000	211	0.13	0.10	6.25
3	31340001	31360000	210	0.13	0.09	6.14
3	104560001	104580000	170	0.11	0.08	5.53
3	51430001	51450000	101	0.11	0.07	5.52
3	31730001	31750000	253	0.11	0.04	5.29
3	104550001	104570000	224	0.11	0.09	5.25
3	31330001	31350000	205	0.10	0.06	5.08
3	31660001	31680000	80	0.10	0.06	5.03
3	31290001	31310000	187	0.10	0.05	4.92
3	30970001	30990000	170	0.10	0.08	4.84
3	103840001	103860000	112	0.10	0.08	4.83
3	103830001	103850000	139	0.10	0.08	4.81
3	31360001	31380000	230	0.10	0.06	4.78
3	49450001	49470000	152	0.09	0.11	4.67
3	31300001	31320000	137	0.09	0.04	4.65
3	103850001	103870000	160	0.09	0.06	4.63
3	31720001	31740000	282	0.09	0.05	4.59
3	104540001	104560000	369	0.09	0.07	4.52
3	103820001	103840000	151	0.09	0.07	4.52
3	31280001	31300000	242	0.09	0.05	4.48
3	104570001	104590000	229	0.09	0.06	4.45
3	31650001	31670000	158	0.09	0.05	4.45
3	34250001	34270000	159	0.09	0.08	4.43
3	40200001	40220000	276	0.09	0.08	4.37
3	31670001	31690000	113	0.09	0.04	4.36
3	31320001	31340000	224	0.09	0.05	4.34
3	30980001	31000000	211	0.08	0.06	4.32
3	103800001	103820000	102	0.08	0.05	4.25
3	104580001	104600000	284	0.08	0.05	4.25
3	31270001	31290000	268	0.08	0.04	4.16
3	31590001	31610000	243	0.08	0.05	4.12
3	36430001	36450000	92	0.08	0.06	4.10

Chr	Window start	Window end	SNP(N)	Weighted Fst	Mean Fst	ZFst
3	34240001	34260000	195	0.08	0.06	4.06
3	104530001	104550000	491	0.08	0.06	4.02
3	103790001	103810000	112	0.08	0.05	4.00
3	104590001	104610000	223	0.08	0.05	3.99
3	69050001	69070000	172	0.08	0.02	3.98
3	104520001	104540000	476	0.08	0.05	3.96
3	94450001	94470000	98	0.08	0.08	3.96
3	49410001	49430000	131	0.08	0.07	3.95
3	68960001	68980000	161	0.07	0.05	3.92
3	31710001	31730000	311	0.07	0.04	3.87
3	51270001	51290000	174	0.07	0.03	3.87
3	104740001	104760000	266	0.07	0.05	3.87
3	31600001	31620000	141	0.07	0.04	3.86
3	31430001	31450000	299	0.07	0.04	3.86
3	68770001	68790000	96	0.07	0.05	3.84
3	38700001	38720000	235	0.07	0.06	3.83
3	31250001	31270000	261	0.07	0.04	3.82
3	31260001	31280000	268	0.07	0.03	3.78
3	31420001	31440000	334	0.07	0.04	3.77
3	68970001	68990000	272	0.07	0.05	3.77
3	30750001	30770000	139	0.07	0.05	3.71
3	31580001	31600000	349	0.07	0.04	3.70
3	68350001	68370000	237	0.07	0.05	3.64
3	30740001	30760000	103	0.07	0.04	3.63
3	68400001	68420000	264	0.07	0.05	3.63
3	104610001	104630000	151	0.07	0.01	3.62
3	104510001	104530000	326	0.07	0.04	3.60
3	28500001	28520000	218	0.07	0.04	3.59
3	66480001	66500000	291	0.07	0.05	3.58
3	31150001	31170000	247	0.07	0.04	3.58
3	51440001	51460000	153	0.07	0.05	3.57
3	51610001	51630000	60	0.07	0.06	3.55
3	68340001	68360000	213	0.07	0.05	3.55
3	34230001	34250000	167	0.07	0.04	3.53
3	103810001	103830000	107	0.06	0.04	3.48
3	36380001	36400000	111	0.06	0.05	3.48
3	68980001	69000000	308	0.06	0.05	3.47
4	88340001	88360000	32	0.10	0.10	4.77
4	88330001	88350000	92	0.09	0.09	4.72
4	63150001	63170000	29	0.09	0.09	4.69
4	52680001	52700000	96	0.09	0.06	4.68
4	45650001	45670000	335	0.09	0.06	4.67
4	52690001	52710000	110	0.09	0.04	4.57
4	88320001	88340000	157	0.09	0.09	4.48
4	45660001	45680000	436	0.08	0.06	4.30

Chr	Window start	Window end	SNP(N)	Weighted Fst	Mean Fst	ZFst
4	58820001	58840000	125	0.08	0.05	4.26
4	52670001	52690000	141	0.08	0.06	4.19
4	58830001	58850000	135	0.08	0.03	3.98
4	63160001	63180000	146	0.07	0.06	3.87
4	88270001	88290000	171	0.07	0.06	3.75
4	45540001	45560000	122	0.07	0.05	3.61
4	52660001	52680000	134	0.07	0.03	3.52
4	58810001	58830000	207	0.06	0.04	3.47
5	32440001	32460000	178	0.15	0.14	7.03
5	32430001	32450000	141	0.15	0.13	6.90
5	32450001	32470000	167	0.14	0.12	6.42
5	29440001	29460000	214	0.11	0.07	5.55
5	29420001	29440000	185	0.11	0.06	5.39
5	29450001	29470000	219	0.10	0.06	5.04
5	29430001	29450000	205	0.10	0.06	4.93
5	34670001	34690000	203	0.10	0.06	4.81
5	32420001	32440000	129	0.10	0.06	4.81
5	36370001	36390000	220	0.09	0.05	4.64
5	29410001	29430000	192	0.09	0.05	4.57
5	33590001	33610000	55	0.09	0.06	4.54
5	34680001	34700000	255	0.09	0.05	4.36
5	36340001	36360000	193	0.09	0.06	4.34
5	32020001	32040000	36	0.08	0.08	4.23
5	36350001	36370000	236	0.08	0.05	4.05
5	34480001	34500000	295	0.08	0.06	4.04
5	34470001	34490000	236	0.08	0.06	4.01
5	35850001	35870000	148	0.08	0.06	3.93
5	33570001	33590000	121	0.07	0.04	3.93
5	29050001	29070000	137	0.07	0.05	3.90
5	36360001	36380000	213	0.07	0.04	3.83
5	37290001	37310000	200	0.07	0.02	3.83
5	33500001	33520000	142	0.07	0.06	3.81
5	33580001	33600000	53	0.07	0.04	3.80
5	37160001	37180000	209	0.07	0.04	3.79
5	34400001	34420000	292	0.07	0.05	3.77
5	32460001	32480000	113	0.07	0.04	3.69
5	29310001	29330000	350	0.07	0.04	3.65
5	33600001	33620000	77	0.07	0.04	3.59
5	31990001	32010000	107	0.07	0.06	3.57
5	34450001	34470000	286	0.06	0.05	3.50
5	29320001	29340000	288	0.06	0.03	3.49
5	42870001	42890000	206	0.06	0.02	3.49
5	33920001	33940000	214	0.06	0.05	3.47
5	31240001	31260000	104	0.06	0.05	3.46
6	23770001	23790000	168	0.07	0.05	3.53

Chr	Window start	Window end	SNP(N)	Weighted Fst	Mean Fst	ZFst
7	6590001	6610000	94	0.17	0.13	7.73
7	6580001	6600000	147	0.13	0.08	6.03
7	6620001	6640000	217	0.13	0.09	5.98
7	9640001	9660000	242	0.12	0.08	5.95
7	10740001	10760000	117	0.12	0.11	5.73
7	6630001	6650000	188	0.12	0.07	5.69
7	6540001	6560000	210	0.12	0.08	5.69
7	6550001	6570000	235	0.12	0.08	5.68
7	9670001	9690000	149	0.12	0.08	5.61
7	6740001	6760000	29	0.11	0.07	5.50
7	10160001	10180000	300	0.11	0.08	5.26
7	6730001	6750000	21	0.10	0.05	5.13
7	25250001	25270000	155	0.10	0.08	5.08
7	31490001	31510000	108	0.10	0.11	5.07
7	8830001	8850000	40	0.10	0.09	4.93
7	6530001	6550000	93	0.10	0.05	4.75
7	9650001	9670000	254	0.09	0.04	4.70
7	31480001	31500000	50	0.09	0.10	4.59
7	25240001	25260000	111	0.09	0.07	4.53
7	10730001	10750000	221	0.09	0.06	4.51
7	10150001	10170000	322	0.09	0.07	4.41
7	9990001	10010000	245	0.09	0.07	4.39
7	9660001	9680000	220	0.09	0.04	4.35
7	25190001	25210000	117	0.09	0.08	4.34
7	25260001	25280000	138	0.08	0.05	4.29
7	6560001	6580000	188	0.08	0.05	4.27
7	10080001	10100000	307	0.08	0.06	4.26
7	6610001	6630000	191	0.08	0.05	4.20
7	11300001	11320000	372	0.08	0.06	4.18
7	6690001	6710000	43	0.08	0.04	4.18
7	5020001	5040000	160	0.08	0.06	4.18
7	13350001	13370000	226	0.08	0.05	4.18
7	9680001	9700000	329	0.08	0.05	4.04
7	6720001	6740000	23	0.08	0.03	4.04
7	9980001	10000000	288	0.08	0.07	3.95
7	13360001	13380000	214	0.08	0.05	3.94
7	25200001	25220000	169	0.07	0.06	3.91
7	25180001	25200000	64	0.07	0.07	3.89
7	11310001	11330000	325	0.07	0.05	3.87
7	25940001	25960000	217	0.07	0.04	3.80
7	9910001	9930000	164	0.07	0.06	3.80
7	6520001	6540000	116	0.07	0.04	3.79
7	6710001	6730000	28	0.07	0.03	3.76
7	13340001	13360000	213	0.07	0.04	3.71
7	5960001	5980000	279	0.07	0.04	3.69

Chr	Window start	Window end	SNP(N)	Weighted Fst	Mean Fst	ZFst
7	5140001	5160000	337	0.07	0.05	3.67
7	9950001	9970000	298	0.07	0.05	3.66
7	10450001	10470000	208	0.07	0.04	3.66
7	4680001	4700000	255	0.07	0.04	3.66
7	10700001	10720000	302	0.07	0.05	3.66
7	6440001	6460000	222	0.07	0.04	3.65
7	10090001	10110000	356	0.07	0.05	3.61
7	25950001	25970000	109	0.07	0.05	3.61
7	9870001	9890000	280	0.07	0.05	3.59
7	9360001	9380000	171	0.07	0.03	3.59
7	10170001	10190000	310	0.07	0.05	3.57
7	4670001	4690000	200	0.07	0.04	3.56
7	25270001	25290000	154	0.07	0.04	3.53
7	9860001	9880000	259	0.06	0.05	3.51
7	9940001	9960000	298	0.06	0.05	3.51
7	10140001	10160000	338	0.06	0.05	3.48
7	9740001	9760000	87	0.06	0.02	3.46
8	1950001	1970000	175	0.16	0.11	7.44
8	1960001	1980000	140	0.15	0.11	7.15
8	1940001	1960000	138	0.15	0.11	7.09
8	1970001	1990000	93	0.12	0.08	5.62
8	26770001	26790000	52	0.11	0.10	5.21
8	26760001	26780000	60	0.10	0.08	4.79
8	26750001	26770000	118	0.09	0.08	4.59
8	26780001	26800000	159	0.09	0.07	4.50
8	1860001	1880000	189	0.09	0.06	4.50
8	21510001	21530000	213	0.09	0.05	4.35
8	21520001	21540000	191	0.08	0.05	4.26
8	26740001	26760000	204	0.08	0.07	4.20
8	1590001	1610000	25	0.08	0.07	4.16
8	23180001	23200000	259	0.07	0.05	3.87
8	23170001	23190000	251	0.07	0.05	3.83
8	23200001	23220000	193	0.07	0.05	3.82
8	23390001	23410000	165	0.07	0.06	3.61
8	23190001	23210000	203	0.06	0.04	3.50
9	9410001	9430000	209	0.16	0.11	7.30
9	12320001	12340000	171	0.15	0.14	6.87
9	12310001	12330000	201	0.14	0.12	6.74
9	12420001	12440000	120	0.14	0.11	6.45
9	9400001	9420000	287	0.12	0.07	5.79
9	12330001	12350000	184	0.12	0.09	5.59
9	12780001	12800000	262	0.11	0.08	5.53
9	12770001	12790000	109	0.11	0.07	5.40
9	12360001	12380000	135	0.11	0.07	5.17
9	11750001	11770000	349	0.11	0.09	5.16

Chr	Window start	Window end	SNP(N)	Weighted Fst	Mean Fst	ZFst
9	11740001	11760000	311	0.10	0.09	5.15
9	11720001	11740000	303	0.10	0.09	5.10
9	12340001	12360000	261	0.10	0.07	5.10
9	12430001	12450000	178	0.10	0.09	5.09
9	12110001	12130000	184	0.10	0.06	5.04
9	11730001	11750000	271	0.10	0.09	5.04
9	11710001	11730000	371	0.10	0.08	4.81
9	9180001	9200000	177	0.10	0.07	4.81
9	12350001	12370000	194	0.10	0.07	4.79
9	11690001	11710000	305	0.09	0.08	4.66
9	6770001	6790000	216	0.09	0.08	4.63
9	12100001	12120000	171	0.09	0.07	4.58
9	12410001	12430000	71	0.09	0.09	4.54
9	12370001	12390000	224	0.09	0.06	4.49
9	11700001	11720000	358	0.09	0.08	4.47
9	12390001	12410000	50	0.09	0.08	4.44
9	11680001	11700000	255	0.09	0.09	4.40
9	10340001	10360000	243	0.09	0.04	4.38
9	9420001	9440000	209	0.08	0.04	4.29
9	12790001	12810000	280	0.08	0.06	4.29
9	10680001	10700000	273	0.08	0.07	4.23
9	6440001	6460000	233	0.08	0.05	4.22
9	12010001	12030000	175	0.08	0.07	4.21
9	9170001	9190000	126	0.08	0.05	4.20
9	12380001	12400000	187	0.08	0.06	4.06
9	9320001	9340000	203	0.08	0.07	4.03
9	6450001	6470000	274	0.08	0.05	4.02
9	6910001	6930000	99	0.08	0.05	3.97
9	11760001	11780000	277	0.08	0.08	3.95
9	4020001	4040000	213	0.07	0.07	3.92
9	10690001	10710000	268	0.07	0.05	3.85
9	9190001	9210000	247	0.07	0.06	3.84
9	9330001	9350000	199	0.07	0.07	3.84
9	8050001	8070000	265	0.07	0.04	3.75
9	9590001	9610000	268	0.07	0.05	3.72
9	9580001	9600000	274	0.07	0.04	3.69
9	6780001	6800000	273	0.07	0.06	3.68
9	9360001	9380000	290	0.07	0.05	3.66
9	8820001	8840000	200	0.07	0.06	3.65
9	6490001	6510000	144	0.07	0.04	3.65
9	9270001	9290000	355	0.07	0.05	3.64
9	4030001	4050000	221	0.07	0.05	3.64
9	9830001	9850000	231	0.07	0.05	3.63
9	9800001	9820000	148	0.07	0.07	3.63
9	8810001	8830000	193	0.07	0.06	3.58

Chr	Window start	Window end	SNP(N)	Weighted Fst	Mean Fst	ZFst
9	6800001	6820000	285	0.07	0.05	3.57
9	13800001	13820000	293	0.07	0.05	3.56
9	9280001	9300000	342	0.07	0.05	3.54
9	24030001	24050000	98	0.07	0.06	3.54
9	9300001	9320000	238	0.06	0.05	3.52
9	6760001	6780000	172	0.06	0.06	3.51
9	8040001	8060000	242	0.06	0.03	3.50
9	6400001	6420000	138	0.06	0.04	3.50
9	24040001	24060000	82	0.06	0.05	3.47
10	16110001	16130000	125	0.07	0.03	3.82
10	15560001	15580000	133	0.07	0.07	3.77
11	13540001	13560000	71	0.12	0.11	5.67
11	13530001	13550000	30	0.12	0.11	5.67
11	1550001	1570000	353	0.10	0.04	5.00
11	13550001	13570000	99	0.10	0.09	4.91
11	1540001	1560000	373	0.07	0.01	3.61
11	1020001	1040000	365	0.07	0.03	3.60
11	1560001	1580000	231	0.07	0.03	3.55
12	15700001	15720000	230	0.09	0.05	4.44
12	9640001	9660000	157	0.09	0.08	4.38
12	15710001	15730000	251	0.09	0.04	4.34
12	15690001	15710000	192	0.07	0.03	3.81
12	9630001	9650000	190	0.07	0.06	3.76
13	17640001	17660000	109	0.07	0.07	3.93
13	17650001	17670000	75	0.07	0.07	3.92
13	17670001	17690000	120	0.07	0.07	3.90
13	17660001	17680000	90	0.07	0.07	3.85
13	17680001	17700000	142	0.07	0.07	3.78
13	2100001	2120000	113	0.07	0.05	3.72
13	17630001	17650000	139	0.07	0.06	3.61
15	11010001	11030000	264	0.07	0.04	3.70
17	4620001	4640000	225	0.07	0.04	3.54
22	1660001	1680000	98	0.12	0.09	5.77
22	520001	540000	27	0.12	0.06	5.59
22	510001	530000	28	0.11	0.07	5.29
22	1650001	1670000	147	0.10	0.07	5.09
22	940001	960000	24	0.10	0.06	4.79
22	780001	800000	36	0.09	0.04	4.42
22	950001	970000	24	0.08	0.06	4.27
22	580001	600000	25	0.08	0.05	4.26
22	1250001	1270000	55	0.07	0.04	3.60
22	1830001	1850000	72	0.07	0.04	3.59
23	4930001	4950000	189	0.07	0.05	3.81
24	6040001	6060000	147	0.13	0.07	6.03
24	6050001	6070000	104	0.11	0.09	5.43

Chr	Window start	Window end	SNP(N)	Weighted Fst	Mean Fst	ZFst
24	4550001	4570000	242	0.11	0.07	5.39
24	6030001	6050000	188	0.11	0.07	5.33
24	6210001	6230000	148	0.11	0.07	5.18
24	5820001	5840000	212	0.10	0.09	5.11
24	5810001	5830000	259	0.10	0.07	4.88
24	5800001	5820000	286	0.09	0.05	4.73
24	4560001	4580000	197	0.09	0.05	4.43
24	5790001	5810000	269	0.09	0.06	4.41
24	5770001	5790000	124	0.09	0.07	4.38
24	5860001	5880000	182	0.09	0.06	4.35
24	5110001	5130000	160	0.08	0.06	4.14
24	6200001	6220000	148	0.08	0.06	4.08
24	6060001	6080000	92	0.08	0.05	3.97
24	5050001	5070000	150	0.07	0.05	3.83
24	6220001	6240000	184	0.07	0.02	3.75
24	5830001	5850000	187	0.07	0.07	3.74
24	5850001	5870000	135	0.07	0.06	3.72
24	5120001	5140000	176	0.07	0.05	3.72
24	5780001	5800000	203	0.07	0.05	3.67
24	5760001	5780000	146	0.07	0.07	3.61
24	4540001	4560000	287	0.07	0.04	3.52
24	4630001	4650000	214	0.06	0.03	3.51
27	5480001	5500000	25	0.09	0.10	4.65
27	5540001	5560000	28	0.08	0.10	4.30
27	5470001	5490000	25	0.08	0.06	4.25
27	5530001	5550000	28	0.07	0.09	3.74
28	3730001	3750000	148	0.11	0.08	5.24
28	4800001	4820000	24	0.10	0.09	4.89
28	3720001	3740000	87	0.09	0.08	4.62
28	4790001	4810000	32	0.09	0.08	4.61
28	3740001	3760000	215	0.09	0.06	4.47
28	3840001	3860000	124	0.08	0.06	4.15
28	3600001	3620000	224	0.08	0.06	4.14
28	2820001	2840000	258	0.08	0.05	4.10
28	4780001	4800000	30	0.08	0.06	4.02
28	2830001	2850000	209	0.08	0.04	4.00
28	4810001	4830000	27	0.08	0.06	3.98
28	3710001	3730000	96	0.08	0.06	3.96
28	4860001	4880000	32	0.07	0.05	3.90
28	3610001	3630000	203	0.07	0.05	3.80
28	3630001	3650000	201	0.07	0.05	3.70
28	2700001	2720000	206	0.07	0.04	3.68
28	4920001	4940000	23	0.07	0.04	3.67
28	4850001	4870000	32	0.07	0.04	3.62
28	3620001	3640000	245	0.07	0.04	3.57

Chr	Window start	Window end	SNP(N)	Weighted Fst	Mean Fst	ZFst
28	4870001	4890000	27	0.06	0.05	3.50
28	3850001	3870000	153	0.06	0.04	3.48

Chr = Chromosome; N= count

Table S 60. List of candidate genes in Improved Horro and Local Horro.

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
1	ENSGALG00000016185	109473644	109505549	SLC37A1	protein
1	ENSGALG00000026573	113257661	113257760		miRNA
1	ENSGALG00000042604	117839213	117843292	ARX	protein
1	ENSGALG00000016055	107539724	107541289	KCNJ15	protein
1	ENSGALG00000025698	101037458	101037610	RF00002	rRNA
1	ENSGALG00000036114	704038	711778	SMO	protein
1	ENSGALG00000045818	105394214	105399695		protein
1	ENSGALG00000016268	113403070	113433885		protein
1	ENSGALG00000016058	107579587	107693888	ERG	protein
1	ENSGALG00000045430	113452551	113458229		protein
1	ENSGALG00000019261	69904874	69982240	ARHGAP8	protein
1	ENSGALG00000016286	115794507	115795376	CXorf21	protein
1	ENSGALG00000044858	115843688	115847698		protein
1	ENSGALG00000030506	77815472	77816407		protein
1	ENSGALG00000016285	115734786	115768467		protein
1	ENSGALG00000015495	92852810	92868421	POU1F1	protein
1	ENSGALG00000016323	118089639	118139548	PDK3	protein
1	ENSGALG00000012791	55806774	56041222	TBXAS1	protein
1	ENSGALG00000015355	87434456	87455171	CD47	protein
1	ENSGALG00000014213	69763115	69848437	PRR5	protein
1	ENSGALG00000014689	77586269	77592786	FAM131B	protein
1	ENSGALG00000016251	112766328	112855804		protein
1	ENSGALG00000033692	113630516	113665856		protein
1	ENSGALG00000016345	118238433	118307972	KLHL15	protein
1	ENSGALG00000016144	108944327	108958350	TMPRSS2	protein
1	ENSGALG00000042515	113494211	113499362		protein
1	ENSGALG00000045035	931381	933117		protein
1	ENSGALG00000042121	118079947	118080147		protein
1	ENSGALG00000016318	118051229	118071937	PCYT1B	protein
1	ENSGALG00000006489	2002525	2187486	CHCHD3	protein
1	ENSGALG00000016281	114486908	115483002	DMD	protein
1	ENSGALG00000022813	109599316	109606438	NDUFV3	protein
1	ENSGALG00000016187	109577831	109599269	WDR4	protein
1	ENSGALG00000015496	92870771	92882303	CHMP2B	protein
1	ENSGALG00000029670	105440356	105461262	CRYZL1	protein
1	ENSGALG00000036677	105492244	105575073	ITSN1	protein
1	ENSGALG00000015258	84531130	84573579	DCBLD2	protein
1	ENSGALG00000014234	70660407	70756330	ATXN10	protein
1	ENSGALG00000045979	101040149	101040594		protein
1	ENSGALG00000039711	101041201	101041500		protein
1	ENSGALG00000032978	1213840	1214346	UCN3	protein
1	ENSGALG00000016312	117847142	118037119	POLA1	protein
1	ENSGALG00000015353	87305099	87349328	BBX	protein
1	ENSGALG00000038169	101040919	101041077		protein
1	ENSGALG00000014232	70491928	70505475	RIBC2	protein

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
1	ENSGALG00000033199	105330816	105350209		protein
1	ENSGALG00000015271	84737375	84814326		protein
1	ENSGALG00000022819	108164030	108196164	PCP4	protein
1	ENSGALG00000040609	78216893	78220222		protein
1	ENSGALG00000034932	108844363	108894770	BACE2	protein
1	ENSGALG00000014746	77904803	77933908		protein
1	ENSGALG00000016236	112079778	112151195		protein
1	ENSGALG00000031890	78318610	78343166	YBX3	protein
1	ENSGALG00000016138	108236302	108412621	DSCAM	protein
1	ENSGALG00000037076	105352798	105389904	GART	protein
1	ENSGALG00000016265	113222082	113251614	LANCL3	protein
1	ENSGALG00000014233	70545573	70627591	FBLN1	protein
1	ENSGALG00000016266	113283937	113314035	PRRG1	protein
1	ENSGALG00000038649	105433842	105439140	DONSON	protein
1	ENSGALG00000035096	105406560	105430638		protein
1	ENSGALG00000027198	113937248	113961367	TMEM47	protein
1	ENSGALG00000014754	78077450	78225862		protein
1	ENSGALG00000014227	70416011	70422094	UPK3A	protein
1	ENSGALG00000044332	89540456	89541604		protein
1	ENSGALG00000036140	925136	930918		protein
1	ENSGALG00000016052	107063968	107080263	VPS26C	protein
1	ENSGALG00000040488	113326215	113331457		protein
1	ENSGALG00000016287	115909469	115911505	NR0B1	protein
1	ENSGALG00000014749	77978178	78032477	EPHB6	protein
1	ENSGALG00000016050	107001974	107060482	TTC3	protein
1	ENSGALG00000014228	70455565	70491589	SMC1B	protein
1	ENSGALG00000008036	933552	945389	TMEM209	protein
1	ENSGALG00000016288	116055337	116671490	IL1RAPL1	protein
1	ENSGALG00000044129	117435791	117441378		protein
1	ENSGALG00000015519	96895939	97053385	ROBO2	protein
1	ENSGALG00000023942	947930	951486		protein
1	ENSGALG00000017106	176737697	177046618	ATP8A2	protein
1	ENSGALG00000046179	70310954	70375330		lincRNA
1	ENSGALG00000046340	77450263	77461548		lincRNA
1	ENSGALG00000032654	78268586	78290816		lincRNA
1	ENSGALG00000033000	101034873	101074782		lincRNA
1	ENSGALG00000043418	105578706	105580665		lincRNA
1	ENSGALG00000031795	112688883	112696578		lincRNA
1	ENSGALG00000041297	113387301	113390563		lincRNA
1	ENSGALG00000038250	115098166	115101343		lincRNA
1	ENSGALG00000035313	116733214	116733791		lincRNA
2	ENSGALG00000033254	129000072	129034245	SPAG1	protein
2	ENSGALG00000041043	131615461	131620601	ABRA	protein
2	ENSGALG00000027894	127449716	127449795		miRNA
2	ENSGALG00000040325	132351058	132385978	EMC2	protein
2	ENSGALG00000037997	128915167	128970668	RGS22	protein
2	ENSGALG00000029983	131784819	131949415	ANGPT1	protein

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
2	ENSGALG00000025532	131521313	131521398	gga-mir-	miRNA
2	ENSGALG00000038022	144646756	144875068	COL22A1	protein
2	ENSGALG00000039011	130564107	130592497	DPYS	protein
2	ENSGALG00000031387	129241561	129267480	YWHAZ	protein
2	ENSGALG00000033438	144239804	144239910		miRNA
2	ENSGALG00000034618	130034484	130057124	DCAF13	protein
2	ENSGALG00000040921	129686126	129700944	RRM2B	protein
2	ENSGALG00000041200	129336386	129343185	ZNF706	protein
2	ENSGALG00000030030	132121027	132231350	RSPO2	protein
2	ENSGALG00000038772	129040782	129061227	RNF19A	protein
2	ENSGALG00000041445	129153464	129170102		protein
2	ENSGALG00000031578	133691901	134258240	CSMD3	protein
2	ENSGALG00000030322	42336011	42350205		protein
2	ENSGALG00000041553	132477229	132478179	TMEM74	protein
2	ENSGALG00000039533	141406000	141466443	EFR3A	protein
2	ENSGALG00000043415	42357024	42375913		protein
2	ENSGALG00000030280	129199347	129213966	PABPC1	protein
2	ENSGALG00000040879	132583137	132607011	NUDCD1	protein
2	ENSGALG00000039013	135959509	136122463	EXT1	protein
2	ENSGALG00000033630	130599464	130659121	LRP12	protein
2	ENSGALG00000030128	141470034	141488999		protein
2	ENSGALG00000031282	129708232	129786771	UBR5	protein
2	ENSGALG00000036618	132606889	132612643	ENY2	protein
2	ENSGALG00000034099	129894934	129916432	ATP6V1C1	protein
2	ENSGALG00000040256	130153028	130517067	RIMS2	protein
2	ENSGALG00000009686	23744767	23815855		protein
2	ENSGALG00000033351	130013430	130018289	CTHRC1	protein
2	ENSGALG00000035761	22663994	22676382		protein
2	ENSGALG00000040079	130901436	131209122	ZFPM2	protein
2	ENSGALG00000039831	144356967	144479127	FAM135B	protein
2	ENSGALG00000037687	129435468	129485773	GRHL2	protein
2	ENSGALG00000040891	20027818	20125211	RSU1	protein
2	ENSGALG00000039882	130019558	130034422	SLC25A32	protein
2	ENSGALG00000042182	131549781	131579894	OXR1	protein
2	ENSGALG00000032518	129501286	129543306	NCALD	protein
2	ENSGALG00000032504	131588439	131609614		protein
2	ENSGALG00000039843	128974062	128976455		lincRNA
2	ENSGALG00000037317	129214619	129215026		lincRNA
2	ENSGALG00000039449	130862553	130864296		lincRNA
2	ENSGALG00000043785	131145205	131154767		lincRNA
2	ENSGALG00000030036	133259610	133653226		lincRNA
2	ENSGALG00000044971	134267681	134321609		lincRNA
3	ENSGALG00000016500	104621983	104668401	FKBP1B	protein
3	ENSGALG00000010435	31145552	31183812	RASGRP3	protein
3	ENSGALG00000010541	31572475	31748573	BIRC6	protein
3	ENSGALG00000039575	66496131	66511020	AMD1	protein
3	ENSGALG00000010341	30965058	30992748	XPO5	protein

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
3	ENSGALG00000010448	31210825	31393401	LTBP1	protein
3	ENSGALG00000013683	51335816	51624319	ARID1B	protein
3	ENSGALG00000010349	30993718	30997091	POLR1C	protein
3	ENSGALG00000037872	104447300	104516627	ATAD2B	protein
3	ENSGALG00000015387	68405534	68477842	ATG5	protein
3	ENSGALG00000016497	104524268	104541302	UBXN2A	protein
3	ENSGALG00000015405	68876701	69004270	PREP	protein
3	ENSGALG00000031427	36312761	36477609	FMN2	protein
3	ENSGALG00000013505	49318532	49488810		protein
3	ENSGALG00000011098	40214428	40230986	TAF5L	protein
3	ENSGALG00000015410	69051906	69078558	BVES	protein
3	ENSGALG00000016498	104544323	104575302	MFSD2B	protein
3	ENSGALG00000015345	68326420	68390064		protein
3	ENSGALG00000019867	104581179	104588806	WDCP	protein
3	ENSGALG00000016499	104597130	104611882		protein
3	ENSGALG00000010538	31444899	31547261	TTC27	protein
3	ENSGALG00000010290	30739147	30759022	VEGFA	protein
3	ENSGALG00000041037	30997145	31002240	YIPF3	protein
3	ENSGALG00000029553	28447222	28667979		lincRNA
3	ENSGALG00000036544	28450739	28526039		lincRNA
4	ENSGALG00000043675	45520827	45620890	ANTXR2	protein
4	ENSGALG00000015966	88306184	88383710		protein
4	ENSGALG00000012216	58732964	58968719	BMPR1B	protein
4	ENSGALG00000013590	63176150	63184079		protein
5	ENSGALG00000044423	34491589	34492617		protein
5	ENSGALG00000010088	36275772	36390043	RALGAPA1	protein
5	ENSGALG00000027121	34499921	34500032		miRNA
5	ENSGALG00000043908	29050505	29056371		protein
5	ENSGALG00000009946	34359921	34412246	HECTD1	protein
5	ENSGALG00000010118	37030439	37188796	MIPOL1	protein
5	ENSGALG00000009587	29066545	29333320	GPHN	protein
5	ENSGALG00000009847	32441311	32495180	STXBP6	protein
5	ENSGALG00000039118	31240857	31409344	MEIS2	protein
5	ENSGALG00000031586	34471731	34492378		protein
5	ENSGALG00000020438	31996234	32173952	DPH6	protein
5	ENSGALG00000009900	33848550	33962481	PRKD1	protein
5	ENSGALG00000014537	29410988	29430989	BMF	protein
6	ENSGALG00000008281	23723779	23800324	NEURL1	protein
6	ENSGALG00000008265	23612168	23824013		protein
7	ENSGALG00000025571	6580437	6580522	gga-mir-	miRNA
7	ENSGALG00000037678	9698247	9701468		protein
7	ENSGALG00000007958	10009681	10029718	GTF3C3	protein
7	ENSGALG00000020876	11289758	11332344	AOX2	protein
7	ENSGALG00000004394	6693921	6709659	PCBP3	protein
7	ENSGALG00000004302	6535126	6575704	NDUFA10	protein
7	ENSGALG00000007841	9683028	9794746	DNAH7	protein
7	ENSGALG00000042117	4668050	4670981		protein

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
7	ENSGALG00000021031	5036416	5041363	ACKR3	protein
7	ENSGALG00000003980	5085191	5163120	IQCA1	protein
7	ENSGALG00000007777	9564789	9679908	SLC39A10	protein
7	ENSGALG00000003862	4682652	4717918		protein
7	ENSGALG00000005974	6723053	6744124	COL6A1	protein
7	ENSGALG00000023742	6580483	6603208	AHR2	protein
7	ENSGALG00000011630	25930783	26109391	GLI2	protein
7	ENSGALG00000007996	10074592	10185212	ANKRD44	protein
7	ENSGALG00000004272	5973865	5983496	ASB1	protein
7	ENSGALG00000007944	9831319	9937960	HECW2	protein
7	ENSGALG00000038311	6633230	6662722	COL18A1	protein
7	ENSGALG00000004322	6604479	6617381	AHR1B	protein
7	ENSGALG00000043345	8756092	8880668		lincRNA
7	ENSGALG00000033329	9273897	9443440		lincRNA
7	ENSGALG00000035909	9641479	9643660		lincRNA
8	ENSGALG00000045609	26758266	26759747		protein
8	ENSGALG00000011413	26796821	26810573		protein
8	ENSGALG00000036909	22774073	23612126	AGBL4	protein
8	ENSGALG00000010335	21504570	21529508		protein
8	ENSGALG00000011394	26763424	26794681	CYP2J23	protein
8	ENSGALG00000010889	26728370	26751231	HOOK1	protein
8	ENSGALG00000002182	1592876	1687096	NR5A2	protein
9	ENSGALG00000002963	9846033	9924167	PID1	protein
9	ENSGALG00000040598	12336436	12336545	gga-mir-	miRNA
9	ENSGALG00000038612	9384943	9430089	COL4A3	protein
9	ENSGALG00000006241	24033681	24037038		protein
9	ENSGALG00000038512	12398415	12430615	AGTR1	protein
9	ENSGALG00000038446	12791624	12817886	XXYLT1	protein
9	ENSGALG00000006843	12448872	12485514	NCBP2	protein
9	ENSGALG00000004957	9276974	9300051	RHBDD1	protein
9	ENSGALG00000035535	24044046	24059098	GYG1	protein
9	ENSGALG00000025759	10338213	10382351	TFDP2	protein
9	ENSGALG00000003079	9434454	9456535	MFF	protein
9	ENSGALG00000007040	12721876	12778586	ACAP2	protein
9	ENSGALG00000005217	8038070	8049501	MOGAT1	protein
9	ENSGALG00000043175	9308914	9310262		protein
9	ENSGALG00000004946	9318986	9370173		protein
9	ENSGALG00000040089	24002562	24031230	HPS3	protein
9	ENSGALG00000034507	10685168	10685803	CHST2	protein
9	ENSGALG00000004966	8727389	8844775	NYAP2	protein
9	ENSGALG00000005283	6763875	6794340	SLC25A36	protein
9	ENSGALG00000045497	6794703	6804886		protein
9	ENSGALG00000002974	9572308	9638300	SPHKAP	protein
9	ENSGALG00000029102	6796763	6897692	PXYLP1	protein
9	ENSGALG00000041879	9200204	9244990		lincRNA
9	ENSGALG00000040423	9836593	9841383		lincRNA
9	ENSGALG00000030000	10355033	10369237		lincRNA

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
9	ENSGALG00000032040	10685845	10687118		lincRNA
9	ENSGALG00000043388	10702824	10777782		lincRNA
9	ENSGALG00000034521	12099991	12132543		lincRNA
11	ENSGALG00000001647	1010935	1031465	PSKH1	protein
11	ENSGALG00000035368	1036239	1037901	CTRL	protein
11	ENSGALG00000002356	1571363	1573654	CMTR2	protein
11	ENSGALG00000026903	1547073	1551636	CALB2	protein
11	ENSGALG00000044146	1554680	1560904	PNP	protein
11	ENSGALG00000001702	1039643	1046923	EXOC3L1	protein
11	ENSGALG00000002321	1534043	1544632	GOT2	protein
12	ENSGALG00000032736	9622177	9678239	MGLL	protein
12	ENSGALG00000007741	15680951	15722117	MDFIC2	protein
13	ENSGALG00000007404	17642827	17649925	YIPF5	protein
13	ENSGALG00000012322	17658234	17692276	KCTD16	protein
13	ENSGALG00000037523	17650088	17655423		lincRNA
15	ENSGALG00000008051	10983392	11057802	MTMR3	protein
22	ENSGALG00000043405	531919	545332	BNIP3L	protein
22	ENSGALG00000001608	1798072	1927838	UNC5D	protein
22	ENSGALG00000000235	551092	584895	PPP2R2A	protein
22	ENSGALG00000036854	1250416	1257995	R3HCC1	protein
22	ENSGALG00000000409	1264837	1273235	CHMP7	protein
22	ENSGALG00000000314	952291	957139	NEFL	protein
22	ENSGALG00000000317	961851	965751	NEFM	protein
23	ENSGALG00000018302	4947355	4947443	gga-mir-	miRNA
23	ENSGALG00000018301	4946132	4946227	gga-mir-30e	miRNA
23	ENSGALG00000003189	4927211	4955061	NFYC	protein
24	ENSGALG00000007017	4561032	4564457	RBM7	protein
24	ENSGALG00000032467	6200315	6206582	C11orf52	protein
24	ENSGALG00000040842	6209231	6210762	HSPB2	protein
24	ENSGALG00000007144	5115506	5186106	SIK3	protein
24	ENSGALG00000007945	6212347	6216461	CRYAB	protein
24	ENSGALG00000007950	6217278	6218903	C11orf1	protein
24	ENSGALG00000007967	6220268	6224769	FDXACB1	protein
24	ENSGALG00000007833	5765420	5775028		protein
24	ENSGALG00000021174	6226906	6251930		protein
24	ENSGALG00000007114	5110448	5112102	APOA1	protein
24	ENSGALG00000035980	4564832	4570788	REXO2	protein
24	ENSGALG00000007839	5780707	5862536	NCAM1	protein
24	ENSGALG00000037459	4559838	4560959		lincRNA
24	ENSGALG00000034862	6036961	6038353		lincRNA
27	ENSGALG00000002804	5549486	5564038	RND2	protein
27	ENSGALG00000034345	5473594	5474209	COA3	protein
27	ENSGALG00000046412	5494647	5500006		protein
27	ENSGALG00000043285	5473787	5477716	CNTD1	protein
27	ENSGALG00000033522	5499722	5504356		protein
27	ENSGALG00000002973	5478574	5483356	BECN1	protein
27	ENSGALG00000002937	5483514	5490234	PSME3	protein

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
27	ENSGALG00000032191	5462100	5472837	WNK4	protein
27	ENSGALG00000044770	5532343	5534366		protein
27	ENSGALG00000002818	5538068	5543804	VAT1	protein
28	ENSGALG00000021722	3623171	3623258	gga-mir-9-1	miRNA
28	ENSGALG00000025492	3621530	3621611	gga-mir-	miRNA
28	ENSGALG00000025443	3620263	3620333	gga-mir-	miRNA
28	ENSGALG00000033270	3867485	3873055	KLHL26	protein
28	ENSGALG00000034592	4813319	4843107		protein
28	ENSGALG00000025809	3646007	3649991	TMEM161A	protein
28	ENSGALG00000044632	4869939	4874272		protein
28	ENSGALG00000034271	4846978	4859149	UHRF1	protein
28	ENSGALG00000003153	3739329	3744161	COPE	protein
28	ENSGALG00000001962	2817697	2846212	PTBP1	protein
28	ENSGALG00000001342	2711394	2723081	HCN2	protein
28	ENSGALG00000026850	4877060	4879564	TICAM1	protein
28	ENSGALG00000003304	3825550	3857837	CRTC1	protein
28	ENSGALG00000038529	2848507	2852387	PLPPR3	protein
28	ENSGALG00000004168	4883400	4886316	FEM1A	protein
28	ENSGALG00000003130	3733488	3739178	DDX49	protein
28	ENSGALG00000025766	3596017	3600340		protein
28	ENSGALG00000004200	4925539	4944851	DPP9	protein
28	ENSGALG00000037558	3608217	3609544		protein
28	ENSGALG00000003160	3746346	3756801	CERS1	protein
28	ENSGALG00000001328	2698084	2709095	BSG	protein
28	ENSGALG00000003161	3758227	3760332	GDF3	protein
28	ENSGALG00000043371	3758353	3758688		protein
28	ENSGALG00000003074	3704908	3725461	HOMER3	protein
28	ENSGALG00000038755	3618921	3643301		lincRNA
28	ENSGALG00000043409	3727817	3728983		lincRNA
28	ENSGALG00000032462	4882319	4883273		lincRNA
28	ENSGALG00000038462	4914645	4923495		lincRNA

Chr = Chromosome; N= count

Table S 61. Top pairwise Fst values (1%) in Improved Horro and Jarso chickens.

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
1	19420001	19440000	162	0.72	0.54	5.61
1	191090001	191110000	34	0.69	0.27	5.33
1	19410001	19430000	128	0.69	0.43	5.32
1	146780001	146800000	85	0.68	0.40	5.29
1	146770001	146790000	74	0.68	0.35	5.29
1	19430001	19450000	108	0.68	0.56	5.26
1	191130001	191150000	165	0.68	0.50	5.22
1	124200001	124220000	251	0.68	0.50	5.21
1	146790001	146810000	135	0.67	0.38	5.18
1	101180001	101200000	167	0.67	0.66	5.18
1	146810001	146830000	96	0.67	0.31	5.17
1	191100001	191120000	29	0.67	0.53	5.14
1	146760001	146780000	87	0.67	0.41	5.11
1	151690001	151710000	207	0.66	0.41	5.08
1	151680001	151700000	182	0.66	0.36	5.04
1	146800001	146820000	119	0.66	0.30	5.04
1	191140001	191160000	80	0.66	0.55	5.01
1	149050001	149070000	175	0.65	0.52	4.94
1	191120001	191140000	149	0.65	0.44	4.91
1	101150001	101170000	166	0.63	0.52	4.79
1	146820001	146840000	153	0.63	0.29	4.73
1	146990001	147010000	91	0.62	0.42	4.64
1	117150001	117170000	113	0.62	0.54	4.62
1	101160001	101180000	188	0.62	0.52	4.62
1	190870001	190890000	153	0.62	0.42	4.61
1	101190001	101210000	180	0.61	0.51	4.59
1	117140001	117160000	90	0.61	0.44	4.58
1	191110001	191130000	66	0.61	0.45	4.55
1	101170001	101190000	175	0.61	0.57	4.54
1	147080001	147100000	144	0.61	0.33	4.54
1	190880001	190900000	122	0.61	0.40	4.54
1	147110001	147130000	185	0.61	0.33	4.53
1	147090001	147110000	179	0.60	0.36	4.45
1	147100001	147120000	209	0.60	0.36	4.45
1	147990001	148010000	166	0.60	0.44	4.40
1	5240001	5260000	141	0.58	0.29	4.27
1	117130001	117150000	62	0.58	0.34	4.27
1	5210001	5230000	164	0.58	0.35	4.24
1	147960001	147980000	253	0.58	0.44	4.24
1	152810001	152830000	46	0.58	0.41	4.23
1	5220001	5240000	139	0.58	0.33	4.22
1	147980001	148000000	240	0.58	0.34	4.20
1	5230001	5250000	124	0.58	0.29	4.20

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
1	35320001	35340000	262	0.57	0.40	4.19
1	147070001	147090000	175	0.57	0.36	4.16
1	194260001	194280000	79	0.57	0.30	4.14
1	100540001	100560000	221	0.57	0.40	4.12
1	146980001	147000000	155	0.57	0.40	4.10
1	5250001	5270000	179	0.56	0.29	4.09
1	181790001	181810000	200	0.56	0.35	4.06
1	147060001	147080000	207	0.56	0.38	4.06
1	146830001	146850000	157	0.56	0.27	4.04
1	19330001	19350000	114	0.56	0.33	4.04
1	151670001	151690000	154	0.56	0.24	4.04
1	147010001	147030000	180	0.56	0.31	4.02
1	191080001	191100000	128	0.56	0.16	4.01
1	181800001	181820000	294	0.56	0.36	4.01
1	147950001	147970000	147	0.56	0.40	4.01
1	147020001	147040000	200	0.56	0.34	4.00
1	100530001	100550000	240	0.55	0.39	3.98
1	147000001	147020000	92	0.55	0.24	3.97
1	181840001	181860000	289	0.55	0.30	3.96
1	19310001	19330000	129	0.55	0.36	3.96
1	146890001	146910000	120	0.55	0.30	3.95
1	190890001	190910000	145	0.55	0.32	3.92
1	190910001	190930000	219	0.55	0.25	3.92
1	147030001	147050000	196	0.55	0.31	3.92
1	5390001	5410000	179	0.55	0.27	3.91
1	148000001	148020000	171	0.55	0.41	3.91
1	146140001	146160000	222	0.55	0.34	3.91
1	147040001	147060000	184	0.55	0.29	3.91
1	147050001	147070000	184	0.55	0.30	3.91
1	117160001	117180000	93	0.55	0.48	3.89
1	146900001	146920000	183	0.54	0.30	3.87
1	117120001	117140000	54	0.54	0.43	3.86
1	146750001	146770000	73	0.54	0.30	3.86
1	194570001	194590000	292	0.54	0.37	3.85
1	147970001	147990000	314	0.54	0.35	3.85
1	100520001	100540000	292	0.54	0.38	3.85
1	120600001	120620000	403	0.54	0.33	3.84
1	146920001	146940000	195	0.54	0.29	3.82
1	194590001	194610000	271	0.54	0.38	3.82
1	19340001	19360000	76	0.54	0.32	3.82
1	194600001	194620000	356	0.54	0.41	3.81
1	5200001	5220000	176	0.54	0.32	3.81
1	64110001	64130000	243	0.54	0.28	3.80
1	190860001	190880000	181	0.53	0.38	3.78
1	148750001	148770000	69	0.53	0.34	3.78

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
1	147940001	147960000	201	0.53	0.35	3.78
1	5260001	5280000	163	0.53	0.25	3.76
1	151750001	151770000	191	0.53	0.39	3.76
1	152580001	152600000	206	0.53	0.26	3.76
1	146130001	146150000	233	0.53	0.28	3.76
1	181480001	181500000	223	0.53	0.31	3.74
1	146110001	146130000	203	0.53	0.32	3.74
1	64120001	64140000	200	0.53	0.33	3.72
1	147120001	147140000	159	0.53	0.25	3.72
1	96580001	96600000	149	0.53	0.30	3.71
1	146970001	146990000	150	0.53	0.34	3.70
1	151660001	151680000	161	0.53	0.22	3.69
1	100510001	100530000	252	0.52	0.39	3.69
1	149040001	149060000	183	0.52	0.39	3.69
1	19320001	19340000	114	0.52	0.32	3.68
1	181490001	181510000	255	0.52	0.35	3.67
1	63520001	63540000	136	0.52	0.31	3.67
1	146910001	146930000	213	0.52	0.30	3.67
1	89460001	89480000	91	0.52	0.38	3.66
1	5160001	5180000	148	0.52	0.34	3.65
1	17890001	17910000	131	0.52	0.32	3.64
1	190900001	190920000	200	0.52	0.25	3.63
1	175710001	175730000	374	0.52	0.31	3.62
1	61330001	61350000	321	0.52	0.31	3.62
1	19540001	19560000	147	0.52	0.34	3.60
1	151540001	151560000	114	0.52	0.31	3.60
1	148160001	148180000	108	0.52	0.41	3.60
1	137500001	137520000	418	0.52	0.23	3.60
1	147930001	147950000	249	0.51	0.35	3.57
1	151630001	151650000	95	0.51	0.30	3.56
1	175720001	175740000	447	0.51	0.29	3.56
1	154530001	154550000	220	0.51	0.30	3.55
1	39050001	39070000	257	0.51	0.33	3.55
1	182720001	182740000	223	0.51	0.29	3.54
1	152590001	152610000	259	0.51	0.20	3.53
1	190920001	190940000	183	0.51	0.20	3.53
1	120590001	120610000	276	0.51	0.33	3.53
1	151620001	151640000	83	0.51	0.30	3.53
1	194580001	194600000	253	0.51	0.33	3.52
1	5150001	5170000	194	0.51	0.36	3.50
1	19700001	19720000	163	0.51	0.34	3.50
1	5190001	5210000	161	0.51	0.29	3.50
1	124190001	124210000	379	0.50	0.35	3.49
1	151700001	151720000	217	0.50	0.34	3.47
1	146840001	146860000	118	0.50	0.31	3.47

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
1	35330001	35350000	270	0.50	0.29	3.46
1	146120001	146140000	171	0.50	0.23	3.45
1	19620001	19640000	184	0.50	0.29	3.45
1	159870001	159890000	207	0.50	0.34	3.45
1	61340001	61360000	287	0.50	0.27	3.44
1	137510001	137530000	368	0.50	0.26	3.44
1	64100001	64120000	263	0.50	0.22	3.44
1	146100001	146120000	357	0.50	0.29	3.43
1	100550001	100570000	290	0.50	0.35	3.43
1	124210001	124230000	309	0.50	0.32	3.42
1	19460001	19480000	141	0.50	0.32	3.40
1	175640001	175660000	385	0.50	0.31	3.40
1	148010001	148030000	198	0.50	0.36	3.39
1	5180001	5200000	125	0.49	0.29	3.38
1	151610001	151630000	80	0.49	0.29	3.38
1	175760001	175780000	296	0.49	0.31	3.37
1	140930001	140950000	123	0.49	0.34	3.36
1	140590001	140610000	272	0.49	0.30	3.36
1	151740001	151760000	254	0.49	0.39	3.35
1	181850001	181870000	286	0.49	0.26	3.34
1	148250001	148270000	147	0.49	0.38	3.34
1	111860001	111880000	156	0.49	0.30	3.34
1	152600001	152620000	282	0.49	0.23	3.34
1	142930001	142950000	302	0.49	0.29	3.33
1	61320001	61340000	329	0.49	0.29	3.33
1	146880001	146900000	75	0.49	0.31	3.32
1	137450001	137470000	358	0.49	0.33	3.32
1	152820001	152840000	69	0.49	0.34	3.32
1	171270001	171290000	256	0.49	0.27	3.30
1	19400001	19420000	118	0.49	0.20	3.30
1	148260001	148280000	147	0.48	0.37	3.29
1	19570001	19590000	145	0.48	0.30	3.28
1	181310001	181330000	204	0.48	0.30	3.27
1	146150001	146170000	256	0.48	0.31	3.26
1	140940001	140960000	104	0.48	0.33	3.24
1	148640001	148660000	91	0.48	0.31	3.24
1	39040001	39060000	272	0.48	0.30	3.24
1	5380001	5400000	180	0.48	0.24	3.23
1	194380001	194400000	267	0.48	0.23	3.23
1	148630001	148650000	103	0.48	0.33	3.23
1	137390001	137410000	444	0.48	0.30	3.22
1	45640001	45660000	283	0.48	0.27	3.22
1	194250001	194270000	37	0.48	0.25	3.22
1	175770001	175790000	301	0.48	0.30	3.22
1	27200001	27220000	253	0.48	0.30	3.21

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
1	5170001	5190000	120	0.48	0.28	3.20
1	145560001	145580000	239	0.48	0.31	3.20
1	1610001	1630000	293	0.48	0.26	3.19
1	175650001	175670000	386	0.48	0.30	3.19
1	145440001	145460000	416	0.48	0.27	3.19
1	1620001	1640000	153	0.48	0.27	3.19
1	82330001	82350000	280	0.47	0.26	3.18
1	63530001	63550000	106	0.47	0.26	3.18
1	96590001	96610000	195	0.47	0.25	3.17
1	148730001	148750000	93	0.47	0.31	3.16
1	111830001	111850000	208	0.47	0.21	3.16
1	27190001	27210000	265	0.47	0.27	3.14
1	151550001	151570000	171	0.47	0.31	3.14
1	143690001	143710000	322	0.47	0.29	3.14
1	146850001	146870000	162	0.47	0.31	3.14
1	149360001	149380000	106	0.47	0.28	3.14
1	19380001	19400000	77	0.47	0.21	3.14
1	63510001	63530000	141	0.47	0.32	3.14
1	111840001	111860000	149	0.47	0.22	3.13
1	55830001	55850000	252	0.47	0.28	3.12
1	191180001	191200000	157	0.47	0.42	3.11
1	78270001	78290000	189	0.47	0.25	3.10
1	64090001	64110000	225	0.47	0.20	3.10
1	137490001	137510000	406	0.47	0.19	3.09
1	177250001	177270000	267	0.47	0.28	3.09
1	149060001	149080000	158	0.47	0.33	3.09
1	148680001	148700000	74	0.46	0.24	3.08
1	159080001	159100000	150	0.46	0.30	3.08
1	19450001	19470000	139	0.46	0.31	3.08
1	159070001	159090000	181	0.46	0.31	3.08
1	84400001	84420000	405	0.46	0.29	3.07
1	19690001	19710000	167	0.46	0.22	3.07
1	137440001	137460000	329	0.46	0.31	3.06
2	142890001	142910000	61	0.73	0.28	5.76
2	142910001	142930000	186	0.71	0.35	5.57
2	61580001	61600000	144	0.71	0.52	5.54
2	142900001	142920000	142	0.70	0.28	5.49
2	142810001	142830000	59	0.70	0.42	5.46
2	143610001	143630000	210	0.68	0.34	5.23
2	143320001	143340000	61	0.68	0.46	5.20
2	142920001	142940000	184	0.64	0.31	4.82
2	143570001	143590000	187	0.64	0.32	4.80
2	133300001	133320000	167	0.63	0.46	4.78
2	143600001	143620000	205	0.62	0.28	4.67
2	133330001	133350000	129	0.61	0.48	4.51

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
2	133290001	133310000	185	0.60	0.36	4.45
2	21240001	21260000	148	0.59	0.48	4.39
2	142800001	142820000	189	0.59	0.32	4.39
2	21990001	22010000	260	0.59	0.33	4.33
2	143580001	143600000	126	0.59	0.29	4.32
2	143560001	143580000	188	0.59	0.25	4.31
2	133070001	133090000	181	0.58	0.38	4.26
2	133320001	133340000	149	0.58	0.42	4.20
2	139700001	139720000	232	0.57	0.27	4.18
2	50210001	50230000	87	0.57	0.37	4.17
2	132910001	132930000	183	0.57	0.42	4.10
2	50200001	50220000	105	0.56	0.35	4.08
2	21250001	21270000	171	0.56	0.46	4.06
2	21260001	21280000	137	0.56	0.44	4.06
2	57870001	57890000	293	0.56	0.33	4.05
2	54810001	54830000	246	0.56	0.42	4.01
2	143590001	143610000	136	0.55	0.24	3.98
2	82270001	82290000	158	0.55	0.40	3.97
2	142270001	142290000	256	0.55	0.39	3.96
2	49690001	49710000	64	0.55	0.34	3.91
2	142260001	142280000	314	0.55	0.36	3.91
2	143620001	143640000	196	0.55	0.23	3.91
2	132920001	132940000	199	0.54	0.41	3.88
2	61570001	61590000	323	0.54	0.30	3.86
2	143330001	143350000	102	0.54	0.38	3.85
2	142320001	142340000	242	0.54	0.36	3.82
2	131340001	131360000	132	0.54	0.30	3.80
2	82260001	82280000	161	0.54	0.37	3.80
2	146070001	146090000	170	0.54	0.36	3.79
2	133310001	133330000	173	0.53	0.35	3.78
2	146060001	146080000	191	0.53	0.34	3.78
2	82280001	82300000	143	0.53	0.35	3.73
2	82250001	82270000	151	0.53	0.37	3.73
2	142460001	142480000	364	0.53	0.33	3.73
2	15940001	15960000	452	0.53	0.27	3.72
2	133270001	133290000	195	0.53	0.36	3.71
2	142940001	142960000	149	0.53	0.36	3.71
2	57860001	57880000	259	0.53	0.35	3.70
2	15340001	15360000	316	0.53	0.33	3.70
2	133280001	133300000	222	0.52	0.31	3.69
2	62480001	62500000	317	0.52	0.32	3.67
2	62490001	62510000	253	0.52	0.35	3.66
2	142540001	142560000	332	0.52	0.29	3.65
2	145990001	146010000	290	0.52	0.31	3.65
2	144380001	144400000	118	0.52	0.43	3.63

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
2	57720001	57740000	169	0.52	0.31	3.63
2	147310001	147330000	133	0.52	0.26	3.63
2	15330001	15350000	363	0.52	0.31	3.61
2	142330001	142350000	214	0.52	0.32	3.61
2	57730001	57750000	155	0.52	0.37	3.61
2	21980001	22000000	291	0.52	0.28	3.61
2	143190001	143210000	217	0.52	0.36	3.61
2	62390001	62410000	247	0.52	0.34	3.61
2	15950001	15970000	306	0.52	0.25	3.59
2	82240001	82260000	131	0.51	0.32	3.58
2	145980001	146000000	341	0.51	0.29	3.58
2	62380001	62400000	296	0.51	0.35	3.57
2	8010001	8030000	306	0.51	0.33	3.56
2	57790001	57810000	223	0.51	0.39	3.55
2	141780001	141800000	290	0.51	0.30	3.55
2	145970001	145990000	376	0.51	0.29	3.53
2	145960001	145980000	233	0.51	0.31	3.53
2	143360001	143380000	103	0.51	0.33	3.52
2	8020001	8040000	325	0.51	0.36	3.52
2	143340001	143360000	109	0.51	0.40	3.52
2	50220001	50240000	153	0.51	0.35	3.52
2	143350001	143370000	111	0.50	0.36	3.48
2	133080001	133100000	221	0.50	0.35	3.44
2	142280001	142300000	274	0.50	0.37	3.43
2	49680001	49700000	106	0.50	0.34	3.43
2	133040001	133060000	116	0.50	0.33	3.42
2	38420001	38440000	230	0.49	0.37	3.39
2	111910001	111930000	244	0.49	0.31	3.37
2	11690001	11710000	92	0.49	0.23	3.36
2	144370001	144390000	121	0.49	0.43	3.36
2	146180001	146200000	356	0.49	0.31	3.35
2	147320001	147340000	138	0.49	0.36	3.34
2	146990001	147010000	169	0.49	0.29	3.33
2	125510001	125530000	238	0.49	0.32	3.31
2	142470001	142490000	307	0.49	0.27	3.29
2	62430001	62450000	300	0.48	0.29	3.28
2	147000001	147020000	219	0.48	0.32	3.28
2	143640001	143660000	221	0.48	0.28	3.28
2	50050001	50070000	142	0.48	0.33	3.25
2	21270001	21290000	171	0.48	0.35	3.25
2	49890001	49910000	70	0.48	0.34	3.25
2	78330001	78350000	293	0.48	0.29	3.24
2	142450001	142470000	355	0.48	0.30	3.24
2	143200001	143220000	193	0.48	0.36	3.23
2	82800001	82820000	172	0.48	0.36	3.22

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
2	62440001	62460000	295	0.48	0.28	3.21
2	61870001	61890000	320	0.48	0.32	3.20
2	142210001	142230000	213	0.48	0.31	3.20
2	15930001	15950000	416	0.48	0.27	3.19
2	145940001	145960000	359	0.47	0.25	3.17
2	21230001	21250000	120	0.47	0.33	3.17
2	23010001	23030000	250	0.47	0.23	3.16
2	104450001	104470000	409	0.47	0.29	3.15
2	111900001	111920000	279	0.47	0.34	3.15
2	82790001	82810000	165	0.47	0.38	3.14
2	82820001	82840000	154	0.47	0.36	3.14
2	50230001	50250000	208	0.47	0.29	3.13
2	62360001	62380000	340	0.47	0.30	3.13
2	146170001	146190000	361	0.47	0.28	3.12
2	143630001	143650000	220	0.47	0.22	3.11
2	104460001	104480000	395	0.47	0.29	3.11
2	82350001	82370000	155	0.47	0.31	3.11
2	50020001	50040000	157	0.47	0.40	3.10
2	57880001	57900000	280	0.47	0.25	3.09
2	55020001	55040000	190	0.46	0.20	3.08
2	50080001	50100000	177	0.46	0.33	3.08
2	145930001	145950000	480	0.46	0.26	3.07
2	82810001	82830000	177	0.46	0.34	3.07
2	132990001	133010000	172	0.46	0.31	3.07
2	145620001	145640000	308	0.46	0.30	3.07
2	142290001	142310000	217	0.46	0.34	3.07
3	80060001	80080000	192	0.71	0.48	5.57
3	80070001	80090000	199	0.70	0.51	5.48
3	37940001	37960000	280	0.68	0.36	5.29
3	90980001	91000000	104	0.68	0.50	5.26
3	37950001	37970000	276	0.67	0.37	5.11
3	80080001	80100000	174	0.66	0.45	5.01
3	90520001	90540000	72	0.65	0.48	4.93
3	37910001	37930000	432	0.65	0.39	4.91
3	37920001	37940000	378	0.64	0.38	4.88
3	80050001	80070000	232	0.63	0.37	4.76
3	80590001	80610000	300	0.63	0.33	4.72
3	37930001	37950000	289	0.63	0.35	4.71
3	92220001	92240000	224	0.62	0.45	4.64
3	98130001	98150000	171	0.60	0.36	4.48
3	80020001	80040000	223	0.59	0.36	4.35
3	80600001	80620000	232	0.59	0.30	4.32
3	80010001	80030000	221	0.58	0.28	4.29
3	51270001	51290000	279	0.58	0.28	4.28
3	11320001	11340000	215	0.58	0.33	4.28

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
3	80040001	80060000	253	0.58	0.31	4.23
3	80030001	80050000	254	0.58	0.33	4.22
3	92230001	92250000	256	0.58	0.41	4.21
3	72010001	72030000	245	0.58	0.43	4.21
3	80090001	80110000	122	0.58	0.35	4.19
3	80810001	80830000	330	0.57	0.32	4.18
3	63980001	64000000	288	0.57	0.35	4.16
3	91460001	91480000	62	0.57	0.41	4.14
3	35180001	35200000	305	0.57	0.35	4.12
3	51480001	51500000	282	0.57	0.36	4.10
3	53590001	53610000	124	0.56	0.32	4.08
3	50770001	50790000	278	0.56	0.32	4.06
3	79800001	79820000	300	0.56	0.30	4.05
3	80000001	80020000	263	0.56	0.28	4.04
3	38370001	38390000	103	0.56	0.42	4.04
3	84140001	84160000	156	0.56	0.49	4.00
3	45970001	45990000	317	0.56	0.38	4.00
3	80450001	80470000	89	0.55	0.26	3.96
3	63990001	64010000	258	0.55	0.29	3.96
3	80840001	80860000	243	0.55	0.36	3.95
3	90990001	91010000	104	0.55	0.33	3.93
3	35170001	35190000	295	0.55	0.34	3.92
3	84150001	84170000	152	0.55	0.44	3.89
3	37390001	37410000	143	0.54	0.34	3.88
3	51470001	51490000	231	0.54	0.37	3.86
3	90970001	90990000	126	0.54	0.38	3.85
3	53610001	53630000	131	0.54	0.28	3.83
3	85600001	85620000	63	0.54	0.33	3.82
3	51280001	51300000	266	0.54	0.27	3.82
3	93710001	93730000	78	0.54	0.35	3.80
3	84040001	84060000	153	0.54	0.25	3.80
3	37350001	37370000	117	0.54	0.22	3.79
3	65840001	65860000	280	0.53	0.33	3.78
3	80750001	80770000	356	0.53	0.28	3.78
3	90510001	90530000	128	0.53	0.40	3.77
3	53600001	53620000	117	0.53	0.30	3.77
3	92190001	92210000	302	0.53	0.34	3.76
3	84160001	84180000	146	0.53	0.40	3.73
3	80770001	80790000	409	0.53	0.23	3.72
3	80760001	80780000	329	0.53	0.26	3.72
3	37340001	37360000	113	0.53	0.23	3.71
3	80740001	80760000	370	0.52	0.28	3.68
3	50810001	50830000	198	0.52	0.32	3.65
3	80800001	80820000	379	0.52	0.26	3.64
3	49960001	49980000	187	0.52	0.30	3.63

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
3	98140001	98160000	149	0.52	0.27	3.62
3	84050001	84070000	153	0.52	0.30	3.60
3	8100001	8120000	257	0.52	0.27	3.60
3	37380001	37400000	139	0.52	0.28	3.60
3	78560001	78580000	356	0.52	0.26	3.60
3	84130001	84150000	109	0.51	0.44	3.58
3	90810001	90830000	188	0.51	0.41	3.58
3	80420001	80440000	367	0.51	0.20	3.57
3	53620001	53640000	138	0.51	0.24	3.56
3	90360001	90380000	217	0.51	0.40	3.55
3	63970001	63990000	296	0.51	0.35	3.54
3	50760001	50780000	439	0.51	0.35	3.54
3	50780001	50800000	210	0.51	0.28	3.53
3	65850001	65870000	198	0.51	0.29	3.51
3	80780001	80800000	446	0.51	0.25	3.51
3	8090001	8110000	328	0.51	0.29	3.50
3	50000001	50020000	240	0.51	0.32	3.50
3	89680001	89700000	209	0.51	0.39	3.49
3	49970001	49990000	175	0.51	0.29	3.49
3	80440001	80460000	209	0.50	0.18	3.47
3	92390001	92410000	273	0.50	0.31	3.47
3	37900001	37920000	480	0.50	0.29	3.46
3	65880001	65900000	221	0.50	0.38	3.46
3	50010001	50030000	176	0.50	0.34	3.45
3	72000001	72020000	248	0.50	0.33	3.44
3	80870001	80890000	323	0.50	0.30	3.43
3	80850001	80870000	310	0.50	0.31	3.42
3	62650001	62670000	245	0.50	0.38	3.42
3	80820001	80840000	347	0.50	0.29	3.42
3	88840001	88860000	266	0.50	0.32	3.39
3	89840001	89860000	237	0.50	0.35	3.39
3	92200001	92220000	283	0.50	0.30	3.39
3	37960001	37980000	280	0.49	0.28	3.39
3	63960001	63980000	207	0.49	0.36	3.39
3	52390001	52410000	354	0.49	0.23	3.38
3	3070001	3090000	147	0.49	0.24	3.37
3	87890001	87910000	288	0.49	0.36	3.37
3	11330001	11350000	340	0.49	0.28	3.37
3	79810001	79830000	317	0.49	0.28	3.36
3	98150001	98170000	155	0.49	0.30	3.36
3	65860001	65880000	242	0.49	0.34	3.35
3	8030001	8050000	356	0.49	0.27	3.35
3	50800001	50820000	214	0.49	0.26	3.34
3	62550001	62570000	189	0.49	0.44	3.34
3	3060001	3080000	96	0.49	0.26	3.34

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
3	84300001	84320000	159	0.49	0.42	3.33
3	80790001	80810000	401	0.49	0.28	3.32
3	51260001	51280000	275	0.49	0.22	3.32
3	79730001	79750000	340	0.49	0.25	3.32
3	62660001	62680000	209	0.49	0.40	3.32
3	84170001	84190000	139	0.49	0.33	3.31
3	79990001	80010000	300	0.49	0.26	3.30
3	90950001	90970000	31	0.49	0.43	3.30
3	80580001	80600000	316	0.48	0.27	3.28
3	80430001	80450000	314	0.48	0.17	3.27
3	68790001	68810000	176	0.48	0.29	3.27
3	79680001	79700000	339	0.48	0.26	3.26
3	50060001	50080000	112	0.48	0.45	3.26
3	80460001	80480000	140	0.48	0.29	3.25
3	98120001	98140000	199	0.48	0.31	3.25
3	41190001	41210000	370	0.48	0.28	3.25
3	92210001	92230000	241	0.48	0.33	3.24
3	79790001	79810000	300	0.48	0.29	3.24
3	80880001	80900000	319	0.48	0.29	3.24
3	51490001	51510000	283	0.48	0.24	3.22
3	64070001	64090000	154	0.48	0.32	3.20
3	90350001	90370000	243	0.48	0.36	3.19
3	90530001	90550000	124	0.47	0.35	3.18
3	49990001	50010000	230	0.47	0.27	3.18
3	3090001	3110000	193	0.47	0.23	3.17
3	89330001	89350000	251	0.47	0.36	3.17
3	65910001	65930000	371	0.47	0.32	3.17
3	52370001	52390000	362	0.47	0.26	3.17
3	53580001	53600000	148	0.47	0.27	3.17
3	79670001	79690000	424	0.47	0.26	3.16
3	90500001	90520000	177	0.47	0.35	3.16
3	53640001	53660000	123	0.47	0.18	3.16
3	80410001	80430000	392	0.47	0.19	3.16
3	50750001	50770000	590	0.47	0.33	3.16
3	49980001	50000000	178	0.47	0.27	3.16
3	91380001	91400000	171	0.47	0.33	3.16
3	90960001	90980000	89	0.47	0.33	3.15
3	50820001	50840000	282	0.47	0.32	3.15
3	27050001	27070000	278	0.47	0.28	3.14
3	65870001	65890000	252	0.47	0.34	3.14
3	94240001	94260000	178	0.47	0.32	3.14
3	98160001	98180000	205	0.47	0.31	3.13
3	52380001	52400000	383	0.47	0.21	3.12
3	79960001	79980000	303	0.47	0.30	3.12
3	80660001	80680000	336	0.47	0.27	3.12

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
3	84310001	84330000	152	0.47	0.37	3.11
3	89690001	89710000	192	0.47	0.37	3.11
3	79950001	79970000	276	0.47	0.31	3.11
3	90620001	90640000	219	0.47	0.24	3.11
3	65890001	65910000	288	0.47	0.32	3.10
3	50050001	50070000	97	0.47	0.42	3.10
3	92240001	92260000	366	0.47	0.33	3.09
3	94690001	94710000	174	0.47	0.24	3.09
3	64530001	64550000	194	0.47	0.33	3.09
3	79420001	79440000	358	0.46	0.21	3.09
3	92400001	92420000	296	0.46	0.31	3.09
3	80830001	80850000	326	0.46	0.25	3.07
3	33110001	33130000	314	0.46	0.31	3.06
4	27910001	27930000	87	0.75	0.64	5.94
4	27890001	27910000	61	0.74	0.59	5.89
4	27880001	27900000	108	0.74	0.60	5.87
4	27900001	27920000	31	0.73	0.51	5.80
4	28010001	28030000	36	0.73	0.70	5.78
4	27870001	27890000	109	0.73	0.45	5.77
4	28000001	28020000	26	0.73	0.71	5.76
4	27990001	28010000	24	0.73	0.62	5.72
4	39730001	39750000	422	0.72	0.43	5.69
4	39720001	39740000	372	0.72	0.44	5.60
4	27920001	27940000	106	0.71	0.60	5.56
4	28020001	28040000	42	0.71	0.61	5.55
4	26340001	26360000	277	0.70	0.30	5.49
4	28030001	28050000	84	0.70	0.58	5.47
4	28040001	28060000	120	0.70	0.59	5.44
4	27980001	28000000	22	0.70	0.57	5.43
4	26350001	26370000	332	0.70	0.30	5.42
4	27860001	27880000	83	0.70	0.26	5.42
4	28050001	28070000	118	0.69	0.60	5.34
4	28230001	28250000	141	0.67	0.43	5.18
4	26360001	26380000	271	0.67	0.28	5.14
4	26300001	26320000	135	0.67	0.35	5.10
4	28060001	28080000	123	0.66	0.52	5.09
4	28700001	28720000	145	0.66	0.50	5.07
4	26280001	26300000	147	0.66	0.34	5.06
4	28670001	28690000	132	0.66	0.49	5.02
4	26310001	26330000	155	0.66	0.28	5.02
4	26330001	26350000	241	0.65	0.25	4.98
4	41780001	41800000	141	0.65	0.38	4.97
4	39700001	39720000	215	0.65	0.41	4.96
4	39710001	39730000	299	0.65	0.43	4.95
4	28710001	28730000	120	0.65	0.48	4.90

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
4	28220001	28240000	166	0.65	0.53	4.90
4	26290001	26310000	120	0.64	0.35	4.85
4	41790001	41810000	70	0.64	0.35	4.80
4	28120001	28140000	97	0.63	0.41	4.75
4	41770001	41790000	171	0.63	0.32	4.74
4	28680001	28700000	148	0.62	0.47	4.68
4	39170001	39190000	173	0.62	0.46	4.64
4	27830001	27850000	52	0.62	0.51	4.64
4	28660001	28680000	95	0.62	0.35	4.64
4	28160001	28180000	22	0.62	0.51	4.59
4	28750001	28770000	216	0.61	0.43	4.58
4	28740001	28760000	119	0.61	0.34	4.58
4	28690001	28710000	149	0.61	0.43	4.58
4	28760001	28780000	179	0.61	0.41	4.55
4	28170001	28190000	79	0.61	0.49	4.54
4	28110001	28130000	118	0.61	0.39	4.54
4	28190001	28210000	134	0.61	0.43	4.53
4	28180001	28200000	123	0.61	0.45	4.53
4	41830001	41850000	112	0.61	0.45	4.52
4	27840001	27860000	51	0.61	0.31	4.52
4	28070001	28090000	129	0.61	0.37	4.51
4	28090001	28110000	153	0.61	0.36	4.50
4	41800001	41820000	62	0.60	0.32	4.49
4	39740001	39760000	402	0.60	0.31	4.48
4	27820001	27840000	46	0.60	0.44	4.47
4	28770001	28790000	106	0.60	0.35	4.46
4	28080001	28100000	160	0.60	0.38	4.45
4	28200001	28220000	143	0.60	0.47	4.44
4	28210001	28230000	164	0.60	0.50	4.43
4	28130001	28150000	50	0.60	0.35	4.41
4	41820001	41840000	109	0.60	0.37	4.40
4	27850001	27870000	54	0.59	0.15	4.39
4	26170001	26190000	231	0.59	0.28	4.36
4	41850001	41870000	101	0.59	0.41	4.36
4	41840001	41860000	97	0.59	0.41	4.34
4	37810001	37830000	167	0.59	0.36	4.30
4	26320001	26340000	208	0.59	0.20	4.30
4	39620001	39640000	375	0.59	0.52	4.29
4	39690001	39710000	179	0.59	0.25	4.29
4	27660001	27680000	128	0.58	0.53	4.28
4	26270001	26290000	175	0.58	0.24	4.27
4	41810001	41830000	100	0.58	0.30	4.26
4	27930001	27950000	69	0.58	0.44	4.24
4	39610001	39630000	346	0.58	0.50	4.23
4	27040001	27060000	100	0.58	0.32	4.21

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
4	28100001	28120000	128	0.57	0.30	4.18
4	42060001	42080000	44	0.57	0.47	4.17
4	28510001	28530000	65	0.57	0.33	4.13
4	27030001	27050000	144	0.57	0.34	4.12
4	26140001	26160000	193	0.57	0.22	4.12
4	87460001	87480000	280	0.57	0.34	4.12
4	27670001	27690000	70	0.57	0.48	4.12
4	28590001	28610000	122	0.57	0.41	4.11
4	28500001	28520000	75	0.56	0.37	4.07
4	27650001	27670000	118	0.56	0.48	4.06
4	28520001	28540000	75	0.56	0.31	4.05
4	27950001	27970000	21	0.56	0.45	4.04
4	28730001	28750000	111	0.56	0.22	4.03
4	28490001	28510000	55	0.55	0.36	3.96
4	28240001	28260000	126	0.55	0.20	3.96
4	28720001	28740000	127	0.55	0.29	3.95
4	27970001	27990000	26	0.55	0.42	3.95
4	41900001	41920000	141	0.55	0.41	3.94
4	41910001	41930000	128	0.55	0.41	3.94
4	28530001	28550000	86	0.55	0.28	3.94
4	26380001	26400000	189	0.55	0.24	3.93
4	27810001	27830000	34	0.55	0.28	3.91
4	26160001	26180000	225	0.55	0.22	3.90
4	28800001	28820000	217	0.54	0.27	3.89
4	27680001	27700000	82	0.54	0.46	3.88
4	26040001	26060000	189	0.54	0.26	3.86
4	87470001	87490000	207	0.54	0.37	3.86
4	37870001	37890000	339	0.54	0.35	3.85
4	26390001	26410000	199	0.54	0.26	3.82
4	27730001	27750000	24	0.54	0.42	3.81
4	28600001	28620000	122	0.54	0.32	3.80
4	41860001	41880000	129	0.53	0.31	3.78
4	39660001	39680000	324	0.53	0.30	3.78
4	27710001	27730000	60	0.53	0.40	3.77
4	39400001	39420000	462	0.53	0.37	3.77
4	28810001	28830000	162	0.53	0.22	3.74
4	28370001	28390000	77	0.53	0.26	3.74
4	26180001	26200000	203	0.53	0.22	3.72
4	37670001	37690000	310	0.53	0.25	3.72
4	28410001	28430000	76	0.53	0.22	3.71
4	27740001	27760000	25	0.53	0.31	3.71
4	27690001	27710000	112	0.53	0.45	3.69
4	39390001	39410000	484	0.53	0.37	3.69
4	26150001	26170000	199	0.52	0.20	3.68
4	27700001	27720000	95	0.52	0.44	3.68

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
4	39210001	39230000	286	0.52	0.35	3.68
4	25260001	25280000	216	0.52	0.33	3.67
4	27940001	27960000	37	0.52	0.41	3.64
4	27590001	27610000	102	0.52	0.42	3.64
4	27720001	27740000	32	0.52	0.35	3.63
4	28340001	28360000	127	0.52	0.27	3.62
4	39600001	39620000	301	0.52	0.41	3.61
4	27600001	27620000	81	0.52	0.43	3.61
4	87480001	87500000	256	0.52	0.40	3.60
4	28380001	28400000	101	0.51	0.23	3.58
4	28780001	28800000	138	0.51	0.22	3.57
4	27020001	27040000	144	0.51	0.30	3.57
4	26370001	26390000	159	0.51	0.16	3.57
4	37660001	37680000	384	0.51	0.26	3.55
4	28350001	28370000	108	0.51	0.27	3.53
4	27800001	27820000	37	0.51	0.23	3.53
4	28430001	28450000	77	0.51	0.30	3.52
4	28790001	28810000	185	0.51	0.23	3.52
4	28400001	28420000	88	0.51	0.23	3.51
4	28540001	28560000	91	0.51	0.22	3.50
4	27540001	27560000	106	0.51	0.39	3.50
4	26450001	26470000	137	0.50	0.26	3.49
4	27760001	27780000	39	0.50	0.25	3.47
4	41890001	41910000	120	0.50	0.30	3.47
4	27490001	27510000	97	0.50	0.31	3.47
4	28420001	28440000	81	0.50	0.27	3.46
4	39670001	39690000	346	0.50	0.23	3.43
4	49170001	49190000	368	0.50	0.35	3.43
4	39590001	39610000	353	0.50	0.40	3.41
4	27790001	27810000	42	0.50	0.25	3.41
4	27750001	27770000	34	0.50	0.25	3.41
4	26130001	26150000	160	0.50	0.18	3.40
4	42070001	42090000	62	0.49	0.36	3.39
4	27610001	27630000	71	0.49	0.37	3.38
4	25270001	25290000	277	0.49	0.30	3.38
4	39160001	39180000	228	0.49	0.35	3.36
4	16450001	16470000	254	0.49	0.30	3.35
4	39380001	39400000	482	0.49	0.34	3.35
4	27960001	27980000	27	0.49	0.38	3.34
4	27400001	27420000	72	0.49	0.24	3.33
4	25190001	25210000	259	0.49	0.30	3.33
4	26080001	26100000	194	0.49	0.25	3.33
4	27410001	27430000	90	0.49	0.25	3.32
4	27530001	27550000	84	0.49	0.36	3.31
4	87580001	87600000	113	0.49	0.39	3.30

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
4	26210001	26230000	168	0.49	0.14	3.30
4	41920001	41940000	85	0.49	0.32	3.29
4	37720001	37740000	401	0.49	0.32	3.29
4	27620001	27640000	81	0.49	0.35	3.29
4	39630001	39650000	336	0.48	0.37	3.27
4	26050001	26070000	212	0.48	0.21	3.27
4	26030001	26050000	165	0.48	0.28	3.26
4	87450001	87470000	316	0.48	0.25	3.26
4	28920001	28940000	185	0.48	0.32	3.26
4	25180001	25200000	215	0.48	0.27	3.26
4	26440001	26460000	182	0.48	0.21	3.26
4	26460001	26480000	133	0.48	0.24	3.24
4	27550001	27570000	115	0.48	0.34	3.24
4	27780001	27800000	29	0.48	0.26	3.24
4	28360001	28380000	88	0.48	0.25	3.24
4	7580001	7600000	184	0.48	0.31	3.23
4	25230001	25250000	229	0.48	0.28	3.23
4	37700001	37720000	394	0.48	0.27	3.23
4	7570001	7590000	138	0.48	0.23	3.22
4	37730001	37750000	349	0.48	0.29	3.21
4	26520001	26540000	144	0.48	0.24	3.21
4	27770001	27790000	25	0.48	0.23	3.20
4	39990001	40010000	328	0.48	0.24	3.20
4	28460001	28480000	45	0.48	0.24	3.20
4	26560001	26580000	150	0.48	0.29	3.20
4	27010001	27030000	152	0.48	0.23	3.20
4	37680001	37700000	359	0.48	0.23	3.19
4	39200001	39220000	244	0.48	0.32	3.19
4	57310001	57330000	246	0.47	0.30	3.19
4	26620001	26640000	84	0.47	0.17	3.18
4	16460001	16480000	200	0.47	0.34	3.17
4	26200001	26220000	164	0.47	0.13	3.17
4	26430001	26450000	182	0.47	0.20	3.16
4	28390001	28410000	112	0.47	0.20	3.16
4	53630001	53650000	73	0.47	0.27	3.16
4	26220001	26240000	137	0.47	0.18	3.15
4	28440001	28460000	61	0.47	0.24	3.15
4	27270001	27290000	90	0.47	0.19	3.15
4	37880001	37900000	318	0.47	0.28	3.15
4	37690001	37710000	387	0.47	0.24	3.14
4	14270001	14290000	305	0.47	0.19	3.13
4	27480001	27500000	133	0.47	0.29	3.13
4	27580001	27600000	96	0.47	0.31	3.13
4	53610001	53630000	341	0.47	0.26	3.12
4	30260001	30280000	172	0.47	0.31	3.11

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
4	37710001	37730000	383	0.47	0.28	3.11
4	87540001	87560000	333	0.47	0.34	3.11
4	27520001	27540000	95	0.47	0.30	3.11
4	28610001	28630000	145	0.46	0.19	3.08
4	28580001	28600000	123	0.46	0.26	3.07
4	39410001	39430000	400	0.46	0.32	3.07
5	26450001	26470000	316	0.57	0.30	4.18
5	9450001	9470000	313	0.55	0.35	3.92
5	26460001	26480000	323	0.55	0.28	3.91
5	40550001	40570000	158	0.55	0.39	3.90
5	26310001	26330000	194	0.55	0.37	3.90
5	5550001	5570000	375	0.53	0.33	3.71
5	26170001	26190000	264	0.53	0.33	3.70
5	26640001	26660000	255	0.53	0.27	3.70
5	1900001	1920000	236	0.52	0.30	3.65
5	26320001	26340000	226	0.52	0.38	3.60
5	12680001	12700000	372	0.51	0.27	3.58
5	25870001	25890000	171	0.51	0.28	3.56
5	7150001	7170000	324	0.51	0.26	3.51
5	40560001	40580000	212	0.51	0.30	3.51
5	520001	540000	407	0.51	0.28	3.50
5	9440001	9460000	341	0.50	0.32	3.49
5	5560001	5580000	391	0.50	0.35	3.47
5	12690001	12710000	336	0.50	0.23	3.47
5	41200001	41220000	152	0.50	0.44	3.42
5	5540001	5560000	323	0.49	0.28	3.39
5	21830001	21850000	227	0.49	0.30	3.37
5	41210001	41230000	127	0.49	0.44	3.32
5	40580001	40600000	135	0.49	0.37	3.31
5	16790001	16810000	254	0.49	0.30	3.31
5	6990001	7010000	305	0.49	0.28	3.30
5	16730001	16750000	207	0.48	0.34	3.29
5	15570001	15590000	352	0.48	0.24	3.28
5	5380001	5400000	264	0.48	0.29	3.27
5	25880001	25900000	145	0.48	0.25	3.25
5	26180001	26200000	287	0.48	0.27	3.23
5	5390001	5410000	300	0.48	0.21	3.19
5	6980001	7000000	306	0.47	0.27	3.14
5	40480001	40500000	210	0.47	0.34	3.13
5	1830001	1850000	394	0.47	0.32	3.09
5	1890001	1910000	275	0.46	0.30	3.08
6	13810001	13830000	98	0.66	0.37	5.02
6	27660001	27680000	339	0.62	0.38	4.65
6	27670001	27690000	240	0.55	0.25	3.94
6	13820001	13840000	108	0.53	0.32	3.74

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
6	13800001	13820000	85	0.53	0.24	3.70
6	16560001	16580000	125	0.53	0.29	3.69
6	25850001	25870000	348	0.52	0.27	3.60
6	13830001	13850000	133	0.51	0.33	3.52
6	16550001	16570000	155	0.49	0.22	3.29
6	5760001	5780000	440	0.48	0.27	3.25
6	25840001	25860000	372	0.48	0.24	3.20
6	12870001	12890000	116	0.47	0.39	3.17
6	13840001	13860000	146	0.47	0.33	3.15
6	13160001	13180000	475	0.47	0.32	3.12
6	13340001	13360000	104	0.46	0.22	3.07
7	32520001	32540000	225	0.76	0.44	6.01
7	32530001	32550000	224	0.74	0.46	5.89
7	32540001	32560000	215	0.70	0.39	5.42
7	32550001	32570000	164	0.68	0.32	5.20
7	32560001	32580000	230	0.57	0.30	4.17
7	32510001	32530000	189	0.56	0.30	4.01
7	29650001	29670000	341	0.54	0.39	3.86
7	32570001	32590000	350	0.54	0.30	3.80
7	29440001	29460000	332	0.53	0.37	3.76
7	29430001	29450000	173	0.53	0.43	3.75
7	29450001	29470000	350	0.50	0.36	3.42
7	6600001	6620000	123	0.49	0.38	3.36
7	2630001	2650000	330	0.49	0.33	3.36
7	29600001	29620000	360	0.49	0.26	3.33
7	10600001	10620000	237	0.49	0.30	3.30
7	28160001	28180000	281	0.49	0.29	3.30
7	2620001	2640000	279	0.48	0.32	3.28
7	29420001	29440000	94	0.48	0.30	3.25
7	31690001	31710000	323	0.48	0.29	3.24
7	32450001	32470000	324	0.48	0.26	3.21
7	14150001	14170000	343	0.47	0.27	3.18
7	32580001	32600000	352	0.47	0.25	3.17
7	2590001	2610000	184	0.47	0.34	3.16
7	29610001	29630000	377	0.47	0.24	3.15
7	2560001	2580000	254	0.47	0.28	3.09
8	15490001	15510000	154	0.76	0.48	6.06
8	15500001	15520000	148	0.73	0.47	5.74
8	15510001	15530000	121	0.66	0.41	5.03
8	15480001	15500000	135	0.66	0.28	5.03
8	15530001	15550000	173	0.63	0.41	4.71
8	15520001	15540000	150	0.62	0.39	4.68
8	15450001	15470000	143	0.61	0.31	4.52
8	15540001	15560000	160	0.60	0.40	4.44
8	15440001	15460000	198	0.59	0.34	4.38

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
8	15460001	15480000	109	0.56	0.21	4.01
8	1100001	1120000	218	0.54	0.41	3.84
8	16170001	16190000	344	0.53	0.29	3.70
8	15430001	15450000	208	0.52	0.28	3.62
8	16160001	16180000	287	0.51	0.27	3.51
8	16180001	16200000	363	0.50	0.29	3.43
8	1090001	1110000	268	0.49	0.38	3.34
8	1060001	1080000	212	0.48	0.31	3.26
8	3560001	3580000	472	0.48	0.33	3.23
8	21170001	21190000	337	0.48	0.27	3.22
8	15550001	15570000	169	0.47	0.30	3.17
9	10340001	10360000	245	0.60	0.37	4.44
9	4500001	4520000	376	0.58	0.33	4.22
9	10350001	10370000	208	0.56	0.40	4.05
9	13800001	13820000	415	0.56	0.32	4.03
9	4520001	4540000	193	0.52	0.25	3.61
9	4510001	4530000	306	0.52	0.26	3.60
9	9570001	9590000	174	0.51	0.38	3.58
9	10330001	10350000	210	0.51	0.23	3.55
9	4490001	4510000	410	0.50	0.30	3.48
9	13790001	13810000	370	0.50	0.28	3.39
9	6580001	6600000	194	0.49	0.30	3.38
9	6500001	6520000	238	0.48	0.32	3.27
9	7810001	7830000	207	0.47	0.29	3.18
9	9490001	9510000	168	0.46	0.29	3.07
9	7800001	7820000	191	0.46	0.32	3.07
11	13520001	13540000	185	0.56	0.45	4.08
11	13530001	13550000	199	0.54	0.40	3.80
11	19060001	19080000	245	0.52	0.33	3.62
11	19050001	19070000	286	0.51	0.31	3.52
11	19070001	19090000	221	0.51	0.35	3.50
11	4480001	4500000	203	0.47	0.20	3.16
11	4490001	4510000	182	0.47	0.21	3.14
12	3710001	3730000	218	0.60	0.45	4.48
12	3720001	3740000	235	0.59	0.41	4.35
12	3700001	3720000	98	0.57	0.47	4.18
12	3690001	3710000	113	0.57	0.44	4.17
12	3730001	3750000	173	0.54	0.38	3.82
12	3740001	3760000	127	0.49	0.28	3.37
12	180001	200000	104	0.46	0.26	3.08
13	1760001	1780000	74	0.67	0.50	5.12
13	2200001	2220000	200	0.63	0.38	4.70
13	2210001	2230000	189	0.62	0.34	4.61
13	1750001	1770000	116	0.58	0.40	4.23
13	2150001	2170000	256	0.57	0.32	4.15

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
13	2280001	2300000	293	0.55	0.29	3.92
13	2310001	2330000	315	0.51	0.25	3.54
13	2270001	2290000	271	0.50	0.27	3.44
13	1990001	2010000	364	0.50	0.25	3.40
13	2320001	2340000	245	0.50	0.28	3.39
13	1970001	1990000	393	0.49	0.23	3.31
13	2000001	2020000	382	0.48	0.24	3.28
13	17750001	17770000	292	0.48	0.30	3.27
14	12270001	12290000	318	0.64	0.32	4.85
14	4590001	4610000	279	0.62	0.40	4.64
14	12260001	12280000	203	0.60	0.28	4.42
14	14900001	14920000	183	0.58	0.33	4.27
14	14890001	14910000	200	0.57	0.32	4.12
14	12400001	12420000	352	0.54	0.31	3.83
14	14910001	14930000	236	0.53	0.31	3.73
14	4580001	4600000	266	0.51	0.31	3.51
14	5300001	5320000	232	0.50	0.27	3.49
14	12690001	12710000	340	0.50	0.21	3.43
14	12700001	12720000	291	0.50	0.22	3.39
14	14880001	14900000	263	0.49	0.31	3.34
14	12390001	12410000	322	0.48	0.23	3.23
14	10690001	10710000	166	0.47	0.26	3.16
14	14400001	14420000	435	0.47	0.25	3.10
15	730001	750000	137	0.55	0.34	3.89
15	720001	740000	116	0.52	0.33	3.60
15	790001	810000	111	0.51	0.29	3.51
15	800001	820000	116	0.50	0.30	3.47
15	820001	840000	88	0.49	0.26	3.29
15	760001	780000	212	0.48	0.25	3.26
15	810001	830000	102	0.48	0.26	3.25
17	2130001	2150000	286	0.49	0.22	3.34
20	4800001	4820000	388	0.56	0.36	4.05
20	12180001	12200000	368	0.52	0.32	3.59
20	4790001	4810000	348	0.50	0.29	3.41
20	4810001	4830000	321	0.47	0.25	3.14
20	13370001	13390000	132	0.47	0.31	3.12
21	1590001	1610000	227	0.51	0.29	3.56
21	1600001	1620000	207	0.49	0.27	3.36
22	4410001	4430000	373	0.49	0.36	3.37
22	3510001	3530000	42	0.47	0.34	3.15
23	20001	40000	82	0.64	0.35	4.81
23	90001	110000	59	0.63	0.41	4.73
23	100001	120000	47	0.60	0.26	4.47
23	30001	50000	88	0.60	0.32	4.43
23	50001	70000	72	0.59	0.23	4.36

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
23	80001	100000	78	0.59	0.31	4.33
23	10001	30000	52	0.59	0.32	4.33
23	110001	130000	40	0.57	0.18	4.15
23	60001	80000	100	0.57	0.15	4.10
23	40001	60000	83	0.54	0.25	3.85
23	120001	140000	31	0.53	0.15	3.77
23	70001	90000	106	0.50	0.13	3.41
24	5470001	5490000	346	0.60	0.34	4.42
24	5460001	5480000	363	0.52	0.31	3.66
24	5820001	5840000	329	0.49	0.27	3.30
24	350001	370000	243	0.49	0.28	3.30
24	5830001	5850000	323	0.47	0.25	3.19
24	5770001	5790000	195	0.47	0.27	3.14
27	5390001	5410000	21	0.55	0.24	3.92
28	870001	890000	269	0.53	0.33	3.70
28	860001	880000	247	0.52	0.32	3.67

Chr = Chromosome; N= count

Table S 62. List of candidate genes in Improved Horro Vs Jarso chickens.

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
1	ENSGALG00000018250	148023499	148023596	gga-mir-20a	miRNA
1	ENSGALG00000018248	148023263	148023340	gga-mir-92-1	miRNA
1	ENSGALG00000018253	148023974	148024058	gga-mir-17	miRNA
1	ENSGALG00000018252	148023819	148023911	gga-mir-18a	miRNA
1	ENSGALG00000018249	148023376	148023462	gga-mir-19b	miRNA
1	ENSGALG00000018251	148023685	148023765	gga-mir-19a	miRNA
1	ENSGALG00000038995	181192418	181414573	GRIA4	protein coding
1	ENSGALG00000016529	120520180	120619365	CDKL5	protein coding
1	ENSGALG00000039029	191156148	191157083	TAS2R4	protein coding
1	ENSGALG00000012791	55806774	56041222	TBXAS1	protein coding
1	ENSGALG00000017040	171268903	171314194		protein coding
1	ENSGALG00000029145	137385524	137404222	DCUN1D2	protein coding
1	ENSGALG00000008477	1421469	1841500	EXOC4	protein coding
1	ENSGALG00000017086	175631550	175648871		protein coding
1	ENSGALG00000025906	145569379	145570098	HS6ST3	protein coding
1	ENSGALG00000009945	35315781	35347355	CPM	protein coding
1	ENSGALG00000032499	194257667	194259937		protein coding
1	ENSGALG00000043980	194618171	194619163		protein coding
1	ENSGALG00000015511	96489993	96603886	ROBO1	protein coding
1	ENSGALG00000017336	194386026	194399905		protein coding
1	ENSGALG00000038154	182684536	182765393	YAP1	protein coding
1	ENSGALG00000016896	146127088	146275409	ABCC4	protein coding
1	ENSGALG00000045637	194611460	194612407		protein coding
1	ENSGALG00000045274	194599548	194600495		protein coding
1	ENSGALG00000030885	194583674	194584633	OR51M1L	protein coding
1	ENSGALG00000046372	137439551	137445352		protein coding
1	ENSGALG00000030474	194589743	194590690	OR52R1	protein coding
1	ENSGALG00000037697	137487513	137505777	LAMP1	protein coding
1	ENSGALG00000016868	143513191	143715709	NALCN	protein coding
1	ENSGALG00000028273	194567561	194575005	HBBA	protein coding
1	ENSGALG00000035375	194255739	194257541		protein coding
1	ENSGALG00000016900	146527090	147094328	GPC6	protein coding
1	ENSGALG00000016830	137511432	137545754	CUL4A	protein coding
1	ENSGALG00000009480	27184787	27262852	DOCK4	protein coding
1	ENSGALG00000017333	194262382	194288323	LCMT2	protein coding
1	ENSGALG00000017347	194562710	194576539	HBBR	protein coding
1	ENSGALG00000045957	1632719	1633541		protein coding
1	ENSGALG00000031642	194378828	194384235	ILK	protein coding
1	ENSGALG00000017898	117176547	117176682	RF00003	snRNA
1	ENSGALG00000016902	147664506	148027057	GPC5	protein coding

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
1	ENSGALG00000016908	159096610	159285693	PCDH9	protein coding
1	ENSGALG00000016828	137458314	137486611	GRTP1	protein coding
1	ENSGALG00000017089	175782740	175796556	SLC46A3	protein coding
1	ENSGALG00000016602	124175179	124319202	ARHGAP6	protein coding
1	ENSGALG00000042400	111777485	111982403	CASK	protein coding
1	ENSGALG00000013117	64035202	64232501	PIK3C2G	protein coding
1	ENSGALG00000042216	145564574	145566571		lincRNA
1	ENSGALG00000031514	146892901	146893485		lincRNA
1	ENSGALG00000038284	148027203	148029069		lincRNA
1	ENSGALG00000038439	148235079	148427563		lincRNA
1	ENSGALG00000032591	148901423	149090982		lincRNA
1	ENSGALG00000033716	181770866	181805885		lincRNA
1	ENSGALG00000035278	39036722	39056354		lincRNA
1	ENSGALG00000032654	78268586	78290816		lincRNA
2	ENSGALG00000007507	15950427	15966138	MASTL	protein coding
2	ENSGALG00000007519	15968850	15995960	ACBD5	protein coding
2	ENSGALG00000012732	62437754	62509972	PHACTR1	protein coding
2	ENSGALG00000009500	22978146	23047300	VPS50	protein coding
2	ENSGALG00000031741	145815693	145960326	PTK2	protein coding
2	ENSGALG00000012730	62337049	62400206	GFOD1	protein coding
2	ENSGALG00000006372	8000159	8085723	RBM33	protein coding
2	ENSGALG00000031758	50150482	50280221	SUGCT	protein coding
2	ENSGALG00000031170	54881741	55053473	ADCY1	protein coding
2	ENSGALG00000009062	21877225	22125099	CDK14	protein coding
2	ENSGALG00000034971	146149257	146178507	SLC45A4	protein coding
2	ENSGALG00000031713	49640512	49897096	POU6F2	protein coding
2	ENSGALG00000012731	62416160	62431263	TBC1D7	protein coding
2	ENSGALG00000042548	141751641	141782032	LRRC6	protein coding
2	ENSGALG00000007492	15927463	15947552	YME1L1	protein coding
2	ENSGALG00000035281	15342791	15398782	WAC	protein coding
2	ENSGALG00000037773	142197114	142221622	ST3GAL1	protein coding
2	ENSGALG00000037014	147222471	147418330	TSNARE1	protein coding
2	ENSGALG00000044996	141791891	141797962	TMEM71	protein coding
2	ENSGALG00000042766	145515969	145738890	TRAPPC9	protein coding
2	ENSGALG00000031893	50015463	50043388	RALA	protein coding
2	ENSGALG00000015122	104463654	104519187	TAF4B	protein coding
2	ENSGALG00000043243	50062031	50120197	CDK13	protein coding
2	ENSGALG00000039831	144356967	144479127	FAM135B	protein coding
2	ENSGALG00000031519	143191899	143269024	KHDRBS3	protein coding
2	ENSGALG00000035941	133011859	133260252		lincRNA
2	ENSGALG00000030036	133259610	133653226		lincRNA
2	ENSGALG00000044807	82245741	82251690		lincRNA
3	ENSGALG00000032937	91386688	91473055	DLGAP2	protein coding

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
3	ENSGALG00000025589	92233115	92233218	RF00026	snRNA
3	ENSGALG00000016329	88826113	88881081	AGPAT5	protein coding
3	ENSGALG00000008757	11329418	11335309	CNRIP1	protein coding
3	ENSGALG00000008195	3072065	3091482	NPHP1	protein coding
3	ENSGALG00000035230	90162525	90533217	CSMD1	protein coding
3	ENSGALG00000014955	63986937	63988707		protein coding
3	ENSGALG00000028314	80041150	80041257		miRNA
3	ENSGALG00000013747	52365943	52372134	TAGAP	protein coding
3	ENSGALG00000008756	11341790	11356873	PLEK	protein coding
3	ENSGALG00000031763	37886878	37905405	EDARADD	protein coding
3	ENSGALG00000023882	3067765	3070648	MALL	protein coding
3	ENSGALG00000028539	63993333	64012992	TRAPPC3L	protein coding
3	ENSGALG00000016296	87894493	87908044	GFRAL	protein coding
3	ENSGALG00000013683	51335816	51624319	ARID1B	protein coding
3	ENSGALG00000013659	50785550	50822797	NOX3	protein coding
3	ENSGALG00000040000	37916515	37937367	ERO1B	protein coding
3	ENSGALG00000046008	52380917	52389464		protein coding
3	ENSGALG00000014950	63962962	63969961	SOT3A1L	protein coding
3	ENSGALG00000038162	64002722	64010618	FAM26E	protein coding
3	ENSGALG00000044523	8027458	8047827		protein coding
3	ENSGALG00000008233	3107192	3126953	BUB1	protein coding
3	ENSGALG00000013751	52394230	52396956		protein coding
3	ENSGALG00000009052	8095587	8106253	LBH	protein coding
3	ENSGALG00000015864	78537400	78582981	IBTK	protein coding
3	ENSGALG00000008176	3040531	3073125	ASB3	protein coding
3	ENSGALG00000010020	27010043	27167686	TTC7A	protein coding
3	ENSGALG00000015898	80736607	80807004	MYO6	protein coding
3	ENSGALG00000015001	65864380	65965590		protein coding
3	ENSGALG00000015889	79785429	79884137	PHIP	protein coding
3	ENSGALG00000015901	80846328	80912598	SENP6	protein coding
3	ENSGALG00000015880	79746415	79770440	HMGN3	protein coding
3	ENSGALG00000011663	45927228	45991940	FNDC1	protein coding
3	ENSGALG00000014953	63973179	63984264	RWDD1	protein coding
3	ENSGALG00000008198	3091987	3106203	TPCN3	protein coding
3	ENSGALG00000010843	37942007	37967000	GPR137B	protein coding
3	ENSGALG00000040702	79329300	79439703	BCKDHB	protein coding
3	ENSGALG00000010812	37306402	37666241	RYR2	protein coding
3	ENSGALG00000044806	37972758	37973736		protein coding
3	ENSGALG00000014964	64078495	64198524	NT5DC1	protein coding
3	ENSGALG00000016362	92246030	92274846	SH3YL1	protein coding
3	ENSGALG00000013647	50738394	50765171	TFB1M	protein coding
3	ENSGALG00000034081	35081760	35226507	AKT3	protein coding
3	ENSGALG00000015878	79685822	79697524	LCA5	protein coding

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
3	ENSGALG00000014878	62648643	62791218	MAN1A1	protein coding
3	ENSGALG00000015897	80679194	80732860	IMPG1	protein coding
3	ENSGALG00000034684	33116938	33125450		lincRNA
3	ENSGALG00000036733	38389716	38390740		lincRNA
3	ENSGALG00000036112	50058811	50161705		lincRNA
3	ENSGALG00000036541	64483871	64693281		lincRNA
3	ENSGALG00000041312	80383288	80482931		lincRNA
3	ENSGALG00000046621	84306206	84498020		lincRNA
4	ENSGALG00000038140	25162884	25180520		protein coding
4	ENSGALG00000010611	39613075	39632176	CFAP97	protein coding
4	ENSGALG00000009639	25181859	25200923		protein coding
4	ENSGALG00000020210	39752033	39762452	CENPU	protein coding
4	ENSGALG00000009870	30233254	30265397	IL15	protein coding
4	ENSGALG00000010614	39636713	39639533	SLC25A4	protein coding
4	ENSGALG00000039411	37840437	37922607	COL25A1	protein coding
4	ENSGALG00000012044	57097275	57432432	ANK2	protein coding
4	ENSGALG00000010628	39713691	39752253	ACSL1	protein coding
4	ENSGALG00000008517	16449974	16457382	MCTS1	protein coding
4	ENSGALG00000008404	14268127	14292407		protein coding
4	ENSGALG00000008559	16458726	16479086	CUL4B	protein coding
4	ENSGALG00000031591	16479446	16482772		lincRNA
4	ENSGALG00000029613	27043314	27051634		lincRNA
4	ENSGALG00000032527	27396660	27628525		lincRNA
4	ENSGALG00000031625	27600624	27601331		lincRNA
4	ENSGALG00000035886	27788185	27825157		lincRNA
4	ENSGALG00000036104	28160838	28173463		lincRNA
4	ENSGALG00000034709	28904779	28987118		lincRNA
4	ENSGALG00000033902	39639654	39646229		lincRNA
4	ENSGALG00000042431	39652919	39669988		lincRNA
5	ENSGALG00000007178	16777263	16794363	FADS2	protein coding
5	ENSGALG00000027255	40155940	40505519	NRXN3	protein coding
5	ENSGALG00000026386	26193022	26193130	gga-mir-6587	miRNA
5	ENSGALG00000025793	1896796	1896969	RF02271	misc_RNA
5	ENSGALG00000026686	40498715	40498826		miRNA
5	ENSGALG00000011695	6907801	6997396	HIPK3	protein coding
5	ENSGALG00000009345	26454626	26467002		protein coding
5	ENSGALG00000005840	9422736	9478597	DENND5A	protein coding
5	ENSGALG00000020485	16740019	16749937		protein coding
5	ENSGALG00000032584	21810345	21834715	ALX4	protein coding
5	ENSGALG00000003999	1910717	1996488	NAV2	protein coding
5	ENSGALG00000026005	40594965	40606615	DIO2	protein coding
5	ENSGALG00000040761	520312	526176	DRD4	protein coding
5	ENSGALG00000037020	533877	538465	SCT	protein coding

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
5	ENSGALG00000007203	16802946	16816245	RAB3IL1	protein coding
5	ENSGALG00000006368	12685002	12717134	PTPN5	protein coding
5	ENSGALG00000012103	5540164	5584404	CCDC73	protein coding
5	ENSGALG00000023243	26166529	26171162		protein coding
5	ENSGALG00000009292	26171455	26176330		protein coding
5	ENSGALG00000020454	26192258	26194122	C5H14ORF169	protein coding
5	ENSGALG00000009315	26297611	26324915	PAPLN	protein coding
5	ENSGALG00000011685	6997540	7041138	CSTF3	protein coding
5	ENSGALG00000009352	26488837	26646463	DPF3	protein coding
5	ENSGALG00000041460	16801352	16802718		lincRNA
5	ENSGALG00000042882	21829440	21830894		lincRNA
5	ENSGALG00000041420	25881336	25883509		lincRNA
5	ENSGALG00000034752	26199697	26200631		lincRNA
5	ENSGALG00000033973	26652505	26660856		lincRNA
6	ENSGALG00000008555	25836094	25887995	MXI1	protein coding
6	ENSGALG00000023925	16567737	16581736	CYP2C45	protein coding
6	ENSGALG00000046543	27677917	27680388		protein coding
6	ENSGALG00000008949	27679147	27680421	ADRB1	protein coding
6	ENSGALG00000020899	16538881	16556264		protein coding
6	ENSGALG00000004980	13362771	13800472	KCNMA1	protein coding
6	ENSGALG00000005462	16560253	16564764	ZP4	protein coding
6	ENSGALG00000004947	13158194	13188974	POLR3A	protein coding
6	ENSGALG00000034133	13321781	13363451		lincRNA
7	ENSGALG00000012045	28138613	28160700	SLC12A8	protein coding
7	ENSGALG00000012156	29342320	29524384	DPP10	protein coding
7	ENSGALG00000039730	2562997	2593595		protein coding
7	ENSGALG00000041563	2614780	2681771		protein coding
7	ENSGALG00000023742	6580483	6603208	AHR2	protein coding
7	ENSGALG00000008896	14159350	14200241	PPP1R1C	protein coding
7	ENSGALG00000004322	6604479	6617381	AHR1B	protein coding
7	ENSGALG00000045127	28175773	28181470		lincRNA
8	ENSGALG00000042744	3575631	3578451	RGS2	protein coding
8	ENSGALG00000006864	16125706	16215909	COL24A1	protein coding
8	ENSGALG00000039327	992070	1140063	VAV3	protein coding
8	ENSGALG00000010230	21118192	21176057	TESK2	protein coding
9	ENSGALG00000006488	4479194	4530082	RYK	protein coding
9	ENSGALG00000005256	7630571	7841500	EPHA4	protein coding
9	ENSGALG00000025759	10338213	10382351	TFDP2	protein coding
9	ENSGALG00000003052	9475461	9510946	AGFG1	protein coding
9	ENSGALG00000032053	6576886	6663551	SPSB4	protein coding
9	ENSGALG00000002974	9572308	9638300	SPHKAP	protein coding
9	ENSGALG00000030000	10355033	10369237		lincRNA
11	ENSGALG00000000059	19086513	19089789		protein coding

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
11	ENSGALG00000025712	19089858	19093054	DEF8	protein coding
11	ENSGALG00000000129	19064511	19086448	TCF25	protein coding
11	ENSGALG00000000516	19022589	19054970	FANCA	protein coding
11	ENSGALG00000000521	19057727	19063586	SPIRE2	protein coding
12	ENSGALG00000034572	133147	204669	POC1A	protein coding
12	ENSGALG00000030908	3752214	4001595	ATP2B2	protein coding
12	ENSGALG00000043361	116859	196969		lincRNA
13	ENSGALG00000038029	1741593	1756665		protein coding
13	ENSGALG00000041692	1763965	1767318		protein coding
13	ENSGALG00000040751	1773042	1775759		protein coding
13	ENSGALG00000035257	1725583	1768857		lincRNA
13	ENSGALG00000034005	1969580	1974487		lincRNA
14	ENSGALG00000002350	14899419	14963460	DNAH3	protein coding
14	ENSGALG00000038884	12712422	12731398	SRL	protein coding
14	ENSGALG00000036819	12286477	12288978	ARHGDIG	protein coding
14	ENSGALG00000042322	12387144	12392905	NAA60	protein coding
14	ENSGALG00000029817	4588547	4676355		protein coding
14	ENSGALG00000040648	12289815	12294043	RGS11	protein coding
14	ENSGALG00000039779	12396961	12399421	NUDT16L1	protein coding
14	ENSGALG00000002267	14864772	14882612	DCUN1D3	protein coding
14	ENSGALG00000001866	14407361	14411064	MCHR2	protein coding
14	ENSGALG00000005215	5264613	5339317	CACNA1H	protein coding
14	ENSGALG00000002273	14882642	14893170	LYRM1	protein coding
14	ENSGALG00000040070	12282289	12286205	PDIA2	protein coding
14	ENSGALG00000029402	12212172	12280905	AXIN1	protein coding
14	ENSGALG00000007779	12641712	12700251	ADCY9	protein coding
14	ENSGALG00000037492	12399639	12448114	MGRN1	protein coding
14	ENSGALG00000045141	12274279	12275343		protein coding
15	ENSGALG00000025197	749632	749731	gga-mir-1673	miRNA
15	ENSGALG00000001688	742948	780197	SEPT5	protein coding
15	ENSGALG00000025533	762734	762804	gga-mir-1729	miRNA
15	ENSGALG00000001652	711033	740520	SEPT2L	protein coding
17	ENSGALG00000008736	2080863	2196807	PNPLA7	protein coding
20	ENSGALG00000007709	12178522	12199808	RTFDC1	protein coding
20	ENSGALG00000007717	12185922	12192543	GCNT7	protein coding
20	ENSGALG00000007912	13326260	13374406	ATP9A	protein coding
20	ENSGALG00000034664	13375980	13380558		lincRNA
22	ENSGALG00000026948	3524231	3543372	ADD2	protein coding
22	ENSGALG00000046059	3521490	3523034		lincRNA
23	ENSGALG00000037136	117566	147202	RPS6KA1L	protein coding
23	ENSGALG00000039883	24815	28245	PIGV	protein coding
23	ENSGALG00000029316	33777	89058		protein coding
24	ENSGALG00000007438	5484062	5488400		protein coding

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
24	ENSGALG00000035419	323205	352144	CDON	protein coding
24	ENSGALG00000007833	5765420	5775028		protein coding
24	ENSGALG00000007430	5475477	5483503	ARCN1	protein coding
24	ENSGALG00000007839	5780707	5862536	NCAM1	protein coding
24	ENSGALG00000040155	5460918	5470400	ZW10	protein coding
24	ENSGALG00000007418	5457626	5460103	CD3D	protein coding
27	ENSGALG00000003162	5398850	5404671	RETREG3	protein coding
27	ENSGALG00000030003	5405581	5413027		protein coding
27	ENSGALG00000003199	5390278	5394159	MLX	protein coding
27	ENSGALG00000019741	5394153	5396864	PSMC3IP	protein coding
28	ENSGALG00000000629	875633	876795		protein coding
28	ENSGALG00000000621	863498	872099	KANK3	protein coding
28	ENSGALG00000026161	883272	885709		protein coding
28	ENSGALG00000043928	867852	869483		protein coding
28	ENSGALG00000037408	885913	888150	ADMP	protein coding
28	ENSGALG00000024398	874867	875414	RPS28	protein coding
28	ENSGALG00000021688	877655	881866	CD320	protein coding

Chr = Chromosome; N = count; LincRNA = Long intergenic noncoding RNAs

Table S 63. Top pairwise Fst values (1%) in Improved Horro and Hugub chickens.

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
1	181310001	181330000	157	0.70	0.47	5.46
1	35320001	35340000	266	0.68	0.43	5.30
1	147080001	147100000	158	0.66	0.45	5.08
1	126310001	126330000	134	0.66	0.55	5.04
1	147090001	147110000	183	0.65	0.42	4.96
1	146790001	146810000	104	0.64	0.49	4.89
1	146760001	146780000	102	0.64	0.43	4.88
1	59250001	59270000	76	0.64	0.52	4.87
1	146780001	146800000	84	0.64	0.43	4.86
1	151690001	151710000	148	0.63	0.47	4.82
1	151680001	151700000	114	0.63	0.47	4.78
1	33410001	33430000	307	0.63	0.33	4.77
1	146800001	146820000	103	0.62	0.39	4.65
1	126320001	126340000	130	0.61	0.53	4.63
1	146770001	146790000	96	0.61	0.34	4.61
1	152810001	152830000	55	0.61	0.39	4.58
1	181320001	181340000	172	0.61	0.38	4.55
1	19310001	19330000	125	0.61	0.43	4.54
1	159520001	159540000	107	0.60	0.47	4.52
1	43210001	43230000	134	0.60	0.46	4.51

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
1	146990001	147010000	92	0.60	0.43	4.47
1	126300001	126320000	135	0.59	0.50	4.43
1	19300001	19320000	175	0.59	0.41	4.36
1	146810001	146830000	108	0.59	0.33	4.35
1	103250001	103270000	129	0.58	0.40	4.29
1	35330001	35350000	233	0.58	0.40	4.24
1	150310001	150330000	35	0.57	0.45	4.23
1	196010001	196030000	227	0.57	0.40	4.19
1	33400001	33420000	324	0.57	0.36	4.19
1	43200001	43220000	128	0.57	0.40	4.16
1	179030001	179050000	260	0.57	0.38	4.15
1	147050001	147070000	211	0.56	0.37	4.12
1	147100001	147120000	208	0.56	0.37	4.10
1	147040001	147060000	189	0.56	0.33	4.10
1	147020001	147040000	205	0.56	0.38	4.10
1	181840001	181860000	200	0.56	0.42	4.09
1	146920001	146940000	189	0.56	0.31	4.08
1	147010001	147030000	179	0.56	0.36	4.08
1	19380001	19400000	66	0.56	0.34	4.07
1	189490001	189510000	255	0.56	0.32	4.07
1	159110001	159130000	100	0.56	0.36	4.06
1	59230001	59250000	101	0.56	0.29	4.05
1	159530001	159550000	97	0.55	0.37	4.03
1	61340001	61360000	211	0.55	0.32	4.02
1	146980001	147000000	157	0.55	0.41	4.01
1	152790001	152810000	63	0.55	0.37	3.99
1	151630001	151650000	74	0.55	0.37	3.98
1	100530001	100550000	185	0.55	0.48	3.96
1	146910001	146930000	210	0.55	0.32	3.96
1	100540001	100560000	174	0.55	0.47	3.96
1	151620001	151640000	68	0.54	0.35	3.94
1	151670001	151690000	92	0.54	0.35	3.93
1	181850001	181870000	195	0.54	0.38	3.93
1	147030001	147050000	200	0.54	0.35	3.90
1	126240001	126260000	96	0.54	0.47	3.90
1	146130001	146150000	278	0.54	0.27	3.89
1	100520001	100540000	236	0.54	0.45	3.88
1	153460001	153480000	330	0.54	0.41	3.88
1	33850001	33870000	287	0.54	0.33	3.88
1	33880001	33900000	257	0.54	0.34	3.87
1	147110001	147130000	190	0.54	0.42	3.86
1	152800001	152820000	32	0.54	0.33	3.86

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
1	196020001	196040000	244	0.54	0.38	3.86
1	126330001	126350000	116	0.54	0.48	3.85
1	103240001	103260000	113	0.53	0.40	3.82
1	146750001	146770000	66	0.53	0.41	3.80
1	33860001	33880000	287	0.53	0.35	3.77
1	181800001	181820000	248	0.53	0.39	3.76
1	181790001	181810000	169	0.53	0.38	3.76
1	189480001	189500000	247	0.52	0.25	3.74
1	196000001	196020000	281	0.52	0.35	3.74
1	39100001	39120000	276	0.52	0.37	3.73
1	33870001	33890000	299	0.52	0.34	3.73
1	146970001	146990000	152	0.52	0.35	3.71
1	153450001	153470000	353	0.52	0.39	3.71
1	146140001	146160000	270	0.52	0.30	3.70
1	177170001	177190000	152	0.52	0.29	3.70
1	39040001	39060000	270	0.52	0.35	3.70
1	151540001	151560000	99	0.52	0.34	3.69
1	126150001	126170000	185	0.52	0.38	3.69
1	179040001	179060000	252	0.52	0.33	3.69
1	39050001	39070000	255	0.52	0.33	3.68
1	146820001	146840000	176	0.52	0.31	3.68
1	126160001	126180000	196	0.52	0.36	3.67
1	33840001	33860000	303	0.52	0.32	3.67
1	147070001	147090000	196	0.52	0.36	3.66
1	152820001	152840000	86	0.52	0.33	3.66
1	100510001	100530000	230	0.52	0.42	3.65
1	147060001	147080000	242	0.52	0.37	3.65
1	147000001	147020000	89	0.51	0.32	3.62
1	177300001	177320000	328	0.51	0.32	3.60
1	132710001	132730000	244	0.51	0.38	3.60
1	151750001	151770000	160	0.51	0.45	3.59
1	146900001	146920000	195	0.51	0.30	3.58
1	159510001	159530000	66	0.51	0.35	3.58
1	146840001	146860000	114	0.51	0.38	3.56
1	159080001	159100000	113	0.50	0.31	3.55
1	19420001	19440000	158	0.50	0.41	3.54
1	5390001	5410000	176	0.50	0.26	3.53
1	151610001	151630000	66	0.50	0.33	3.53
1	19320001	19340000	105	0.50	0.37	3.53
1	126250001	126270000	109	0.50	0.42	3.52
1	178670001	178690000	350	0.50	0.32	3.52
1	19350001	19370000	90	0.50	0.28	3.48

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
1	147120001	147140000	162	0.50	0.41	3.48
1	19410001	19430000	123	0.50	0.36	3.47
1	85100001	85120000	125	0.50	0.25	3.47
1	126290001	126310000	133	0.50	0.42	3.45
1	142920001	142940000	298	0.50	0.28	3.45
1	151700001	151720000	183	0.49	0.36	3.45
1	36360001	36380000	384	0.49	0.32	3.44
1	146830001	146850000	164	0.49	0.33	3.43
1	178920001	178940000	288	0.49	0.23	3.42
1	146960001	146980000	144	0.49	0.20	3.42
1	179050001	179070000	229	0.49	0.30	3.40
1	177310001	177330000	333	0.49	0.31	3.40
1	177160001	177180000	151	0.49	0.23	3.38
1	19360001	19380000	112	0.49	0.25	3.38
1	19370001	19390000	76	0.49	0.28	3.37
1	151660001	151680000	87	0.49	0.33	3.36
1	142930001	142950000	292	0.49	0.28	3.36
1	150300001	150320000	76	0.49	0.36	3.35
1	177180001	177200000	163	0.49	0.32	3.35
1	5210001	5230000	174	0.49	0.34	3.35
1	82330001	82350000	243	0.48	0.33	3.34
1	78800001	78820000	362	0.48	0.33	3.34
1	179020001	179040000	263	0.48	0.26	3.34
1	190910001	190930000	96	0.48	0.40	3.33
1	39110001	39130000	265	0.48	0.28	3.33
1	28470001	28490000	401	0.48	0.30	3.32
1	153440001	153460000	275	0.48	0.37	3.32
1	177330001	177350000	405	0.48	0.34	3.29
1	140930001	140950000	115	0.48	0.36	3.29
1	177560001	177580000	236	0.48	0.33	3.28
1	5220001	5240000	132	0.48	0.33	3.27
1	126260001	126280000	105	0.48	0.39	3.27
1	67450001	67470000	443	0.48	0.27	3.26
1	177550001	177570000	277	0.48	0.34	3.26
2	73570001	73590000	184	0.82	0.61	6.63
2	73580001	73600000	168	0.81	0.60	6.59
2	21240001	21260000	140	0.80	0.58	6.47
2	73560001	73580000	135	0.78	0.50	6.28
2	139700001	139720000	119	0.76	0.60	6.09
2	73590001	73610000	142	0.75	0.53	5.96
2	21250001	21270000	165	0.75	0.51	5.93
2	149180001	149200000	705	0.74	0.64	5.91

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
2	149170001	149190000	715	0.73	0.63	5.80
2	21260001	21280000	137	0.72	0.52	5.68
2	149190001	149210000	677	0.72	0.61	5.66
2	73520001	73540000	79	0.71	0.51	5.61
2	73530001	73550000	112	0.71	0.48	5.59
2	21230001	21250000	110	0.71	0.46	5.58
2	70870001	70890000	250	0.71	0.56	5.53
2	149200001	149220000	659	0.70	0.59	5.45
2	149160001	149180000	567	0.70	0.57	5.45
2	149210001	149230000	462	0.69	0.57	5.35
2	70880001	70900000	174	0.69	0.52	5.33
2	21270001	21290000	168	0.69	0.51	5.33
2	21990001	22010000	214	0.68	0.48	5.29
2	141780001	141800000	256	0.67	0.37	5.20
2	73550001	73570000	106	0.67	0.33	5.18
2	149220001	149240000	223	0.67	0.52	5.17
2	70860001	70880000	225	0.67	0.51	5.15
2	21980001	22000000	232	0.67	0.46	5.15
2	73650001	73670000	76	0.67	0.54	5.14
2	73540001	73560000	115	0.66	0.35	5.12
2	147720001	147740000	189	0.66	0.37	5.09
2	21970001	21990000	231	0.66	0.46	5.07
2	73600001	73620000	120	0.65	0.43	4.99
2	73660001	73680000	80	0.65	0.53	4.94
2	149150001	149170000	278	0.65	0.47	4.94
2	21950001	21970000	190	0.64	0.48	4.90
2	111910001	111930000	213	0.63	0.38	4.80
2	70850001	70870000	216	0.63	0.43	4.78
2	21220001	21240000	192	0.63	0.46	4.78
2	147710001	147730000	171	0.63	0.42	4.77
2	21960001	21980000	189	0.63	0.46	4.75
2	21820001	21840000	319	0.63	0.43	4.74
2	147730001	147750000	190	0.62	0.30	4.69
2	73610001	73630000	106	0.62	0.38	4.68
2	73640001	73660000	95	0.61	0.42	4.63
2	21830001	21850000	309	0.61	0.41	4.56
2	141790001	141810000	283	0.61	0.28	4.55
2	146070001	146090000	153	0.61	0.44	4.55
2	111900001	111920000	257	0.60	0.42	4.51
2	73670001	73690000	90	0.60	0.45	4.51
2	146060001	146080000	170	0.60	0.42	4.50
2	147700001	147720000	171	0.59	0.40	4.43

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
2	21210001	21230000	212	0.59	0.43	4.36
2	139710001	139730000	165	0.59	0.42	4.36
2	141820001	141840000	242	0.58	0.25	4.32
2	147310001	147330000	129	0.58	0.53	4.28
2	141770001	141790000	331	0.58	0.28	4.26
2	141740001	141760000	297	0.57	0.33	4.21
2	22610001	22630000	317	0.56	0.36	4.12
2	21280001	21300000	240	0.56	0.42	4.09
2	141810001	141830000	423	0.56	0.20	4.07
2	81210001	81230000	154	0.55	0.30	4.02
2	81220001	81240000	188	0.55	0.29	3.99
2	73620001	73640000	118	0.55	0.29	3.96
2	141750001	141770000	337	0.55	0.32	3.95
2	70840001	70860000	254	0.54	0.39	3.92
2	20090001	20110000	195	0.54	0.36	3.91
2	149230001	149250000	107	0.54	0.37	3.89
2	141800001	141820000	444	0.54	0.18	3.86
2	142260001	142280000	314	0.53	0.37	3.83
2	147350001	147370000	163	0.53	0.48	3.83
2	147300001	147320000	140	0.53	0.45	3.77
2	83410001	83430000	211	0.53	0.38	3.77
2	81200001	81220000	196	0.53	0.28	3.76
2	111890001	111910000	250	0.52	0.40	3.72
2	147390001	147410000	241	0.52	0.42	3.71
2	142270001	142290000	231	0.52	0.37	3.70
2	141730001	141750000	390	0.52	0.28	3.69
2	21810001	21830000	295	0.52	0.38	3.69
2	73630001	73650000	122	0.52	0.29	3.68
2	147360001	147380000	220	0.52	0.45	3.67
2	70890001	70910000	115	0.52	0.36	3.67
2	142910001	142930000	154	0.52	0.30	3.65
2	23010001	23030000	206	0.51	0.33	3.63
2	83420001	83440000	238	0.51	0.25	3.61
2	147400001	147420000	199	0.51	0.41	3.61
2	139690001	139710000	114	0.51	0.39	3.60
2	21880001	21900000	315	0.51	0.38	3.58
2	147340001	147360000	144	0.51	0.44	3.55
2	141830001	141850000	194	0.50	0.23	3.54
2	21940001	21960000	245	0.50	0.38	3.54
2	147690001	147710000	226	0.50	0.36	3.51
2	146180001	146200000	358	0.50	0.35	3.50
2	146880001	146900000	91	0.50	0.43	3.50

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
2	62440001	62460000	302	0.50	0.33	3.50
2	20080001	20100000	254	0.50	0.38	3.46
2	71050001	71070000	137	0.50	0.38	3.45
2	147380001	147400000	263	0.49	0.37	3.45
2	22000001	22020000	291	0.49	0.34	3.45
2	147210001	147230000	109	0.49	0.48	3.44
2	83800001	83820000	360	0.49	0.27	3.44
2	110950001	110970000	316	0.49	0.31	3.43
2	147370001	147390000	259	0.49	0.39	3.43
2	62450001	62470000	274	0.49	0.33	3.40
2	141760001	141780000	394	0.49	0.26	3.39
2	110940001	110960000	309	0.48	0.34	3.31
2	147290001	147310000	124	0.48	0.40	3.29
2	70950001	70970000	163	0.48	0.32	3.29
2	61580001	61600000	211	0.48	0.28	3.29
2	148500001	148520000	279	0.48	0.24	3.28
2	141840001	141860000	263	0.48	0.26	3.28
2	22100001	22120000	191	0.48	0.34	3.27
2	81230001	81250000	180	0.48	0.28	3.27
3	90980001	91000000	98	0.79	0.58	6.32
3	90520001	90540000	67	0.75	0.55	5.96
3	90990001	91010000	88	0.70	0.47	5.50
3	89840001	89860000	206	0.68	0.54	5.31
3	89330001	89350000	247	0.68	0.46	5.30
3	90810001	90830000	184	0.67	0.54	5.15
3	89680001	89700000	204	0.65	0.48	4.96
3	90510001	90530000	125	0.64	0.48	4.88
3	89850001	89870000	197	0.64	0.45	4.87
3	86440001	86460000	136	0.64	0.43	4.87
3	89690001	89710000	186	0.64	0.49	4.85
3	90970001	90990000	123	0.63	0.44	4.80
3	89340001	89360000	231	0.63	0.42	4.74
3	91010001	91030000	95	0.62	0.40	4.73
3	90950001	90970000	21	0.62	0.55	4.69
3	91020001	91040000	94	0.61	0.41	4.59
3	90060001	90080000	138	0.61	0.39	4.57
3	35300001	35320000	330	0.60	0.43	4.51
3	86430001	86450000	244	0.60	0.38	4.45
3	90500001	90520000	171	0.59	0.44	4.44
3	86450001	86470000	67	0.59	0.32	4.41
3	92220001	92240000	226	0.59	0.40	4.37
3	90620001	90640000	186	0.59	0.34	4.34

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
3	86460001	86480000	97	0.58	0.32	4.32
3	86470001	86490000	111	0.58	0.30	4.30
3	88320001	88340000	72	0.58	0.45	4.24
3	86480001	86500000	144	0.58	0.34	4.24
3	91000001	91020000	92	0.57	0.35	4.17
3	86390001	86410000	187	0.57	0.30	4.17
3	91050001	91070000	94	0.57	0.47	4.16
3	86270001	86290000	129	0.57	0.27	4.16
3	90360001	90380000	194	0.57	0.48	4.15
3	90800001	90820000	162	0.57	0.47	4.15
3	88840001	88860000	269	0.57	0.45	4.15
3	90960001	90980000	85	0.57	0.39	4.15
3	90530001	90550000	120	0.56	0.41	4.13
3	90630001	90650000	205	0.56	0.33	4.11
3	81240001	81260000	237	0.56	0.36	4.10
3	86380001	86400000	151	0.56	0.29	4.09
3	92190001	92210000	266	0.56	0.40	4.07
3	89320001	89340000	211	0.56	0.37	4.05
3	35290001	35310000	277	0.56	0.37	4.05
3	35310001	35330000	373	0.55	0.40	4.04
3	53590001	53610000	122	0.55	0.31	4.00
3	86300001	86320000	195	0.55	0.29	3.98
3	90820001	90840000	181	0.55	0.45	3.96
3	91040001	91060000	107	0.55	0.45	3.96
3	86370001	86390000	107	0.55	0.36	3.96
3	89670001	89690000	179	0.55	0.40	3.95
3	86280001	86300000	130	0.55	0.26	3.95
3	61470001	61490000	317	0.54	0.27	3.94
3	86530001	86550000	182	0.54	0.42	3.93
3	33110001	33130000	278	0.54	0.40	3.91
3	92200001	92220000	274	0.54	0.35	3.90
3	86200001	86220000	149	0.54	0.39	3.90
3	90050001	90070000	143	0.54	0.36	3.90
3	86310001	86330000	210	0.54	0.24	3.87
3	88180001	88200000	159	0.53	0.31	3.83
3	86210001	86230000	181	0.53	0.37	3.83
3	86360001	86380000	93	0.53	0.35	3.82
3	86490001	86510000	160	0.53	0.35	3.79
3	90350001	90370000	223	0.53	0.42	3.78
3	86220001	86240000	207	0.53	0.31	3.78
3	92210001	92230000	263	0.53	0.33	3.77
3	86420001	86440000	229	0.53	0.27	3.76

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
3	90690001	90710000	121	0.52	0.43	3.74
3	86520001	86540000	189	0.52	0.43	3.72
3	86540001	86560000	176	0.52	0.38	3.71
3	91030001	91050000	88	0.52	0.37	3.70
3	50060001	50080000	110	0.52	0.49	3.69
3	53600001	53620000	113	0.52	0.30	3.69
3	90640001	90660000	164	0.52	0.31	3.68
3	53610001	53630000	122	0.52	0.29	3.67
3	79800001	79820000	280	0.52	0.35	3.66
3	33100001	33120000	231	0.51	0.35	3.64
3	86230001	86250000	303	0.51	0.26	3.63
3	91340001	91360000	278	0.51	0.36	3.63
3	35280001	35300000	229	0.51	0.36	3.62
3	86550001	86570000	150	0.51	0.35	3.60
3	81160001	81180000	227	0.51	0.37	3.60
3	86400001	86420000	187	0.51	0.24	3.57
3	81250001	81270000	225	0.50	0.31	3.52
3	86240001	86260000	277	0.50	0.22	3.48
3	90210001	90230000	132	0.50	0.37	3.46
3	91060001	91080000	104	0.50	0.28	3.45
3	78560001	78580000	290	0.50	0.31	3.45
3	87340001	87360000	189	0.50	0.33	3.45
3	88850001	88870000	283	0.49	0.41	3.44
3	86350001	86370000	122	0.49	0.22	3.43
3	91460001	91480000	61	0.49	0.38	3.43
3	43680001	43700000	253	0.49	0.28	3.43
3	91330001	91350000	348	0.49	0.34	3.42
3	87350001	87370000	265	0.49	0.34	3.42
3	90840001	90860000	159	0.49	0.41	3.40
3	104600001	104620000	254	0.49	0.37	3.40
3	12210001	12230000	76	0.49	0.34	3.37
3	90610001	90630000	143	0.49	0.32	3.37
3	90370001	90390000	183	0.49	0.41	3.36
3	10720001	10740000	219	0.49	0.31	3.36
3	90830001	90850000	154	0.49	0.41	3.35
3	81290001	81310000	185	0.48	0.36	3.33
3	91380001	91400000	159	0.48	0.37	3.31
3	86560001	86580000	133	0.48	0.24	3.30
3	27560001	27580000	221	0.48	0.36	3.30
3	10690001	10710000	130	0.48	0.33	3.29
3	81260001	81280000	239	0.48	0.28	3.28
3	84880001	84900000	48	0.48	0.42	3.28

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
3	89040001	89060000	226	0.48	0.30	3.28
3	81280001	81300000	218	0.48	0.35	3.28
3	84870001	84890000	119	0.48	0.43	3.27
4	27880001	27900000	133	0.78	0.53	6.26
4	27890001	27910000	77	0.78	0.50	6.25
4	27870001	27890000	124	0.75	0.45	5.95
4	28010001	28030000	56	0.74	0.51	5.88
4	27990001	28010000	42	0.73	0.42	5.82
4	27910001	27930000	123	0.73	0.48	5.79
4	28020001	28040000	57	0.73	0.50	5.78
4	27980001	28000000	31	0.72	0.48	5.71
4	28700001	28720000	147	0.72	0.51	5.68
4	28710001	28730000	114	0.71	0.52	5.55
4	28000001	28020000	49	0.71	0.43	5.53
4	27920001	27940000	133	0.71	0.50	5.53
4	28670001	28690000	138	0.70	0.50	5.49
4	27900001	27920000	52	0.70	0.33	5.47
4	28230001	28250000	127	0.70	0.51	5.44
4	28220001	28240000	160	0.68	0.60	5.27
4	28030001	28050000	93	0.68	0.52	5.24
4	27840001	27860000	64	0.67	0.29	5.22
4	27830001	27850000	96	0.67	0.34	5.22
4	28490001	28510000	68	0.67	0.36	5.22
4	28500001	28520000	92	0.67	0.36	5.22
4	28680001	28700000	161	0.67	0.46	5.19
4	27660001	27680000	127	0.67	0.61	5.19
4	20010001	20030000	31	0.67	0.46	5.15
4	27860001	27880000	90	0.67	0.30	5.14
4	28690001	28710000	164	0.67	0.43	5.14
4	28660001	28680000	102	0.66	0.35	5.08
4	20160001	20180000	36	0.66	0.45	5.07
4	28750001	28770000	211	0.66	0.45	5.04
4	28740001	28760000	116	0.65	0.34	4.99
4	28760001	28780000	174	0.65	0.43	4.99
4	27650001	27670000	116	0.65	0.56	4.99
4	27670001	27690000	64	0.65	0.57	4.98
4	28770001	28790000	103	0.65	0.39	4.94
4	27490001	27510000	89	0.64	0.44	4.92
4	28510001	28530000	69	0.64	0.36	4.91
4	27820001	27840000	96	0.64	0.28	4.89
4	25710001	25730000	345	0.64	0.34	4.87
4	28040001	28060000	133	0.64	0.50	4.87

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
4	20150001	20170000	44	0.64	0.43	4.85
4	19790001	19810000	36	0.63	0.48	4.81
4	28120001	28140000	97	0.63	0.47	4.79
4	28210001	28230000	165	0.63	0.54	4.78
4	19770001	19790000	41	0.63	0.40	4.78
4	28430001	28450000	75	0.63	0.35	4.77
4	19550001	19570000	23	0.62	0.44	4.73
4	28050001	28070000	130	0.62	0.51	4.73
4	19610001	19630000	54	0.62	0.38	4.71
4	28410001	28430000	65	0.62	0.30	4.70
4	28060001	28080000	125	0.62	0.49	4.70
4	28590001	28610000	117	0.62	0.46	4.69
4	20000001	20020000	41	0.62	0.41	4.66
4	27540001	27560000	107	0.62	0.47	4.64
4	19780001	19800000	45	0.61	0.41	4.63
4	28130001	28150000	47	0.61	0.43	4.61
4	26040001	26060000	192	0.61	0.31	4.60
4	19860001	19880000	44	0.61	0.39	4.60
4	27400001	27420000	52	0.61	0.36	4.57
4	20070001	20090000	30	0.61	0.39	4.56
4	28090001	28110000	158	0.61	0.41	4.56
4	28200001	28220000	144	0.61	0.49	4.55
4	27270001	27290000	83	0.61	0.26	4.55
4	28420001	28440000	72	0.60	0.33	4.52
4	27590001	27610000	89	0.60	0.54	4.52
4	28520001	28540000	70	0.60	0.36	4.52
4	28080001	28100000	181	0.60	0.37	4.52
4	20140001	20160000	36	0.60	0.40	4.51
4	20130001	20150000	48	0.60	0.39	4.51
4	17980001	18000000	62	0.60	0.45	4.50
4	37730001	37750000	243	0.60	0.47	4.50
4	27600001	27620000	77	0.60	0.52	4.50
4	19530001	19550000	31	0.60	0.39	4.50
4	28720001	28740000	125	0.60	0.31	4.49
4	27850001	27870000	58	0.60	0.18	4.49
4	19940001	19960000	55	0.60	0.39	4.49
4	27530001	27550000	81	0.60	0.43	4.48
4	19850001	19870000	40	0.60	0.43	4.48
4	19990001	20010000	48	0.60	0.37	4.48
4	19460001	19480000	24	0.60	0.43	4.47
4	19980001	20000000	45	0.60	0.37	4.47
4	27410001	27430000	67	0.60	0.40	4.46

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
4	19670001	19690000	53	0.60	0.44	4.45
4	19680001	19700000	63	0.60	0.40	4.45
4	27480001	27500000	125	0.60	0.40	4.45
4	37720001	37740000	314	0.60	0.43	4.44
4	20020001	20040000	28	0.60	0.39	4.44
4	28170001	28190000	83	0.59	0.49	4.44
4	19350001	19370000	27	0.59	0.39	4.44
4	28180001	28200000	127	0.59	0.46	4.43
4	28530001	28550000	72	0.59	0.34	4.42
4	28160001	28180000	24	0.59	0.49	4.41
4	19410001	19430000	36	0.59	0.34	4.41
4	17970001	17990000	64	0.59	0.47	4.41
4	28190001	28210000	135	0.59	0.45	4.40
4	28460001	28480000	48	0.59	0.26	4.40
4	19820001	19840000	45	0.59	0.36	4.40
4	19440001	19460000	30	0.59	0.42	4.40
4	28400001	28420000	74	0.59	0.31	4.37
4	19700001	19720000	21	0.59	0.36	4.37
4	28600001	28620000	116	0.59	0.36	4.37
4	28440001	28460000	61	0.59	0.27	4.37
4	20060001	20080000	45	0.59	0.41	4.36
4	19520001	19540000	47	0.59	0.41	4.36
4	19560001	19580000	38	0.59	0.39	4.35
4	19800001	19820000	42	0.59	0.38	4.35
4	28730001	28750000	110	0.59	0.21	4.35
4	20310001	20330000	55	0.59	0.38	4.35
4	27040001	27060000	93	0.59	0.36	4.35
4	26490001	26510000	143	0.58	0.34	4.34
4	28110001	28130000	119	0.58	0.40	4.33
4	20170001	20190000	25	0.58	0.38	4.33
4	27720001	27740000	30	0.58	0.44	4.33
4	20220001	20240000	40	0.58	0.35	4.33
4	19970001	19990000	38	0.58	0.35	4.32
4	19470001	19490000	47	0.58	0.38	4.31
4	27930001	27950000	90	0.58	0.37	4.31
4	19640001	19660000	48	0.58	0.32	4.31
4	19960001	19980000	49	0.58	0.37	4.30
4	27550001	27570000	113	0.58	0.42	4.30
4	16450001	16470000	259	0.58	0.39	4.30
4	20230001	20250000	38	0.58	0.36	4.29
4	41830001	41850000	107	0.58	0.45	4.28
4	19620001	19640000	61	0.58	0.34	4.27

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
4	28920001	28940000	185	0.58	0.36	4.26
4	25720001	25740000	331	0.58	0.28	4.26
4	7420001	7440000	136	0.58	0.52	4.26
4	27680001	27700000	74	0.58	0.50	4.26
4	20100001	20120000	55	0.58	0.41	4.26
4	27610001	27630000	69	0.58	0.45	4.25
4	19690001	19710000	52	0.58	0.34	4.25
4	26120001	26140000	139	0.58	0.31	4.25
4	16460001	16480000	233	0.58	0.46	4.24
4	27970001	27990000	40	0.58	0.34	4.24
4	19650001	19670000	56	0.57	0.33	4.24
4	19870001	19890000	44	0.57	0.37	4.24
4	20120001	20140000	51	0.57	0.35	4.23
4	19950001	19970000	61	0.57	0.38	4.23
4	27810001	27830000	51	0.57	0.25	4.23
4	27620001	27640000	81	0.57	0.40	4.22
4	28070001	28090000	145	0.57	0.34	4.21
4	26050001	26070000	213	0.57	0.27	4.20
4	27030001	27050000	138	0.57	0.37	4.19
4	19810001	19830000	49	0.57	0.35	4.19
4	26030001	26050000	184	0.57	0.30	4.18
4	25680001	25700000	372	0.57	0.31	4.18
4	20300001	20320000	41	0.57	0.41	4.18
4	26500001	26520000	128	0.57	0.31	4.18
4	39730001	39750000	377	0.57	0.42	4.17
4	27280001	27300000	121	0.57	0.34	4.16
4	20110001	20130000	50	0.57	0.40	4.16
4	25730001	25750000	304	0.57	0.28	4.15
4	75370001	75390000	175	0.57	0.38	4.15
4	7410001	7430000	147	0.56	0.51	4.14
4	27260001	27280000	91	0.56	0.31	4.14
4	20080001	20100000	34	0.56	0.38	4.13
4	27580001	27600000	84	0.56	0.42	4.13
4	7720001	7740000	257	0.56	0.24	4.12
4	25670001	25690000	422	0.56	0.29	4.12
4	27750001	27770000	31	0.56	0.29	4.10
4	20210001	20230000	47	0.56	0.32	4.10
4	20180001	20200000	24	0.56	0.36	4.10
4	39720001	39740000	331	0.56	0.42	4.10
4	19840001	19860000	34	0.56	0.39	4.10
4	27520001	27540000	79	0.56	0.41	4.09
4	20290001	20310000	31	0.56	0.40	4.09

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
4	20090001	20110000	50	0.56	0.36	4.08
4	19480001	19500000	51	0.56	0.30	4.07
4	28370001	28390000	87	0.56	0.27	4.07
4	41840001	41860000	95	0.56	0.40	4.07
4	27690001	27710000	108	0.56	0.49	4.07
4	39700001	39720000	192	0.56	0.43	4.06
4	19830001	19850000	36	0.56	0.35	4.06
4	20320001	20340000	54	0.56	0.30	4.06
4	27390001	27410000	86	0.56	0.39	4.06
4	19580001	19600000	62	0.56	0.35	4.06
4	27630001	27650000	78	0.56	0.35	4.05
4	19570001	19590000	56	0.55	0.35	4.04
4	26070001	26090000	250	0.55	0.32	4.03
4	26080001	26100000	201	0.55	0.28	4.03
4	19660001	19680000	50	0.55	0.36	4.03
4	25700001	25720000	328	0.55	0.22	4.02
4	28540001	28560000	78	0.55	0.25	4.01
4	7580001	7600000	141	0.55	0.41	4.01
4	28380001	28400000	90	0.55	0.28	4.00
4	25740001	25760000	358	0.55	0.32	3.99
4	27640001	27660000	71	0.55	0.34	3.99
4	19400001	19420000	40	0.55	0.30	3.99
4	28800001	28820000	241	0.55	0.26	3.99
4	27730001	27750000	23	0.55	0.45	3.99
4	41820001	41840000	98	0.55	0.38	3.99
4	27710001	27730000	57	0.55	0.45	3.99
4	7430001	7450000	151	0.55	0.49	3.98
4	27760001	27780000	44	0.55	0.26	3.97
4	6620001	6640000	102	0.55	0.47	3.97
4	28780001	28800000	142	0.55	0.23	3.97
4	41850001	41870000	93	0.55	0.42	3.97
4	27700001	27720000	92	0.55	0.49	3.96
4	27790001	27810000	55	0.55	0.23	3.95
4	54030001	54050000	206	0.55	0.33	3.95
4	28450001	28470000	60	0.55	0.25	3.94
4	26110001	26130000	206	0.55	0.29	3.94
4	19600001	19620000	48	0.54	0.31	3.94
4	20050001	20070000	52	0.54	0.38	3.93
4	19510001	19530000	50	0.54	0.35	3.93
4	28360001	28380000	95	0.54	0.29	3.93
4	28350001	28370000	102	0.54	0.34	3.93
4	26700001	26720000	133	0.54	0.30	3.92

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
4	20030001	20050000	24	0.54	0.40	3.91
4	26060001	26080000	266	0.54	0.31	3.91
4	28100001	28120000	128	0.54	0.33	3.91
4	27800001	27820000	47	0.54	0.21	3.90
4	27780001	27800000	44	0.54	0.22	3.89
4	27740001	27760000	23	0.54	0.34	3.89
4	39710001	39730000	268	0.54	0.44	3.89
4	26690001	26710000	135	0.54	0.32	3.88
4	19590001	19610000	51	0.54	0.34	3.87
4	26020001	26040000	194	0.54	0.25	3.87
4	20200001	20220000	34	0.54	0.29	3.87
4	20240001	20260000	45	0.54	0.31	3.86
4	42060001	42080000	45	0.54	0.45	3.85
4	26480001	26500000	144	0.54	0.31	3.85
4	28910001	28930000	133	0.54	0.35	3.85
4	28810001	28830000	197	0.54	0.20	3.84
4	17960001	17980000	84	0.53	0.38	3.83
4	28240001	28260000	120	0.53	0.28	3.82
4	53580001	53600000	198	0.53	0.34	3.82
4	19360001	19380000	43	0.53	0.31	3.82
4	19500001	19520000	49	0.53	0.31	3.81
4	40530001	40550000	286	0.53	0.42	3.80
4	27940001	27960000	48	0.53	0.35	3.79
4	28390001	28410000	89	0.53	0.28	3.77
4	19420001	19440000	30	0.53	0.29	3.77
4	37710001	37730000	300	0.53	0.34	3.77
4	19930001	19950000	57	0.53	0.30	3.77
4	7080001	7100000	125	0.53	0.44	3.76
4	27950001	27970000	29	0.53	0.32	3.76
4	27370001	27390000	126	0.52	0.41	3.73
4	17800001	17820000	111	0.52	0.37	3.72
4	19630001	19650000	52	0.52	0.28	3.72
4	19880001	19900000	55	0.52	0.32	3.71
4	27770001	27790000	43	0.52	0.18	3.70
4	27510001	27530000	92	0.52	0.41	3.68
4	40200001	40220000	233	0.52	0.44	3.66
4	37810001	37830000	145	0.52	0.35	3.66
4	27560001	27580000	104	0.52	0.31	3.65
4	25770001	25790000	269	0.52	0.36	3.65
4	28340001	28360000	118	0.51	0.33	3.65
4	7400001	7420000	166	0.51	0.46	3.64
4	28790001	28810000	195	0.51	0.22	3.62

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
4	40210001	40230000	233	0.51	0.39	3.62
4	27420001	27440000	135	0.51	0.38	3.61
4	26710001	26730000	137	0.51	0.27	3.61
4	39740001	39760000	382	0.51	0.39	3.61
4	7570001	7590000	102	0.51	0.32	3.61
4	19380001	19400000	40	0.51	0.31	3.60
4	19490001	19510000	52	0.51	0.27	3.60
4	7440001	7460000	117	0.51	0.46	3.60
4	20400001	20420000	95	0.51	0.39	3.59
4	25780001	25800000	248	0.51	0.38	3.58
4	20040001	20060000	35	0.51	0.33	3.58
4	6610001	6630000	102	0.51	0.38	3.57
4	20270001	20290000	57	0.51	0.31	3.56
4	26460001	26480000	133	0.51	0.27	3.56
4	26720001	26740000	154	0.51	0.27	3.56
4	5860001	5880000	315	0.51	0.38	3.55
4	19390001	19410000	42	0.51	0.29	3.55
4	26090001	26110000	201	0.50	0.24	3.54
4	20260001	20280000	52	0.50	0.30	3.53
4	26450001	26470000	160	0.50	0.25	3.53
4	20650001	20670000	162	0.50	0.32	3.52
4	20280001	20300000	37	0.50	0.33	3.52
4	26430001	26450000	207	0.50	0.20	3.51
4	28580001	28600000	121	0.50	0.28	3.51
4	21670001	21690000	177	0.50	0.38	3.51
4	20390001	20410000	115	0.50	0.37	3.50
4	26440001	26460000	216	0.50	0.20	3.50
4	19430001	19450000	30	0.50	0.31	3.50
4	25940001	25960000	287	0.50	0.33	3.49
4	7070001	7090000	217	0.50	0.36	3.48
4	27360001	27380000	130	0.50	0.33	3.48
4	20610001	20630000	170	0.50	0.31	3.47
4	27290001	27310000	118	0.50	0.33	3.47
4	27570001	27590000	91	0.50	0.28	3.47
4	28610001	28630000	146	0.50	0.20	3.46
4	40520001	40540000	221	0.50	0.37	3.46
4	19910001	19930000	36	0.50	0.35	3.46
4	49170001	49190000	311	0.50	0.41	3.45
4	26470001	26490000	128	0.49	0.26	3.45
4	26010001	26030000	194	0.49	0.20	3.44
4	27250001	27270000	121	0.49	0.31	3.44
4	27120001	27140000	93	0.49	0.36	3.44

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
4	39950001	39970000	383	0.49	0.29	3.43
4	7590001	7610000	132	0.49	0.42	3.43
4	41860001	41880000	121	0.49	0.31	3.42
4	25750001	25770000	412	0.49	0.29	3.42
4	17990001	18010000	70	0.49	0.31	3.41
4	39690001	39710000	166	0.49	0.20	3.40
4	41780001	41800000	129	0.49	0.30	3.38
4	69990001	70010000	204	0.49	0.32	3.38
4	37700001	37720000	311	0.49	0.35	3.37
4	26680001	26700000	134	0.49	0.24	3.36
4	25930001	25950000	235	0.49	0.34	3.35
4	20370001	20390000	83	0.49	0.32	3.35
4	41770001	41790000	164	0.49	0.26	3.35
4	21700001	21720000	155	0.48	0.34	3.35
4	17790001	17810000	118	0.48	0.31	3.34
4	87460001	87480000	219	0.48	0.39	3.33
4	20380001	20400000	107	0.48	0.33	3.33
4	41790001	41810000	62	0.48	0.30	3.33
4	20990001	21010000	137	0.48	0.30	3.32
4	17950001	17970000	88	0.48	0.34	3.31
4	20620001	20640000	115	0.48	0.31	3.30
4	26100001	26120000	216	0.48	0.22	3.30
4	27960001	27980000	44	0.48	0.27	3.30
4	21660001	21680000	183	0.48	0.38	3.30
4	20250001	20270000	43	0.48	0.27	3.29
4	21000001	21020000	219	0.48	0.31	3.29
4	7060001	7080000	196	0.48	0.33	3.29
4	41810001	41830000	90	0.48	0.27	3.29
4	26650001	26670000	106	0.48	0.21	3.28
4	53590001	53610000	207	0.48	0.31	3.28
4	26340001	26360000	281	0.48	0.22	3.27
4	25660001	25680000	302	0.48	0.22	3.26
5	14990001	15010000	32	0.72	0.56	5.64
5	14810001	14830000	103	0.71	0.57	5.55
5	26170001	26190000	240	0.67	0.41	5.19
5	14820001	14840000	127	0.66	0.45	5.06
5	26180001	26200000	228	0.63	0.39	4.82
5	23790001	23810000	145	0.63	0.53	4.76
5	20620001	20640000	183	0.63	0.46	4.75
5	27710001	27730000	199	0.63	0.46	4.74
5	14780001	14800000	85	0.62	0.47	4.71
5	14800001	14820000	94	0.62	0.51	4.68

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
5	14790001	14810000	85	0.62	0.51	4.67
5	14770001	14790000	44	0.62	0.45	4.65
5	14950001	14970000	43	0.61	0.43	4.60
5	14980001	15000000	80	0.61	0.38	4.59
5	15210001	15230000	318	0.60	0.38	4.45
5	15340001	15360000	270	0.59	0.38	4.36
5	26450001	26470000	257	0.59	0.38	4.35
5	15200001	15220000	312	0.58	0.39	4.31
5	14960001	14980000	72	0.58	0.39	4.29
5	26160001	26180000	284	0.58	0.34	4.29
5	15330001	15350000	331	0.57	0.35	4.20
5	32860001	32880000	35	0.57	0.46	4.18
5	4810001	4830000	163	0.56	0.40	4.11
5	28010001	28030000	316	0.56	0.43	4.11
5	32730001	32750000	45	0.56	0.43	4.10
5	23780001	23800000	189	0.56	0.42	4.10
5	28000001	28020000	277	0.56	0.40	4.08
5	27720001	27740000	219	0.56	0.36	4.07
5	32810001	32830000	53	0.56	0.44	4.05
5	15190001	15210000	286	0.56	0.36	4.05
5	27150001	27170000	173	0.55	0.45	4.04
5	32870001	32890000	36	0.55	0.47	3.96
5	32600001	32620000	98	0.54	0.42	3.93
5	32800001	32820000	41	0.54	0.34	3.91
5	15430001	15450000	330	0.54	0.38	3.89
5	26460001	26480000	306	0.54	0.30	3.87
5	15180001	15200000	234	0.54	0.34	3.87
5	15320001	15340000	338	0.54	0.32	3.85
5	32720001	32740000	101	0.54	0.40	3.85
5	15350001	15370000	321	0.53	0.33	3.82
5	27160001	27180000	179	0.53	0.42	3.82
5	20610001	20630000	155	0.53	0.39	3.82
5	32820001	32840000	58	0.53	0.42	3.80
5	49220001	49240000	128	0.53	0.38	3.80
5	24030001	24050000	138	0.53	0.36	3.77
5	26120001	26140000	196	0.53	0.36	3.76
5	15420001	15440000	367	0.52	0.37	3.74
5	23800001	23820000	161	0.52	0.44	3.73
5	32690001	32710000	101	0.52	0.35	3.71
5	32670001	32690000	105	0.52	0.37	3.71
5	1900001	1920000	231	0.52	0.31	3.71
5	32660001	32680000	101	0.52	0.42	3.70

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
5	15290001	15310000	286	0.52	0.33	3.70
5	26640001	26660000	207	0.52	0.36	3.69
5	15280001	15300000	239	0.52	0.26	3.69
5	18570001	18590000	170	0.52	0.28	3.69
5	32710001	32730000	126	0.52	0.37	3.68
5	15360001	15380000	337	0.52	0.33	3.66
5	15270001	15290000	233	0.52	0.24	3.66
5	21120001	21140000	170	0.52	0.42	3.66
5	25910001	25930000	265	0.52	0.31	3.66
5	30810001	30830000	193	0.52	0.27	3.65
5	26190001	26210000	269	0.51	0.31	3.64
5	18560001	18580000	126	0.51	0.31	3.64
5	32680001	32700000	111	0.51	0.30	3.62
5	26350001	26370000	185	0.51	0.33	3.61
5	32850001	32870000	33	0.51	0.42	3.60
5	32740001	32760000	45	0.51	0.37	3.59
5	32790001	32810000	44	0.51	0.35	3.59
5	32700001	32720000	94	0.51	0.36	3.59
5	1830001	1850000	371	0.51	0.35	3.58
5	23820001	23840000	265	0.51	0.43	3.57
5	23810001	23830000	212	0.51	0.45	3.57
5	15170001	15190000	306	0.51	0.35	3.55
5	32590001	32610000	122	0.50	0.42	3.54
5	25900001	25920000	240	0.50	0.34	3.52
5	32630001	32650000	109	0.50	0.35	3.50
5	15310001	15330000	228	0.50	0.31	3.48
5	25930001	25950000	317	0.50	0.29	3.48
5	5540001	5560000	325	0.50	0.29	3.47
5	27500001	27520000	133	0.50	0.35	3.47
5	20630001	20650000	215	0.50	0.37	3.47
5	15260001	15280000	268	0.50	0.30	3.46
5	32830001	32850000	39	0.50	0.39	3.46
5	4820001	4840000	161	0.50	0.39	3.45
5	32620001	32640000	104	0.50	0.34	3.45
5	14890001	14910000	134	0.50	0.36	3.45
5	5550001	5570000	369	0.49	0.33	3.44
5	20720001	20740000	135	0.49	0.42	3.44
5	15440001	15460000	299	0.49	0.33	3.44
5	14840001	14860000	276	0.49	0.33	3.43
5	15220001	15240000	386	0.49	0.31	3.42
5	21780001	21800000	198	0.49	0.38	3.42
5	32650001	32670000	93	0.49	0.38	3.42

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
5	14970001	14990000	81	0.49	0.31	3.42
5	32610001	32630000	84	0.49	0.34	3.41
5	1840001	1860000	350	0.49	0.34	3.41
5	32780001	32800000	47	0.49	0.34	3.41
5	32840001	32860000	30	0.49	0.42	3.40
5	14830001	14850000	223	0.49	0.32	3.40
5	10460001	10480000	242	0.49	0.37	3.38
5	24000001	24020000	160	0.49	0.34	3.37
5	19810001	19830000	56	0.49	0.39	3.37
5	30760001	30780000	222	0.49	0.35	3.36
5	25870001	25890000	125	0.49	0.35	3.36
5	14220001	14240000	367	0.49	0.34	3.36
5	46300001	46320000	257	0.49	0.29	3.36
5	24990001	25010000	258	0.49	0.33	3.35
5	25920001	25940000	334	0.49	0.28	3.35
5	31930001	31950000	73	0.48	0.38	3.35
5	1890001	1910000	299	0.48	0.30	3.34
5	21110001	21130000	253	0.48	0.41	3.33
5	32580001	32600000	117	0.48	0.41	3.32
5	57120001	57140000	269	0.48	0.32	3.31
5	1790001	1810000	158	0.48	0.34	3.30
5	12890001	12910000	185	0.48	0.33	3.28
5	23770001	23790000	223	0.48	0.31	3.27
5	25580001	25600000	395	0.48	0.35	3.26
6	27660001	27680000	341	0.64	0.42	4.84
6	30720001	30740000	413	0.57	0.34	4.15
6	35110001	35130000	137	0.57	0.38	4.15
6	27670001	27690000	242	0.57	0.30	4.14
6	30710001	30730000	338	0.55	0.32	4.01
6	30850001	30870000	244	0.53	0.36	3.83
6	30730001	30750000	385	0.53	0.34	3.81
6	28970001	28990000	203	0.53	0.35	3.77
6	32830001	32850000	296	0.52	0.36	3.74
6	28980001	29000000	241	0.52	0.34	3.74
6	30700001	30720000	333	0.52	0.31	3.73
6	32840001	32860000	286	0.52	0.34	3.69
6	8560001	8580000	333	0.49	0.34	3.44
6	30690001	30710000	369	0.48	0.30	3.34
6	8550001	8570000	319	0.48	0.33	3.27
7	29440001	29460000	217	0.60	0.60	4.50
7	29430001	29450000	142	0.59	0.56	4.35
7	34990001	35010000	262	0.57	0.31	4.24

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
7	29450001	29470000	242	0.54	0.55	3.87
7	35000001	35020000	265	0.53	0.29	3.76
7	29420001	29440000	86	0.52	0.36	3.69
7	34980001	35000000	274	0.52	0.28	3.69
7	31240001	31260000	272	0.49	0.33	3.35
7	19470001	19490000	291	0.48	0.32	3.32
8	16010001	16030000	150	0.65	0.44	4.98
8	16000001	16020000	146	0.63	0.45	4.83
8	16220001	16240000	276	0.61	0.33	4.57
8	15490001	15510000	141	0.58	0.40	4.26
8	12910001	12930000	122	0.57	0.44	4.22
8	15990001	16010000	167	0.57	0.43	4.15
8	15500001	15520000	136	0.55	0.38	4.02
8	16020001	16040000	166	0.55	0.41	3.95
8	15460001	15480000	119	0.55	0.40	3.95
8	16210001	16230000	254	0.54	0.21	3.92
8	15540001	15560000	191	0.54	0.34	3.86
8	8980001	9000000	59	0.52	0.44	3.69
8	15900001	15920000	307	0.52	0.34	3.69
8	15450001	15470000	170	0.52	0.38	3.65
8	17320001	17340000	159	0.51	0.37	3.59
8	17330001	17350000	208	0.50	0.36	3.47
8	17000001	17020000	213	0.49	0.32	3.39
8	13080001	13100000	42	0.49	0.41	3.39
8	15530001	15550000	182	0.49	0.30	3.36
8	19380001	19400000	230	0.48	0.36	3.33
8	13100001	13120000	27	0.48	0.43	3.28
9	13800001	13820000	357	0.63	0.34	4.74
9	13810001	13830000	353	0.52	0.30	3.67
9	6950001	6970000	136	0.51	0.35	3.65
9	13790001	13810000	327	0.50	0.31	3.47
9	18020001	18040000	303	0.48	0.30	3.34
9	9490001	9510000	181	0.48	0.36	3.29
9	6960001	6980000	170	0.48	0.33	3.27
10	12450001	12470000	112	0.68	0.58	5.31
10	12460001	12480000	117	0.66	0.49	5.10
10	12470001	12490000	138	0.64	0.47	4.92
10	12440001	12460000	131	0.60	0.45	4.48
10	12480001	12500000	175	0.60	0.42	4.48
10	17180001	17200000	144	0.57	0.37	4.17
10	11290001	11310000	218	0.52	0.33	3.72
10	17170001	17190000	151	0.51	0.37	3.57

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
10	11300001	11320000	216	0.50	0.34	3.49
10	1680001	1700000	246	0.48	0.32	3.33
10	17190001	17210000	165	0.48	0.30	3.29
11	19050001	19070000	268	0.67	0.46	5.23
11	19060001	19080000	253	0.65	0.43	5.00
11	19070001	19090000	236	0.63	0.44	4.81
11	11030001	11050000	161	0.53	0.41	3.77
11	19040001	19060000	266	0.52	0.36	3.67
11	7040001	7060000	136	0.51	0.35	3.64
11	4660001	4680000	253	0.51	0.33	3.63
11	7050001	7070000	245	0.50	0.33	3.51
11	1610001	1630000	246	0.49	0.29	3.45
11	12990001	13010000	214	0.49	0.36	3.41
11	13520001	13540000	189	0.49	0.40	3.38
11	19080001	19100000	224	0.49	0.37	3.36
11	4650001	4670000	255	0.49	0.30	3.36
11	4670001	4690000	235	0.49	0.32	3.35
12	3860001	3880000	213	0.58	0.43	4.32
12	1210001	1230000	155	0.55	0.40	3.97
12	3710001	3730000	211	0.55	0.45	3.96
12	3850001	3870000	175	0.54	0.42	3.93
12	3980001	4000000	144	0.54	0.36	3.89
12	3720001	3740000	233	0.54	0.42	3.86
12	3970001	3990000	160	0.52	0.36	3.67
12	3690001	3710000	112	0.51	0.42	3.58
12	3960001	3980000	230	0.51	0.35	3.56
12	3700001	3720000	95	0.50	0.44	3.50
12	3870001	3890000	245	0.50	0.33	3.45
12	3950001	3970000	227	0.49	0.32	3.42
12	3990001	4010000	149	0.49	0.30	3.37
12	3680001	3700000	193	0.48	0.41	3.31
12	1200001	1220000	205	0.48	0.30	3.26
13	2150001	2170000	210	0.59	0.43	4.40
13	2270001	2290000	207	0.57	0.35	4.17
13	2280001	2300000	225	0.55	0.35	4.03
14	14780001	14800000	69	0.60	0.50	4.49
14	14770001	14790000	69	0.55	0.43	3.99
14	15550001	15570000	43	0.55	0.34	3.94
14	15560001	15580000	33	0.54	0.28	3.89
14	4590001	4610000	308	0.52	0.41	3.72
14	15540001	15560000	33	0.51	0.28	3.64
14	14760001	14780000	76	0.50	0.37	3.52

Chr	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
23	90001	110000	60	0.55	0.38	3.98
23	4930001	4950000	253	0.48	0.29	3.34
23	100001	120000	41	0.48	0.27	3.32
24	6040001	6060000	203	0.53	0.38	3.83
24	3370001	3390000	203	0.48	0.27	3.29
24	6060001	6080000	157	0.48	0.36	3.29
25	2830001	2850000	55	0.55	0.49	3.99
25	2820001	2840000	75	0.52	0.45	3.74
27	5280001	5300000	153	0.48	0.36	3.30

Chr = Chromosome; N= count

Table S 64. List of candidate genes in Improved Horro and Hugub chickens.

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
1	ENSGALG00000044624	59245579	59246586		protein coding
1	ENSGALG00000017135	178883375	178933935	CRYL1	protein coding
1	ENSGALG00000017119	177513346	177560920	TNFRSF19	protein coding
1	ENSGALG00000035126	150329998	150330064		miRNA
1	ENSGALG00000038995	181192418	181414573	GRIA4	protein coding
1	ENSGALG00000016767	132714633	132747517		protein coding
1	ENSGALG00000009945	35315781	35347355	CPM	protein coding
1	ENSGALG00000009815	33395407	33407028	TMEM5	protein coding
1	ENSGALG00000016896	146127088	146275409	ABCC4	protein coding
1	ENSGALG00000017139	179051034	179094239		protein coding
1	ENSGALG00000045031	59237872	59238879		protein coding
1	ENSGALG00000044524	59241726	59242732		protein coding
1	ENSGALG00000016900	146527090	147094328	GPC6	protein coding
1	ENSGALG00000010177	36351342	36388496	ZFC3H1	protein coding
1	ENSGALG00000039209	33881874	33923658	WIF1	protein coding
1	ENSGALG00000022696	196006397	196006681	KCNE3	protein coding
1	ENSGALG00000015307	84985337	85117095	ABI3BP	protein coding
1	ENSGALG00000017304	196014618	196048973	PGM2L1	protein coding
1	ENSGALG00000016908	159096610	159285693	PCDH9	protein coding
1	ENSGALG00000044959	59249433	59250440		protein coding
1	ENSGALG00000025192	132720340	132720457	RF00619	snRNA
1	ENSGALG00000046239	59253286	59254293		protein coding
1	ENSGALG00000009859	33794056	33841926	TBC1D30	protein coding
1	ENSGALG00000045433	59257140	59258147		protein coding
1	ENSGALG00000027868	177160927	177162801	AMER2	protein coding
1	ENSGALG00000031225	178671358	178682347		protein coding
1	ENSGALG00000032339	150234073	150532403		lincRNA
1	ENSGALG00000040093	159526738	159744910		lincRNA

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
1	ENSGALG00000033716	181770866	181805885		lincRNA
1	ENSGALG00000035278	39036722	39056354		lincRNA
1	ENSGALG00000034873	126246316	126340432		lincRNA
2	ENSGALG00000025664	70897916	70898018	RF00026	snRNA
2	ENSGALG00000012732	62437754	62509972	PHACTR1	protein coding
2	ENSGALG00000009500	22978146	23047300	VPS50	protein coding
2	ENSGALG00000031869	110919658	110976941		protein coding
2	ENSGALG00000012941	73245203	73614065	CDH12	protein coding
2	ENSGALG00000039585	148501300	148505443		protein coding
2	ENSGALG00000013129	83790809	83833193	RPRD1A	protein coding
2	ENSGALG00000009062	21877225	22125099	CDK14	protein coding
2	ENSGALG00000042548	141751641	141782032	LRRC6	protein coding
2	ENSGALG00000031917	22587398	22642927	ANKIB1	protein coding
2	ENSGALG00000037014	147222471	147418330	TSNARE1	protein coding
2	ENSGALG00000044996	141791891	141797962	TMEM71	protein coding
2	ENSGALG00000013124	83340744	83708432	FHOD3	protein coding
2	ENSGALG00000034333	149152445	149152741		protein coding
2	ENSGALG00000039346	149228059	149229441		protein coding
2	ENSGALG00000033205	141806556	141854403	PHF20L1	protein coding
2	ENSGALG00000013100	81116137	81255419	GRB10	protein coding
2	ENSGALG00000040891	20027818	20125211	RSU1	protein coding
2	ENSGALG00000031547	70841747	71110837		lincRNA
3	ENSGALG00000032937	91386688	91473055	DLGAP2	protein coding
3	ENSGALG00000025589	92233115	92233218	RF00026	snRNA
3	ENSGALG00000016329	88826113	88881081	AGPAT5	protein coding
3	ENSGALG00000010039	27486112	27649822	BRE	protein coding
3	ENSGALG00000035230	90162525	90533217	CSMD1	protein coding
3	ENSGALG00000016276	86406473	86714063	KHDRBS2	protein coding
3	ENSGALG00000014868	61471807	61486414	SERINC1	protein coding
3	ENSGALG00000015864	78537400	78582981	IBTK	protein coding
3	ENSGALG00000010713	35235950	35336239	SDCCAG8	protein coding
3	ENSGALG00000015889	79785429	79884137	PHIP	protein coding
3	ENSGALG00000016300	88190798	88234696	TINAG	protein coding
3	ENSGALG00000016289	87201225	87461978	DST	protein coding
3	ENSGALG00000032069	90034820	90054328		protein coding
3	ENSGALG00000015908	81088530	81188721	COL12A1	protein coding
3	ENSGALG00000039606	91341696	91348290	CLN8	protein coding
3	ENSGALG00000016499	104597130	104611882		protein coding
3	ENSGALG00000038420	61487557	61508738	HSF2	protein coding
3	ENSGALG00000034684	33116938	33125450		lincRNA
3	ENSGALG00000036112	50058811	50161705		lincRNA
3	ENSGALG00000044759	81233001	81242848		lincRNA
4	ENSGALG00000009361	20960961	21000658	GUCY1B1	protein coding

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
4	ENSGALG00000010668	40162296	40247894	WWC2	protein coding
4	ENSGALG00000034621	75273238	75452467	KCNIP4	protein coding
4	ENSGALG00000027439	20654247	20654356		miRNA
4	ENSGALG00000042586	19460437	19460523		miRNA
4	ENSGALG00000032953	19548868	19548950		miRNA
4	ENSGALG00000025212	21010293	21010422	RF00548	snRNA
4	ENSGALG00000011844	54036328	54041083	IL21	protein coding
4	ENSGALG00000030791	5837514	5995090	DIAPH2	protein coding
4	ENSGALG00000009085	17775905	17808725	MTMR1	protein coding
4	ENSGALG00000020210	39752033	39762452	CENPU	protein coding
4	ENSGALG00000009192	19424229	19426802	SLITRK2	protein coding
4	ENSGALG00000009692	25668584	25740316	SH3RF1	protein coding
4	ENSGALG00000009207	19996054	20033183	TRIM2	protein coding
4	ENSGALG00000006851	6599257	7006957		protein coding
4	ENSGALG00000009212	20040123	20078631	MND1	protein coding
4	ENSGALG00000009241	20227180	20230889	SFRP2	protein coding
4	ENSGALG00000009230	20091761	20162392	TMEM131L	protein coding
4	ENSGALG00000009714	25756022	25763028	CBR4	protein coding
4	ENSGALG00000030065	40334424	40645412	TENM3	protein coding
4	ENSGALG00000010628	39713691	39752253	ACSL1	protein coding
4	ENSGALG00000009719	27095819	27127946	PCDH10	protein coding
4	ENSGALG00000008517	16449974	16457382	MCTS1	protein coding
4	ENSGALG00000008559	16458726	16479086	CUL4B	protein coding
4	ENSGALG00000041717	69980272	70000045	KLF3	protein coding
4	ENSGALG00000034722	20184996	20199647	TLR2B	protein coding
4	ENSGALG00000042912	5862686	5863323		lincRNA
4	ENSGALG00000031591	16479446	16482772		lincRNA
4	ENSGALG00000040514	18009035	18012307		lincRNA
4	ENSGALG00000033107	19392907	19563891		lincRNA
4	ENSGALG00000033380	19504112	19511619		lincRNA
4	ENSGALG00000041824	19541886	19542585		lincRNA
4	ENSGALG00000039736	19819071	19857159		lincRNA
4	ENSGALG00000039492	19873184	19873825		lincRNA
4	ENSGALG00000032689	26689975	26702258		lincRNA
4	ENSGALG00000029613	27043314	27051634		lincRNA
4	ENSGALG00000032527	27396660	27628525		lincRNA
4	ENSGALG00000031625	27600624	27601331		lincRNA
4	ENSGALG00000035886	27788185	27825157		lincRNA
4	ENSGALG00000036104	28160838	28173463		lincRNA
4	ENSGALG00000034709	28904779	28987118		lincRNA
4	ENSGALG00000045271	39895978	39956315		lincRNA
5	ENSGALG00000011609	18540733	18648374		protein coding
5	ENSGALG00000031542	21728195	21799637	EXT2	protein coding

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
5	ENSGALG00000009320	26365084	26386235	PSEN1	protein coding
5	ENSGALG00000008653	24995617	25023029		protein coding
5	ENSGALG00000030172	25001804	25002247		protein coding
5	ENSGALG00000026386	26193022	26193130	gga-mir-6587	miRNA
5	ENSGALG00000025793	1896796	1896969	RF02271	misc_RNA
5	ENSGALG00000009415	27718429	27835276	SMOC1	protein coding
5	ENSGALG00000009850	32870788	32999065	NOVA1	protein coding
5	ENSGALG00000040897	46303329	46303499	TUNAR	protein coding
5	ENSGALG00000009345	26454626	26467002		protein coding
5	ENSGALG00000038950	14921862	14996500		protein coding
5	ENSGALG00000006830	15151804	15252302	CHID1	protein coding
5	ENSGALG00000012228	56898267	57232790	MDGA2	protein coding
5	ENSGALG00000028203	30752050	30805661	SPRED1	protein coding
5	ENSGALG00000029399	1855519	1880037		protein coding
5	ENSGALG00000008403	23771783	23893510	PHF21A	protein coding
5	ENSGALG00000003999	1910717	1996488	NAV2	protein coding
5	ENSGALG00000008991	25575504	25598610	VPS39	protein coding
5	ENSGALG00000009282	26124345	26142266	ELMSAN1	protein coding
5	ENSGALG00000028568	26150108	26163720	DNAL1	protein coding
5	ENSGALG00000009431	27987462	28003889	PLEKHD1	protein coding
5	ENSGALG00000012103	5540164	5584404	CCDC73	protein coding
5	ENSGALG00000023243	26166529	26171162		protein coding
5	ENSGALG00000017933	32749704	32749858	RF00003	snRNA
5	ENSGALG00000009292	26171455	26176330		protein coding
5	ENSGALG00000009387	27443194	27531009		protein coding
5	ENSGALG00000020454	26192258	26194122	C5H14ORF169	protein coding
5	ENSGALG00000006837	15271751	15336034	TSPAN4	protein coding
5	ENSGALG00000009438	28008500	28025729	SLC39A9	protein coding
5	ENSGALG00000009176	25903704	25937422	TTBK2	protein coding
5	ENSGALG00000009300	26200817	26293922	NUMB	protein coding
5	ENSGALG00000039066	15451610	15451999		protein coding
5	ENSGALG00000017384	28025971	28032991	ERH	protein coding
5	ENSGALG00000009352	26488837	26646463	DPF3	protein coding
5	ENSGALG00000006035	10434605	10509846	PDE3B	protein coding
5	ENSGALG00000035105	26349956	26350342		protein coding
5	ENSGALG00000022531	24001629	24002515		protein coding
5	ENSGALG00000006717	14871236	14911577		protein coding
5	ENSGALG00000009400	27618375	27715349	SLC8A3	protein coding
5	ENSGALG00000031456	24977292	24994712		protein coding
5	ENSGALG00000031737	14760117	14805890		protein coding
5	ENSGALG00000038303	1854102	1858309		lincRNA
5	ENSGALG00000041420	25881336	25883509		lincRNA
5	ENSGALG00000034752	26199697	26200631		lincRNA

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
5	ENSGALG00000033973	26652505	26660856		lincRNA
5	ENSGALG00000032603	32617627	32740415		lincRNA
5	ENSGALG00000030088	32824916	32826865		lincRNA
6	ENSGALG00000025862	8546459	8560943	TMEM26	protein coding
6	ENSGALG00000009254	28990063	29007399	ENO4	protein coding
6	ENSGALG00000046543	27677917	27680388		protein coding
6	ENSGALG00000008949	27679147	27680421	ADRB1	protein coding
6	ENSGALG00000035013	30680913	30714244	WDR11	protein coding
6	ENSGALG00000010493	35098018	35309850	INPP5A	protein coding
7	ENSGALG00000012156	29342320	29524384	DPP10	protein coding
7	ENSGALG00000012462	34961029	35028577	KIF5C	protein coding
7	ENSGALG00000012362	31073812	31346787	THSD7B	protein coding
7	ENSGALG00000010933	19477509	19493971		protein coding
8	ENSGALG00000008658	16222861	16250213	ZNHIT6	protein coding
8	ENSGALG00000006284	15997170	16014128	SH3GLB1	protein coding
8	ENSGALG00000006864	16125706	16215909	COL24A1	protein coding
8	ENSGALG00000028423	15897943	15967214	HS2ST1	protein coding
8	ENSGALG00000006322	16020120	16033702		protein coding
9	ENSGALG00000039182	17991354	18078753	TBL1XR1	protein coding
9	ENSGALG00000003052	9475461	9510946	AGFG1	protein coding
10	ENSGALG00000006041	11295144	11301592	BNC1	protein coding
10	ENSGALG00000006445	12413427	12483133	ARNT2	protein coding
10	ENSGALG00000038688	17119378	17280787	ADAMTS17	protein coding
11	ENSGALG00000000059	19086513	19089789		protein coding
11	ENSGALG00000025712	19089858	19093054	DEF8	protein coding
11	ENSGALG00000000129	19064511	19086448	TCF25	protein coding
11	ENSGALG00000005319	12984674	13144905	CDH8	protein coding
11	ENSGALG00000000516	19022589	19054970	FANCA	protein coding
11	ENSGALG00000004949	11034188	11075126	KIAA0355	protein coding
11	ENSGALG00000004943	11030199	11043197	SS18L2	protein coding
11	ENSGALG00000000521	19057727	19063586	SPIRE2	protein coding
11	ENSGALG00000000540	19097873	19105088	GAS8	protein coding
11	ENSGALG00000000528	19093979	19155591	DBNDD1	protein coding
11	ENSGALG00000002407	1604963	1708650	HYDIN	protein coding
12	ENSGALG00000046270	1156711	1252102		protein coding
12	ENSGALG00000030908	3752214	4001595	ATP2B2	protein coding
14	ENSGALG00000002119	14717931	14809857	VPS35L	protein coding
14	ENSGALG00000029817	4588547	4676355		protein coding
14	ENSGALG00000042581	15534743	15562301		lincRNA
23	ENSGALG00000018302	4947355	4947443	gga-mir-30c-1	miRNA
23	ENSGALG00000018301	4946132	4946227	gga-mir-30e	miRNA
23	ENSGALG00000037136	117566	147202	RPS6KA1L	protein coding
23	ENSGALG00000003189	4927211	4955061	NFYC	protein coding

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
25	ENSGALG00000028478	2848558	2856046		protein coding
25	ENSGALG00000040687	2829873	2845968	SNX27	protein coding
25	ENSGALG00000032955	2816337	2828064	TUFT1	protein coding
27	ENSGALG00000003282	5296817	5306850	STAT5B	protein coding
27	ENSGALG00000011485	5280330	5281387	HCRT	protein coding
27	ENSGALG00000003345	5282575	5292696		protein coding
27	ENSGALG00000003333	5292832	5299192	GHDC	protein coding

Chr = Chromosome

Table S 65. Top pairwise Fst values (1%) in Improved Horro and Arabo chickens.

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
1	59250001	59270000	73	0.68	0.57	6.48
1	59230001	59250000	58	0.66	0.52	6.28
1	147080001	147100000	143	0.62	0.49	5.86
1	150950001	150970000	37	0.61	0.44	5.66
1	150960001	150980000	65	0.61	0.49	5.65
1	150970001	150990000	103	0.60	0.49	5.61
1	150940001	150960000	79	0.59	0.47	5.42
1	150980001	151000000	67	0.58	0.43	5.39
1	162450001	162470000	181	0.58	0.29	5.31
1	181220001	181240000	200	0.56	0.30	5.17
1	162440001	162460000	154	0.56	0.33	5.14
1	19420001	19440000	158	0.56	0.44	5.11
1	19220001	19240000	131	0.56	0.39	5.09
1	149980001	150000000	84	0.56	0.47	5.08
1	147070001	147090000	171	0.56	0.38	5.07
1	149960001	149980000	80	0.55	0.47	5.06
1	19230001	19250000	85	0.55	0.42	5.05
1	149970001	149990000	77	0.55	0.47	5.04
1	142920001	142940000	261	0.55	0.30	5.02

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
1	150910001	150930000	112	0.54	0.45	4.91
1	142930001	142950000	270	0.54	0.28	4.87
1	181840001	181860000	285	0.54	0.33	4.86
1	179030001	179050000	332	0.54	0.38	4.86
1	150920001	150940000	111	0.53	0.46	4.83
1	151610001	151630000	59	0.53	0.42	4.82
1	147090001	147110000	178	0.53	0.31	4.78
1	19300001	19320000	172	0.53	0.37	4.78
1	19190001	19210000	124	0.53	0.44	4.77
1	147060001	147080000	199	0.53	0.33	4.75
1	19430001	19450000	105	0.53	0.45	4.74
1	19380001	19400000	68	0.53	0.30	4.73
1	150930001	150950000	96	0.52	0.44	4.72
1	19410001	19430000	127	0.52	0.35	4.71
1	19310001	19330000	120	0.52	0.37	4.70
1	181230001	181250000	171	0.52	0.30	4.68
1	137510001	137530000	318	0.52	0.29	4.66
1	181240001	181260000	154	0.52	0.33	4.64
1	149950001	149970000	69	0.51	0.44	4.61
1	162400001	162420000	209	0.50	0.28	4.47
1	181800001	181820000	292	0.50	0.35	4.46
1	147050001	147070000	191	0.50	0.31	4.45
1	181790001	181810000	198	0.50	0.32	4.39
1	162410001	162430000	232	0.49	0.29	4.39
1	158930001	158950000	106	0.49	0.41	4.39
1	142910001	142930000	287	0.49	0.23	4.37

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
1	181260001	181280000	310	0.49	0.27	4.35
1	150800001	150820000	163	0.49	0.39	4.33
1	179040001	179060000	354	0.49	0.33	4.32
1	150290001	150310000	104	0.49	0.39	4.31
1	181250001	181270000	219	0.49	0.28	4.30
1	142940001	142960000	251	0.49	0.26	4.29
1	47220001	47240000	127	0.49	0.31	4.29
1	59220001	59240000	240	0.49	0.33	4.29
1	177500001	177520000	307	0.49	0.29	4.28
1	19330001	19350000	105	0.48	0.31	4.25
1	19370001	19390000	78	0.48	0.28	4.25
1	137450001	137470000	292	0.48	0.36	4.21
1	162430001	162450000	197	0.48	0.27	4.19
1	180990001	181010000	229	0.48	0.36	4.18
1	56710001	56730000	393	0.47	0.38	4.15
1	137500001	137520000	366	0.47	0.25	4.14
1	181850001	181870000	291	0.47	0.27	4.14
1	151600001	151620000	130	0.47	0.39	4.11
1	181310001	181330000	210	0.47	0.31	4.10
1	19340001	19360000	71	0.47	0.31	4.09
1	158940001	158960000	119	0.47	0.37	4.07
1	150870001	150890000	119	0.46	0.40	4.02
1	154530001	154550000	235	0.46	0.27	4.01
1	162420001	162440000	230	0.46	0.22	4.00
1	150270001	150290000	108	0.46	0.39	3.98
1	19200001	19220000	147	0.46	0.33	3.98

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
1	150280001	150300000	104	0.46	0.37	3.98
1	156410001	156430000	319	0.46	0.29	3.95
1	177550001	177570000	248	0.45	0.32	3.93
1	151560001	151580000	163	0.45	0.35	3.91
1	179050001	179070000	286	0.45	0.30	3.91
1	56740001	56760000	462	0.45	0.38	3.90
1	151550001	151570000	162	0.45	0.34	3.90
1	177330001	177350000	333	0.45	0.33	3.90
1	177170001	177190000	140	0.45	0.25	3.90
1	181780001	181800000	147	0.45	0.28	3.90
1	110320001	110340000	52	0.45	0.24	3.86
1	19240001	19260000	74	0.45	0.36	3.85
1	19320001	19340000	102	0.45	0.29	3.85
1	19170001	19190000	131	0.45	0.39	3.84
1	59260001	59280000	235	0.45	0.34	3.83
1	179020001	179040000	331	0.45	0.27	3.83
1	56750001	56770000	499	0.44	0.39	3.82
1	151690001	151710000	200	0.44	0.32	3.81
1	4410001	4430000	146	0.44	0.25	3.80
1	177540001	177560000	281	0.44	0.30	3.79
1	19460001	19480000	112	0.44	0.34	3.77
1	151620001	151640000	69	0.44	0.30	3.76
1	151590001	151610000	180	0.44	0.35	3.76
1	150790001	150810000	141	0.44	0.34	3.75
1	153300001	153320000	244	0.44	0.30	3.75
1	177490001	177510000	310	0.44	0.27	3.74

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
1	150810001	150830000	134	0.44	0.32	3.73
1	151010001	151030000	140	0.44	0.25	3.71
1	150300001	150320000	94	0.43	0.34	3.70
1	181770001	181790000	247	0.43	0.27	3.70
1	151540001	151560000	108	0.43	0.32	3.69
1	137440001	137460000	318	0.43	0.30	3.69
1	159520001	159540000	97	0.43	0.37	3.68
1	150990001	151010000	109	0.43	0.23	3.68
1	151680001	151700000	184	0.43	0.27	3.67
1	177320001	177340000	293	0.43	0.32	3.64
1	177180001	177200000	165	0.43	0.27	3.63
1	179060001	179080000	302	0.43	0.30	3.62
1	179100001	179120000	261	0.43	0.31	3.61
1	179070001	179090000	246	0.43	0.29	3.61
1	151000001	151020000	155	0.43	0.24	3.61
1	19360001	19380000	112	0.42	0.22	3.58
1	137360001	137380000	306	0.42	0.23	3.58
1	162460001	162480000	214	0.42	0.22	3.55
1	187440001	187460000	331	0.42	0.28	3.55
1	187430001	187450000	310	0.42	0.28	3.55
1	151630001	151650000	85	0.42	0.29	3.54
1	181000001	181020000	316	0.42	0.30	3.54
1	47250001	47270000	521	0.42	0.29	3.51
1	19180001	19200000	103	0.42	0.35	3.51
1	181210001	181230000	249	0.42	0.28	3.51
1	177340001	177360000	337	0.42	0.30	3.49

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
1	141630001	141650000	40	0.42	0.37	3.49
1	19450001	19470000	127	0.42	0.32	3.49
1	56680001	56700000	303	0.41	0.33	3.47
1	56730001	56750000	446	0.41	0.35	3.46
1	19250001	19270000	131	0.41	0.31	3.45
1	56720001	56740000	380	0.41	0.35	3.44
1	143080001	143100000	315	0.41	0.23	3.44
1	69660001	69680000	330	0.41	0.28	3.43
1	151700001	151720000	227	0.41	0.31	3.43
1	84410001	84430000	404	0.41	0.29	3.42
1	141640001	141660000	21	0.41	0.34	3.40
1	182720001	182740000	200	0.41	0.36	3.39
1	137520001	137540000	307	0.41	0.23	3.38
1	179110001	179130000	249	0.41	0.31	3.38
1	177160001	177180000	162	0.41	0.17	3.37
2	149180001	149200000	721	0.70	0.60	6.72
2	21260001	21280000	159	0.70	0.49	6.71
2	149170001	149190000	743	0.69	0.59	6.61
2	149190001	149210000	681	0.67	0.58	6.43
2	21240001	21260000	183	0.67	0.44	6.34
2	21250001	21270000	214	0.66	0.43	6.24
2	149200001	149220000	674	0.65	0.55	6.15
2	149160001	149180000	610	0.65	0.55	6.12
2	149210001	149230000	494	0.64	0.53	6.07
2	149220001	149240000	238	0.64	0.52	5.99
2	21270001	21290000	178	0.63	0.45	5.93

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
2	36650001	36670000	181	0.63	0.46	5.90
2	149150001	149170000	310	0.59	0.45	5.51
2	36640001	36660000	150	0.59	0.44	5.42
2	21980001	22000000	208	0.57	0.45	5.28
2	125510001	125530000	187	0.56	0.45	5.18
2	21880001	21900000	225	0.56	0.48	5.09
2	21990001	22010000	200	0.56	0.41	5.08
2	36660001	36680000	161	0.55	0.32	4.97
2	21230001	21250000	123	0.54	0.37	4.94
2	21970001	21990000	202	0.54	0.45	4.90
2	21820001	21840000	305	0.53	0.39	4.84
2	21870001	21890000	192	0.52	0.40	4.70
2	21830001	21850000	294	0.52	0.37	4.69
2	22140001	22160000	204	0.52	0.42	4.66
2	21960001	21980000	166	0.52	0.43	4.65
2	22150001	22170000	192	0.52	0.37	4.64
2	146070001	146090000	183	0.51	0.33	4.55
2	142470001	142490000	236	0.51	0.35	4.54
2	142320001	142340000	224	0.51	0.29	4.52
2	146060001	146080000	206	0.51	0.32	4.51
2	142910001	142930000	173	0.50	0.26	4.46
2	142290001	142310000	172	0.50	0.33	4.41
2	24060001	24080000	217	0.50	0.37	4.40
2	142460001	142480000	292	0.49	0.35	4.29
2	31300001	31320000	221	0.48	0.32	4.27
2	49890001	49910000	56	0.48	0.29	4.26

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
2	142330001	142350000	202	0.48	0.29	4.24
2	143190001	143210000	224	0.48	0.32	4.21
2	17460001	17480000	339	0.48	0.30	4.19
2	142280001	142300000	226	0.47	0.32	4.16
2	109720001	109740000	171	0.47	0.39	4.13
2	22080001	22100000	244	0.47	0.37	4.13
2	21220001	21240000	206	0.47	0.36	4.11
2	49880001	49900000	85	0.47	0.27	4.10
2	21430001	21450000	196	0.47	0.33	4.08
2	21950001	21970000	172	0.47	0.39	4.07
2	109730001	109750000	173	0.47	0.38	4.07
2	145960001	145980000	225	0.46	0.33	4.04
2	24070001	24090000	210	0.46	0.33	4.02
2	142270001	142290000	218	0.46	0.34	4.01
2	21280001	21300000	242	0.46	0.37	4.01
2	132120001	132140000	234	0.46	0.28	3.99
2	23010001	23030000	234	0.46	0.27	3.99
2	146050001	146070000	201	0.46	0.26	3.96
2	49960001	49980000	202	0.46	0.21	3.95
2	125500001	125520000	247	0.46	0.31	3.95
2	21890001	21910000	235	0.46	0.37	3.95
2	49870001	49890000	151	0.46	0.27	3.95
2	142260001	142280000	287	0.46	0.32	3.94
2	21810001	21830000	298	0.46	0.31	3.94
2	50200001	50220000	98	0.45	0.32	3.92
2	36670001	36690000	137	0.45	0.24	3.92

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
2	17470001	17490000	278	0.45	0.29	3.92
2	149230001	149250000	109	0.45	0.33	3.91
2	20470001	20490000	309	0.45	0.28	3.91
2	146550001	146570000	250	0.45	0.33	3.90
2	145970001	145990000	364	0.45	0.30	3.88
2	49970001	49990000	263	0.45	0.25	3.87
2	51260001	51280000	63	0.45	0.42	3.87
2	24090001	24110000	235	0.45	0.30	3.84
2	49910001	49930000	145	0.45	0.21	3.83
2	146140001	146160000	387	0.45	0.25	3.83
2	49860001	49880000	206	0.45	0.29	3.83
2	24250001	24270000	329	0.45	0.30	3.82
2	51250001	51270000	65	0.44	0.41	3.81
2	49900001	49920000	97	0.44	0.21	3.81
2	36680001	36700000	115	0.44	0.30	3.80
2	104080001	104100000	216	0.44	0.31	3.79
2	142540001	142560000	306	0.44	0.27	3.78
2	143180001	143200000	233	0.44	0.28	3.78
2	20760001	20780000	152	0.44	0.24	3.76
2	125520001	125540000	230	0.44	0.30	3.76
2	22610001	22630000	330	0.44	0.29	3.76
2	22090001	22110000	240	0.44	0.31	3.76
2	142510001	142530000	339	0.44	0.26	3.73
2	21420001	21440000	175	0.44	0.28	3.73
2	49850001	49870000	182	0.44	0.32	3.73
2	36630001	36650000	131	0.43	0.27	3.71

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
2	21210001	21230000	227	0.43	0.34	3.70
2	49980001	50000000	225	0.43	0.25	3.68
2	142800001	142820000	168	0.43	0.22	3.67
2	21650001	21670000	343	0.43	0.32	3.66
2	49840001	49860000	104	0.43	0.35	3.66
2	23510001	23530000	464	0.43	0.21	3.66
2	24240001	24260000	292	0.43	0.27	3.66
2	147350001	147370000	126	0.43	0.34	3.65
2	49990001	50010000	176	0.43	0.30	3.64
2	144850001	144870000	226	0.43	0.29	3.63
2	20460001	20480000	302	0.42	0.27	3.59
2	23280001	23300000	342	0.42	0.30	3.59
2	145940001	145960000	437	0.42	0.22	3.58
2	147360001	147380000	183	0.42	0.35	3.57
2	21840001	21860000	313	0.42	0.30	3.57
2	145980001	146000000	338	0.42	0.27	3.56
2	57720001	57740000	165	0.42	0.33	3.55
2	104090001	104110000	235	0.42	0.32	3.54
2	23370001	23390000	278	0.42	0.29	3.54
2	30810001	30830000	266	0.42	0.25	3.53
2	143160001	143180000	128	0.42	0.30	3.52
2	50630001	50650000	98	0.42	0.32	3.52
2	147380001	147400000	262	0.42	0.29	3.51
2	146040001	146060000	328	0.42	0.27	3.50
2	143170001	143190000	228	0.42	0.29	3.50
2	55120001	55140000	199	0.42	0.29	3.49

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
2	21720001	21740000	249	0.42	0.30	3.49
2	24100001	24120000	222	0.42	0.26	3.49
2	50210001	50230000	80	0.42	0.31	3.49
2	81890001	81910000	86	0.42	0.30	3.49
2	49800001	49820000	171	0.42	0.21	3.49
2	23500001	23520000	463	0.41	0.22	3.48
2	144860001	144880000	223	0.41	0.27	3.48
2	142210001	142230000	220	0.41	0.24	3.47
2	24080001	24100000	231	0.41	0.26	3.47
2	20090001	20110000	168	0.41	0.29	3.46
2	144520001	144540000	204	0.41	0.28	3.46
2	146540001	146560000	295	0.41	0.32	3.46
2	20080001	20100000	204	0.41	0.35	3.46
2	94310001	94330000	120	0.41	0.33	3.45
2	145990001	146010000	294	0.41	0.26	3.44
2	142900001	142920000	133	0.41	0.18	3.44
2	24050001	24070000	261	0.41	0.29	3.44
2	142200001	142220000	227	0.41	0.23	3.42
2	36560001	36580000	66	0.41	0.31	3.41
2	57730001	57750000	143	0.41	0.34	3.41
2	81620001	81640000	138	0.41	0.24	3.41
2	142920001	142940000	176	0.41	0.20	3.41
2	147390001	147410000	250	0.41	0.27	3.41
2	21170001	21190000	243	0.41	0.30	3.40
2	49920001	49940000	145	0.41	0.15	3.40
2	83420001	83440000	133	0.41	0.31	3.40

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
2	36590001	36610000	97	0.41	0.29	3.40
2	142790001	142810000	245	0.41	0.25	3.40
2	24260001	24280000	414	0.41	0.28	3.39
2	23020001	23040000	347	0.41	0.25	3.39
2	149140001	149160000	67	0.41	0.20	3.39
2	142480001	142500000	265	0.41	0.26	3.38
2	49950001	49970000	179	0.41	0.16	3.38
2	78330001	78350000	247	0.41	0.29	3.38
2	36600001	36620000	79	0.40	0.29	3.37
3	90980001	91000000	120	0.57	0.39	5.19
3	90810001	90830000	209	0.56	0.37	5.13
3	84140001	84160000	145	0.50	0.48	4.44
3	84040001	84060000	101	0.50	0.33	4.40
3	83780001	83800000	74	0.49	0.34	4.35
3	84150001	84170000	122	0.49	0.47	4.32
3	84160001	84180000	103	0.49	0.48	4.31
3	84050001	84070000	110	0.48	0.38	4.26
3	90990001	91010000	119	0.48	0.30	4.24
3	83630001	83650000	99	0.47	0.29	4.14
3	79870001	79890000	206	0.46	0.30	4.02
3	84130001	84150000	101	0.46	0.42	3.98
3	96500001	96520000	235	0.45	0.31	3.91
3	83620001	83640000	101	0.45	0.28	3.89
3	78560001	78580000	319	0.44	0.25	3.81
3	5970001	5990000	230	0.44	0.27	3.80
3	37910001	37930000	426	0.44	0.29	3.79

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
3	84170001	84190000	94	0.44	0.40	3.74
3	90820001	90840000	205	0.44	0.29	3.74
3	12410001	12430000	197	0.44	0.18	3.72
3	83770001	83790000	118	0.43	0.34	3.65
3	90800001	90820000	190	0.43	0.32	3.63
3	90620001	90640000	233	0.42	0.24	3.59
3	4700001	4720000	294	0.42	0.23	3.58
3	35260001	35280000	319	0.42	0.30	3.57
3	37920001	37940000	366	0.42	0.27	3.56
3	89680001	89700000	254	0.42	0.29	3.52
3	72010001	72030000	292	0.42	0.31	3.51
3	12640001	12660000	257	0.42	0.30	3.49
3	104620001	104640000	360	0.41	0.24	3.48
3	79860001	79880000	267	0.41	0.27	3.46
3	84030001	84050000	74	0.41	0.23	3.45
3	79800001	79820000	253	0.41	0.29	3.44
3	90970001	90990000	145	0.41	0.29	3.44
3	35250001	35270000	324	0.41	0.29	3.41
3	82370001	82390000	206	0.41	0.22	3.41
3	86440001	86460000	144	0.41	0.27	3.38
3	90950001	90970000	32	0.41	0.34	3.37
4	27910001	27930000	87	0.80	0.68	7.80
4	27890001	27910000	62	0.79	0.62	7.74
4	27880001	27900000	110	0.79	0.63	7.71
4	27900001	27920000	28	0.78	0.57	7.64
4	27870001	27890000	109	0.78	0.47	7.61

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
4	28010001	28030000	38	0.78	0.71	7.61
4	28000001	28020000	30	0.76	0.66	7.45
4	27920001	27940000	110	0.76	0.64	7.43
4	27990001	28010000	26	0.76	0.61	7.40
4	28020001	28040000	43	0.76	0.63	7.36
4	27980001	28000000	21	0.75	0.64	7.28
4	28030001	28050000	84	0.75	0.62	7.25
4	27860001	27880000	83	0.74	0.27	7.22
4	28700001	28720000	146	0.71	0.53	6.81
4	28670001	28690000	127	0.70	0.54	6.74
4	26040001	26060000	107	0.70	0.57	6.67
4	28710001	28730000	117	0.69	0.51	6.61
4	28230001	28250000	131	0.68	0.53	6.51
4	28040001	28060000	118	0.68	0.57	6.46
4	28680001	28700000	149	0.67	0.49	6.36
4	27830001	27850000	52	0.66	0.54	6.31
4	28220001	28240000	164	0.66	0.58	6.31
4	28690001	28710000	156	0.66	0.46	6.30
4	28660001	28680000	90	0.66	0.40	6.27
4	26070001	26090000	177	0.65	0.46	6.16
4	27840001	27860000	51	0.65	0.33	6.16
4	27930001	27950000	77	0.65	0.46	6.09
4	26060001	26080000	206	0.64	0.42	6.07
4	27820001	27840000	47	0.64	0.48	6.02
4	28770001	28790000	108	0.64	0.36	6.01
4	27850001	27870000	54	0.64	0.15	6.00

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
4	28750001	28770000	218	0.63	0.43	5.97
4	26050001	26070000	134	0.63	0.42	5.96
4	28760001	28780000	178	0.63	0.42	5.96
4	28740001	28760000	120	0.63	0.34	5.91
4	27970001	27990000	25	0.62	0.49	5.81
4	28210001	28230000	165	0.61	0.54	5.74
4	26030001	26050000	131	0.61	0.42	5.72
4	28590001	28610000	124	0.60	0.43	5.63
4	27950001	27970000	22	0.60	0.46	5.60
4	28090001	28110000	173	0.60	0.42	5.59
4	28720001	28740000	129	0.59	0.31	5.50
4	28120001	28140000	95	0.59	0.48	5.49
4	28920001	28940000	200	0.59	0.33	5.48
4	28200001	28220000	145	0.59	0.50	5.46
4	26120001	26140000	108	0.59	0.36	5.44
4	28520001	28540000	67	0.59	0.36	5.43
4	28530001	28550000	72	0.59	0.35	5.41
4	28130001	28150000	48	0.58	0.47	5.38
4	28080001	28100000	189	0.58	0.38	5.37
4	27940001	27960000	44	0.58	0.39	5.37
4	28180001	28200000	123	0.58	0.49	5.32
4	28730001	28750000	110	0.58	0.22	5.32
4	28170001	28190000	78	0.58	0.51	5.31
4	28510001	28530000	59	0.58	0.37	5.31
4	27410001	27430000	93	0.57	0.41	5.28
4	28600001	28620000	123	0.57	0.33	5.27

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
4	28190001	28210000	134	0.57	0.47	5.26
4	28160001	28180000	21	0.56	0.53	5.16
4	27810001	27830000	35	0.56	0.31	5.16
4	28050001	28070000	115	0.56	0.51	5.15
4	27330001	27350000	174	0.56	0.40	5.11
4	28810001	28830000	172	0.56	0.22	5.08
4	28800001	28820000	221	0.55	0.27	5.06
4	26080001	26100000	127	0.55	0.39	5.04
4	28540001	28560000	81	0.55	0.27	5.02
4	26110001	26130000	151	0.55	0.36	4.99
4	28780001	28800000	140	0.55	0.24	4.97
4	26410001	26430000	152	0.54	0.28	4.92
4	27960001	27980000	25	0.54	0.44	4.91
4	39730001	39750000	399	0.54	0.39	4.88
4	26020001	26040000	135	0.54	0.31	4.87
4	27800001	27820000	38	0.54	0.24	4.86
4	28110001	28130000	118	0.54	0.40	4.86
4	27760001	27780000	37	0.53	0.29	4.83
4	27790001	27810000	37	0.53	0.29	4.81
4	27750001	27770000	30	0.53	0.28	4.81
4	26010001	26030000	106	0.53	0.23	4.80
4	28060001	28080000	123	0.53	0.43	4.80
4	27400001	27420000	66	0.53	0.34	4.80
4	27720001	27740000	34	0.53	0.36	4.76
4	28500001	28520000	71	0.53	0.38	4.75
4	28930001	28950000	210	0.52	0.32	4.73

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
4	39720001	39740000	338	0.52	0.38	4.70
4	27020001	27040000	149	0.52	0.30	4.68
4	27260001	27280000	130	0.52	0.28	4.68
4	28910001	28930000	148	0.52	0.29	4.66
4	27320001	27340000	118	0.52	0.37	4.65
4	31170001	31190000	207	0.52	0.38	4.64
4	27030001	27050000	149	0.52	0.32	4.63
4	27780001	27800000	23	0.51	0.36	4.61
4	26420001	26440000	148	0.51	0.27	4.61
4	26090001	26110000	136	0.51	0.31	4.60
4	28240001	28260000	117	0.51	0.35	4.58
4	27770001	27790000	25	0.51	0.28	4.55
4	28100001	28120000	138	0.51	0.35	4.55
4	28790001	28810000	186	0.51	0.23	4.54
4	28490001	28510000	54	0.51	0.36	4.54
4	31180001	31200000	248	0.51	0.37	4.53
4	27610001	27630000	78	0.51	0.39	4.53
4	26100001	26120000	153	0.51	0.28	4.53
4	27040001	27060000	110	0.51	0.28	4.53
4	27590001	27610000	119	0.50	0.36	4.50
4	27340001	27360000	163	0.50	0.37	4.50
4	27360001	27380000	133	0.50	0.38	4.50
4	20310001	20330000	49	0.50	0.35	4.49
4	26430001	26450000	165	0.50	0.25	4.49
4	27600001	27620000	95	0.50	0.37	4.48
4	28370001	28390000	77	0.50	0.29	4.47

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
4	28580001	28600000	125	0.50	0.29	4.46
4	49170001	49190000	347	0.50	0.32	4.45
4	25940001	25960000	229	0.50	0.37	4.42
4	25960001	25980000	207	0.50	0.33	4.42
4	28070001	28090000	148	0.50	0.31	4.40
4	25990001	26010000	98	0.50	0.32	4.40
4	25780001	25800000	314	0.50	0.26	4.39
4	25970001	25990000	172	0.49	0.33	4.39
4	19450001	19470000	24	0.49	0.35	4.38
4	20290001	20310000	31	0.49	0.37	4.37
4	20300001	20320000	39	0.49	0.35	4.37
4	26480001	26500000	146	0.49	0.29	4.35
4	28410001	28430000	70	0.49	0.25	4.34
4	25790001	25810000	302	0.49	0.25	4.34
4	28610001	28630000	145	0.49	0.20	4.31
4	27390001	27410000	68	0.49	0.29	4.30
4	27700001	27720000	94	0.49	0.44	4.29
4	28380001	28400000	103	0.49	0.30	4.28
4	27010001	27030000	181	0.48	0.21	4.27
4	19790001	19810000	41	0.48	0.35	4.27
4	27580001	27600000	108	0.48	0.36	4.27
4	27420001	27440000	167	0.48	0.36	4.26
4	25800001	25820000	316	0.48	0.25	4.26
4	27730001	27750000	24	0.48	0.38	4.25
4	27370001	27390000	88	0.48	0.33	4.25
4	26440001	26460000	159	0.48	0.25	4.24

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
4	27710001	27730000	60	0.48	0.37	4.24
4	26490001	26510000	153	0.48	0.28	4.23
4	19850001	19870000	41	0.48	0.35	4.22
4	17960001	17980000	95	0.48	0.30	4.22
4	28420001	28440000	80	0.48	0.30	4.21
4	39740001	39760000	384	0.48	0.36	4.21
4	26810001	26830000	132	0.48	0.28	4.19
4	20320001	20340000	52	0.47	0.26	4.16
4	25770001	25790000	335	0.47	0.28	4.16
4	19610001	19630000	51	0.47	0.33	4.16
4	27690001	27710000	109	0.47	0.43	4.16
4	27350001	27370000	127	0.47	0.35	4.15
4	28350001	28370000	96	0.47	0.34	4.12
4	25950001	25970000	205	0.47	0.32	4.10
4	28430001	28450000	76	0.47	0.32	4.10
4	27740001	27760000	22	0.47	0.30	4.10
4	27250001	27270000	152	0.47	0.28	4.09
4	27460001	27480000	129	0.47	0.32	4.08
4	28360001	28380000	85	0.47	0.30	4.08
4	17970001	17990000	71	0.47	0.33	4.06
4	19550001	19570000	32	0.47	0.31	4.05
4	28400001	28420000	80	0.46	0.28	4.04
4	17980001	18000000	73	0.46	0.29	4.03
4	27510001	27530000	121	0.46	0.34	4.03
4	19860001	19880000	46	0.46	0.31	4.02
4	27170001	27190000	134	0.46	0.32	4.01

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
4	20280001	20300000	39	0.46	0.25	3.99
4	28820001	28840000	118	0.46	0.17	3.99
4	20270001	20290000	57	0.46	0.24	3.98
4	5060001	5080000	353	0.46	0.26	3.97
4	2240001	2260000	402	0.46	0.35	3.97
4	25930001	25950000	210	0.46	0.33	3.94
4	25840001	25860000	247	0.45	0.27	3.93
4	27450001	27470000	129	0.45	0.32	3.93
4	25980001	26000000	146	0.45	0.31	3.92
4	19530001	19550000	33	0.45	0.29	3.92
4	19840001	19860000	38	0.45	0.31	3.91
4	20260001	20280000	47	0.45	0.26	3.90
4	19780001	19800000	55	0.45	0.29	3.87
4	19460001	19480000	35	0.45	0.30	3.87
4	19440001	19460000	36	0.45	0.33	3.87
4	27620001	27640000	84	0.45	0.36	3.87
4	28630001	28650000	155	0.45	0.16	3.86
4	19670001	19690000	57	0.45	0.33	3.86
4	19520001	19540000	52	0.45	0.30	3.85
4	19700001	19720000	25	0.45	0.29	3.85
4	27180001	27200000	187	0.45	0.27	3.84
4	28280001	28300000	149	0.45	0.28	3.83
4	49180001	49200000	323	0.44	0.29	3.82
4	83500001	83520000	326	0.44	0.30	3.81
4	25850001	25870000	254	0.44	0.22	3.79
4	27470001	27490000	104	0.44	0.29	3.79

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
4	27520001	27540000	87	0.44	0.34	3.77
4	19560001	19580000	48	0.44	0.28	3.76
4	28620001	28640000	162	0.44	0.16	3.76
4	2230001	2250000	333	0.44	0.31	3.75
4	27060001	27080000	192	0.44	0.23	3.75
4	28340001	28360000	113	0.44	0.31	3.74
4	28390001	28410000	110	0.44	0.29	3.74
4	26500001	26520000	137	0.44	0.25	3.71
4	26560001	26580000	122	0.44	0.28	3.71
4	19580001	19600000	67	0.43	0.28	3.70
4	28650001	28670000	117	0.43	0.16	3.70
4	25880001	25900000	241	0.43	0.20	3.69
4	19940001	19960000	66	0.43	0.28	3.69
4	28460001	28480000	45	0.43	0.22	3.68
4	25910001	25930000	244	0.43	0.26	3.68
4	19830001	19850000	42	0.43	0.26	3.68
4	26000001	26020000	64	0.43	0.11	3.67
4	26800001	26820000	136	0.43	0.24	3.67
4	26780001	26800000	96	0.43	0.23	3.67
4	83490001	83510000	446	0.43	0.29	3.67
4	26700001	26720000	169	0.43	0.22	3.66
4	27120001	27140000	132	0.43	0.29	3.66
4	27160001	27180000	119	0.43	0.32	3.65
4	26690001	26710000	151	0.43	0.23	3.65
4	19770001	19790000	50	0.43	0.27	3.65
4	26720001	26740000	148	0.43	0.25	3.63

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
4	83540001	83560000	234	0.43	0.32	3.63
4	28440001	28460000	60	0.43	0.24	3.63
4	19820001	19840000	53	0.43	0.25	3.62
4	19410001	19430000	41	0.43	0.25	3.62
4	27070001	27090000	199	0.43	0.24	3.62
4	26400001	26420000	153	0.43	0.16	3.62
4	19680001	19700000	76	0.43	0.28	3.62
4	26770001	26790000	129	0.43	0.22	3.61
4	2250001	2270000	431	0.43	0.32	3.61
4	26820001	26840000	149	0.43	0.25	3.61
4	19470001	19490000	58	0.42	0.27	3.60
4	26470001	26490000	121	0.42	0.23	3.59
4	19570001	19590000	68	0.42	0.27	3.59
4	26130001	26150000	134	0.42	0.10	3.58
4	28840001	28860000	109	0.42	0.27	3.58
4	28290001	28310000	169	0.42	0.28	3.58
4	28640001	28660000	152	0.42	0.15	3.58
4	83530001	83550000	250	0.42	0.28	3.55
4	17950001	17970000	104	0.42	0.24	3.55
4	19660001	19680000	62	0.42	0.26	3.54
4	19620001	19640000	68	0.42	0.25	3.51
4	27110001	27130000	149	0.42	0.27	3.51
4	19950001	19970000	67	0.42	0.27	3.50
4	82350001	82370000	365	0.42	0.27	3.50
4	27500001	27520000	84	0.42	0.30	3.49
4	19600001	19620000	47	0.42	0.26	3.49

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
4	27560001	27580000	111	0.41	0.32	3.48
4	26840001	26860000	177	0.41	0.24	3.48
4	19690001	19710000	67	0.41	0.26	3.48
4	19540001	19560000	22	0.41	0.24	3.47
4	20650001	20670000	169	0.41	0.26	3.47
4	26710001	26730000	152	0.41	0.23	3.47
4	29000001	29020000	278	0.41	0.22	3.47
4	27570001	27590000	100	0.41	0.32	3.46
4	28550001	28570000	106	0.41	0.16	3.46
4	4100001	4120000	259	0.41	0.25	3.46
4	19590001	19610000	52	0.41	0.26	3.44
4	25900001	25920000	140	0.41	0.28	3.44
4	19870001	19890000	56	0.41	0.27	3.44
4	26680001	26700000	118	0.41	0.20	3.43
4	27440001	27460000	154	0.41	0.22	3.43
4	25870001	25890000	261	0.41	0.20	3.43
4	28560001	28580000	136	0.41	0.16	3.42
4	27550001	27570000	119	0.41	0.32	3.42
4	20560001	20580000	151	0.41	0.21	3.41
4	28450001	28470000	62	0.41	0.21	3.41
4	25830001	25850000	270	0.41	0.24	3.41
4	26880001	26900000	139	0.41	0.23	3.41
4	39750001	39770000	339	0.41	0.32	3.41
4	29010001	29030000	265	0.41	0.22	3.41
4	19510001	19530000	59	0.41	0.25	3.39
4	26870001	26890000	154	0.41	0.22	3.39

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
4	5070001	5090000	382	0.41	0.22	3.38
4	19800001	19820000	49	0.41	0.27	3.37
4	27220001	27240000	196	0.41	0.23	3.37
5	23340001	23360000	167	0.64	0.50	5.99
5	23350001	23370000	173	0.63	0.55	5.91
5	26450001	26470000	191	0.62	0.45	5.75
5	15310001	15330000	196	0.61	0.37	5.74
5	15320001	15340000	299	0.60	0.40	5.63
5	15330001	15350000	311	0.59	0.37	5.51
5	15300001	15320000	245	0.58	0.28	5.39
5	15340001	15360000	259	0.58	0.34	5.37
5	25910001	25930000	219	0.58	0.35	5.37
5	15290001	15310000	253	0.58	0.28	5.33
5	19810001	19830000	60	0.58	0.41	5.30
5	23690001	23710000	164	0.57	0.48	5.29
5	25930001	25950000	254	0.57	0.32	5.29
5	16790001	16810000	315	0.57	0.25	5.28
5	25920001	25940000	238	0.57	0.34	5.26
5	23330001	23350000	113	0.57	0.42	5.22
5	26170001	26190000	245	0.57	0.41	5.21
5	26460001	26480000	251	0.56	0.37	5.18
5	23320001	23340000	111	0.56	0.39	5.11
5	25940001	25960000	201	0.56	0.30	5.08
5	25900001	25920000	239	0.56	0.32	5.08
5	23310001	23330000	203	0.55	0.32	5.07
5	15420001	15440000	383	0.55	0.31	5.02

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
5	16780001	16800000	412	0.55	0.26	4.97
5	19800001	19820000	111	0.54	0.38	4.94
5	16800001	16820000	249	0.54	0.27	4.94
5	15430001	15450000	356	0.54	0.32	4.91
5	25890001	25910000	174	0.54	0.28	4.91
5	23360001	23380000	180	0.54	0.47	4.88
5	23610001	23630000	270	0.54	0.37	4.87
5	16930001	16950000	404	0.54	0.27	4.85
5	16920001	16940000	403	0.54	0.29	4.85
5	26180001	26200000	254	0.54	0.37	4.84
5	15240001	15260000	305	0.53	0.32	4.82
5	25430001	25450000	264	0.53	0.35	4.81
5	23300001	23320000	275	0.53	0.29	4.78
5	21780001	21800000	207	0.53	0.35	4.76
5	23820001	23840000	226	0.53	0.42	4.76
5	25440001	25460000	363	0.53	0.35	4.76
5	23620001	23640000	269	0.53	0.33	4.74
5	23420001	23440000	186	0.53	0.40	4.74
5	5550001	5570000	351	0.53	0.35	4.73
5	15580001	15600000	380	0.53	0.30	4.73
5	22960001	22980000	125	0.52	0.41	4.72
5	21050001	21070000	160	0.52	0.41	4.71
5	16770001	16790000	378	0.52	0.25	4.69
5	23410001	23430000	215	0.52	0.37	4.67
5	23390001	23410000	140	0.52	0.33	4.67
5	15570001	15590000	369	0.52	0.27	4.65

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
5	22950001	22970000	108	0.52	0.44	4.65
5	25880001	25900000	130	0.52	0.27	4.64
5	2320001	2340000	53	0.52	0.45	4.62
5	24000001	24020000	172	0.52	0.34	4.62
5	2310001	2330000	96	0.51	0.46	4.61
5	21820001	21840000	326	0.51	0.28	4.61
5	14090001	14110000	362	0.51	0.30	4.60
5	23680001	23700000	184	0.51	0.35	4.58
5	5540001	5560000	279	0.51	0.34	4.57
5	21000001	21020000	84	0.51	0.39	4.56
5	15410001	15430000	282	0.51	0.26	4.56
5	16910001	16930000	319	0.51	0.29	4.55
5	23400001	23420000	148	0.51	0.33	4.54
5	21810001	21830000	358	0.51	0.30	4.52
5	21120001	21140000	173	0.51	0.41	4.52
5	23700001	23720000	174	0.50	0.41	4.50
5	2300001	2320000	84	0.50	0.43	4.50
5	21790001	21810000	255	0.50	0.32	4.48
5	26160001	26180000	289	0.50	0.31	4.48
5	15350001	15370000	326	0.50	0.27	4.47
5	23170001	23190000	314	0.50	0.34	4.46
5	15520001	15540000	456	0.50	0.28	4.45
5	15560001	15580000	313	0.50	0.28	4.45
5	23600001	23620000	132	0.50	0.34	4.45
5	2290001	2310000	63	0.50	0.42	4.44
5	25870001	25890000	130	0.50	0.32	4.44

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
5	16830001	16850000	431	0.50	0.30	4.43
5	15460001	15480000	306	0.50	0.27	4.42
5	16310001	16330000	218	0.50	0.31	4.42
5	26120001	26140000	195	0.50	0.38	4.42
5	15370001	15390000	350	0.50	0.28	4.39
5	5560001	5580000	364	0.49	0.35	4.38
5	27710001	27730000	241	0.49	0.34	4.37
5	15280001	15300000	235	0.49	0.20	4.37
5	16760001	16780000	378	0.49	0.22	4.36
5	15230001	15250000	352	0.49	0.30	4.34
5	26310001	26330000	193	0.49	0.33	4.33
5	14080001	14100000	406	0.49	0.28	4.31
5	15190001	15210000	342	0.49	0.23	4.29
5	15850001	15870000	225	0.49	0.27	4.29
5	2280001	2300000	63	0.49	0.41	4.28
5	15360001	15380000	363	0.49	0.27	4.28
5	15590001	15610000	361	0.49	0.27	4.28
5	15550001	15570000	373	0.48	0.27	4.27
5	23790001	23810000	146	0.48	0.43	4.27
5	15470001	15490000	318	0.48	0.26	4.26
5	21010001	21030000	127	0.48	0.34	4.26
5	23810001	23830000	195	0.48	0.38	4.24
5	25850001	25870000	250	0.48	0.28	4.24
5	15510001	15530000	452	0.48	0.25	4.24
5	15480001	15500000	344	0.48	0.25	4.22
5	15450001	15470000	264	0.48	0.21	4.22

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
5	15250001	15270000	332	0.48	0.27	4.21
5	25760001	25780000	182	0.48	0.27	4.19
5	22940001	22960000	106	0.48	0.37	4.19
5	15200001	15220000	327	0.48	0.29	4.19
5	24010001	24030000	224	0.48	0.30	4.17
5	25960001	25980000	223	0.47	0.25	4.16
5	21110001	21130000	255	0.47	0.40	4.15
5	23560001	23580000	320	0.47	0.29	4.14
5	16560001	16580000	415	0.47	0.28	4.13
5	16820001	16840000	482	0.47	0.29	4.12
5	23590001	23610000	128	0.47	0.32	4.12
5	15440001	15460000	290	0.47	0.22	4.12
5	20620001	20640000	183	0.47	0.37	4.12
5	16840001	16860000	208	0.47	0.26	4.11
5	22350001	22370000	161	0.47	0.32	4.10
5	22970001	22990000	246	0.47	0.30	4.08
5	15490001	15510000	364	0.47	0.25	4.07
5	15380001	15400000	312	0.47	0.26	4.07
5	22930001	22950000	97	0.46	0.28	4.05
5	44470001	44490000	203	0.46	0.33	4.04
5	16730001	16750000	219	0.46	0.28	4.03
5	21830001	21850000	244	0.46	0.27	4.02
5	16320001	16340000	297	0.46	0.28	4.01
5	25860001	25880000	160	0.46	0.27	4.01
5	15540001	15560000	416	0.46	0.25	4.00
5	26040001	26060000	335	0.46	0.31	4.00

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
5	20030001	20050000	162	0.46	0.38	3.99
5	16810001	16830000	411	0.46	0.27	3.99
5	16740001	16760000	382	0.46	0.27	3.99
5	27720001	27740000	253	0.46	0.26	3.98
5	16940001	16960000	377	0.46	0.24	3.98
5	19790001	19810000	109	0.46	0.33	3.97
5	16960001	16980000	254	0.46	0.25	3.97
5	15530001	15550000	428	0.46	0.25	3.96
5	21800001	21820000	268	0.46	0.29	3.96
5	15220001	15240000	371	0.45	0.27	3.94
5	2260001	2280000	62	0.45	0.28	3.93
5	18500001	18520000	296	0.45	0.28	3.93
5	16900001	16920000	195	0.45	0.23	3.91
5	2130001	2150000	60	0.45	0.33	3.91
5	27150001	27170000	286	0.45	0.26	3.91
5	26190001	26210000	292	0.45	0.31	3.91
5	2140001	2160000	75	0.45	0.19	3.91
5	25750001	25770000	206	0.45	0.32	3.90
5	26320001	26340000	217	0.45	0.35	3.89
5	2270001	2290000	69	0.45	0.32	3.88
5	15600001	15620000	391	0.45	0.24	3.88
5	25780001	25800000	233	0.45	0.27	3.88
5	15400001	15420000	267	0.45	0.23	3.87
5	23290001	23310000	310	0.45	0.24	3.86
5	15210001	15230000	314	0.45	0.25	3.86
5	23650001	23670000	212	0.45	0.34	3.86

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
5	16750001	16770000	422	0.45	0.23	3.85
5	23430001	23450000	232	0.45	0.30	3.84
5	2240001	2260000	57	0.45	0.34	3.84
5	16550001	16570000	385	0.45	0.25	3.84
5	2250001	2270000	54	0.45	0.32	3.83
5	25840001	25860000	288	0.44	0.27	3.82
5	15180001	15200000	312	0.44	0.18	3.81
5	15390001	15410000	318	0.44	0.25	3.79
5	24030001	24050000	160	0.44	0.31	3.79
5	16330001	16350000	274	0.44	0.29	3.77
5	16300001	16320000	237	0.44	0.26	3.77
5	25970001	25990000	229	0.44	0.29	3.77
5	15500001	15520000	400	0.44	0.22	3.75
5	15260001	15280000	301	0.44	0.23	3.74
5	21080001	21100000	264	0.44	0.34	3.74
5	35130001	35150000	167	0.44	0.33	3.74
5	15610001	15630000	404	0.44	0.25	3.73
5	2230001	2250000	63	0.44	0.31	3.72
5	5530001	5550000	152	0.44	0.30	3.72
5	21060001	21080000	182	0.44	0.33	3.71
5	14070001	14090000	463	0.43	0.25	3.70
5	22340001	22360000	166	0.43	0.29	3.70
5	21770001	21790000	201	0.43	0.35	3.69
5	16970001	16990000	283	0.43	0.26	3.68
5	2150001	2170000	103	0.43	0.21	3.68
5	25770001	25790000	214	0.43	0.23	3.68

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
5	10460001	10480000	262	0.43	0.32	3.67
5	22800001	22820000	240	0.43	0.28	3.66
5	14990001	15010000	62	0.43	0.20	3.66
5	15700001	15720000	310	0.43	0.25	3.66
5	5390001	5410000	296	0.43	0.23	3.65
5	16540001	16560000	450	0.43	0.24	3.64
5	22790001	22810000	208	0.43	0.26	3.63
5	21760001	21780000	291	0.43	0.32	3.63
5	25240001	25260000	187	0.43	0.30	3.63
5	45110001	45130000	329	0.43	0.33	3.63
5	19760001	19780000	180	0.43	0.35	3.62
5	26440001	26460000	142	0.43	0.15	3.61
5	23570001	23590000	291	0.43	0.24	3.60
5	21890001	21910000	234	0.42	0.25	3.59
5	27160001	27180000	256	0.42	0.27	3.57
5	18690001	18710000	356	0.42	0.23	3.57
5	27210001	27230000	267	0.42	0.28	3.56
5	23670001	23690000	185	0.42	0.27	3.56
5	27500001	27520000	159	0.42	0.29	3.56
5	21920001	21940000	266	0.42	0.27	3.56
5	21100001	21120000	310	0.42	0.35	3.55
5	2120001	2140000	74	0.42	0.33	3.55
5	23580001	23600000	249	0.42	0.27	3.55
5	23830001	23850000	279	0.42	0.29	3.55
5	25950001	25970000	237	0.42	0.20	3.55
5	27140001	27160000	296	0.42	0.27	3.54

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
5	2160001	2180000	59	0.42	0.25	3.53
5	25450001	25470000	335	0.42	0.31	3.53
5	21020001	21040000	186	0.42	0.29	3.53
5	14100001	14120000	389	0.42	0.27	3.52
5	37410001	37430000	233	0.42	0.30	3.52
5	18570001	18590000	206	0.42	0.22	3.52
5	19770001	19790000	155	0.42	0.34	3.52
5	16460001	16480000	247	0.42	0.31	3.52
5	16530001	16550000	484	0.42	0.25	3.51
5	21880001	21900000	289	0.42	0.25	3.51
5	23510001	23530000	173	0.42	0.27	3.51
5	18510001	18530000	265	0.42	0.27	3.51
5	25150001	25170000	291	0.42	0.23	3.50
5	16270001	16290000	325	0.42	0.21	3.49
5	22140001	22160000	373	0.42	0.24	3.49
5	14150001	14170000	292	0.42	0.24	3.49
5	15270001	15290000	273	0.41	0.17	3.48
5	21040001	21060000	143	0.41	0.32	3.48
5	26150001	26170000	248	0.41	0.25	3.48
5	35430001	35450000	163	0.41	0.26	3.46
5	2190001	2210000	93	0.41	0.33	3.45
5	18560001	18580000	175	0.41	0.22	3.45
5	23660001	23680000	191	0.41	0.31	3.44
5	2040001	2060000	123	0.41	0.31	3.44
5	16570001	16590000	424	0.41	0.23	3.44
5	23780001	23800000	177	0.41	0.35	3.44

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
5	2100001	2120000	119	0.41	0.36	3.43
5	25250001	25270000	214	0.41	0.30	3.42
5	45120001	45140000	326	0.41	0.31	3.42
5	22860001	22880000	161	0.41	0.33	3.42
5	28000001	28020000	327	0.41	0.27	3.42
5	2110001	2130000	82	0.41	0.35	3.41
5	44460001	44480000	249	0.41	0.28	3.41
5	15170001	15190000	309	0.41	0.23	3.41
5	25790001	25810000	269	0.41	0.35	3.41
5	23550001	23570000	338	0.41	0.25	3.41
5	21900001	21920000	289	0.41	0.23	3.41
5	2220001	2240000	66	0.41	0.30	3.40
5	26130001	26150000	184	0.41	0.32	3.40
5	2090001	2110000	118	0.41	0.35	3.40
5	22850001	22870000	98	0.41	0.28	3.40
5	13980001	14000000	175	0.41	0.17	3.39
5	2200001	2220000	82	0.41	0.30	3.39
5	5570001	5590000	349	0.41	0.27	3.39
5	22200001	22220000	316	0.41	0.21	3.38
5	23160001	23180000	325	0.41	0.29	3.37
5	26280001	26300000	119	0.41	0.30	3.37
7	31730001	31750000	307	0.45	0.20	3.89
8	15490001	15510000	114	0.71	0.60	6.79
8	15480001	15500000	127	0.64	0.44	5.98
8	15500001	15520000	130	0.61	0.49	5.73
8	15430001	15450000	230	0.54	0.28	4.93

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
8	15440001	15460000	221	0.50	0.27	4.42
8	15510001	15530000	142	0.49	0.34	4.36
8	15530001	15550000	187	0.48	0.33	4.24
8	15540001	15560000	178	0.47	0.32	4.13
8	22420001	22440000	208	0.47	0.31	4.09
8	15520001	15540000	168	0.46	0.31	4.01
8	15450001	15470000	183	0.45	0.25	3.89
8	22560001	22580000	205	0.45	0.30	3.85
8	22550001	22570000	190	0.42	0.28	3.60
8	15420001	15440000	223	0.42	0.22	3.57
8	15460001	15480000	169	0.41	0.22	3.45
9	13800001	13820000	348	0.44	0.31	3.73
10	12450001	12470000	165	0.63	0.40	5.93
10	12460001	12480000	164	0.59	0.35	5.47
10	12440001	12460000	160	0.57	0.37	5.18
10	12480001	12500000	208	0.56	0.39	5.13
10	12470001	12490000	182	0.55	0.37	5.06
10	12420001	12440000	290	0.50	0.29	4.45
10	16750001	16770000	252	0.49	0.31	4.30
10	12410001	12430000	249	0.48	0.26	4.26
10	12430001	12450000	237	0.48	0.27	4.17
10	16740001	16760000	255	0.43	0.28	3.60
10	2610001	2630000	347	0.42	0.24	3.56
10	2620001	2640000	293	0.42	0.24	3.53
10	610001	630000	102	0.42	0.26	3.53
10	600001	620000	115	0.42	0.27	3.49

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
11	19050001	19070000	272	0.59	0.39	5.47
11	19060001	19080000	242	0.53	0.39	4.75
11	13520001	13540000	175	0.52	0.45	4.70
11	19070001	19090000	229	0.51	0.36	4.52
11	19040001	19060000	278	0.47	0.32	4.08
11	13530001	13550000	151	0.43	0.40	3.70
11	13510001	13530000	150	0.43	0.36	3.69
11	4650001	4670000	272	0.42	0.25	3.49
11	12980001	13000000	149	0.41	0.34	3.40
12	3860001	3880000	213	0.54	0.40	4.90
12	3850001	3870000	172	0.49	0.38	4.37
12	3870001	3890000	245	0.48	0.31	4.17
12	3880001	3900000	238	0.43	0.26	3.63
13	520001	540000	22	0.47	0.45	4.09
13	530001	550000	22	0.47	0.45	4.09
13	13690001	13710000	188	0.41	0.26	3.44
14	3850001	3870000	203	0.49	0.30	4.35
14	3540001	3560000	162	0.48	0.33	4.19
14	3860001	3880000	180	0.44	0.30	3.75
14	3550001	3570000	194	0.43	0.31	3.66
14	3530001	3550000	115	0.42	0.29	3.54
14	3880001	3900000	217	0.41	0.31	3.44
14	3890001	3910000	286	0.41	0.29	3.39
15	7270001	7290000	318	0.51	0.26	4.54
15	7280001	7300000	288	0.48	0.26	4.18
15	7250001	7270000	391	0.41	0.20	3.45

Chromosome	Window start	Window end	SNP (N)	Weighted Fst	Mean Fst	ZFst
15	7260001	7280000	401	0.41	0.18	3.39
17	2670001	2690000	309	0.45	0.29	3.84
17	1070001	1090000	105	0.43	0.34	3.60
20	4720001	4740000	297	0.42	0.24	3.57
20	4710001	4730000	368	0.42	0.24	3.54
23	4540001	4560000	340	0.42	0.25	3.52
27	5280001	5300000	168	0.45	0.25	3.85
27	5270001	5290000	207	0.43	0.23	3.69
27	4090001	4110000	114	0.43	0.29	3.63
27	5370001	5390000	98	0.43	0.27	3.60

N = count

Table S 66. List of candidate genes in |Improved Horro and Arabo chickens.

Chromosome	Gene start (bp)	Gene end (bp)	Gene stable ID	Gene type	Gene name
1	59245579	59246586	ENSGALG00000044624	protein coding	
1	180999373	180999454	ENSGALG00000025213	miRNA	gga-mir-1709
1	177513346	177560920	ENSGALG00000017119	protein coding	TNFRSF19
1	56693093	56705912	ENSGALG00000012847	protein coding	
1	181192418	181414573	ENSGALG00000038995	protein coding	GRIA4
1	56754302	56787545	ENSGALG00000035108	protein coding	KDM7A
1	56680591	56689353	ENSGALG00000034511	protein coding	
1	137351599	137382930	ENSGALG00000016824	protein coding	TMCO3
1	182684536	182765393	ENSGALG00000038154	protein coding	YAP1
1	4402132	4591692	ENSGALG00000029270	protein coding	GATA3
1	179051034	179094239	ENSGALG00000017139	protein coding	
1	59237872	59238879	ENSGALG00000045031	protein coding	
1	59241726	59242732	ENSGALG00000044524	protein coding	
1	137439551	137445352	ENSGALG00000046372	protein coding	
1	137487513	137505777	ENSGALG00000037697	protein coding	LAMP1
1	146527090	147094328	ENSGALG00000016900	protein coding	GPC6
1	47186191	47253542	ENSGALG00000011557	protein coding	UHRF1BP1L
1	137511432	137545754	ENSGALG00000016830	protein coding	CUL4A
1	47268108	47299064	ENSGALG00000011569	protein coding	SCYL2
1	47183349	47267032	ENSGALG00000040976	protein coding	ACTR6
1	110323165	110332874	ENSGALG00000045726	protein coding	

Chromosome	Gene start (bp)	Gene end (bp)	Gene stable ID	Gene type	Gene name
1	110334367	110341333	ENSGALG00000019171	protein coding	C1H21ORF33
1	177503653	177503754	ENSGALG00000025608	snRNA	RF00026
1	137458314	137486611	ENSGALG00000016828	protein coding	GRTP1
1	59249433	59250440	ENSGALG00000044959	protein coding	
1	59253286	59254293	ENSGALG00000046239	protein coding	
1	59257140	59258147	ENSGALG00000045433	protein coding	
1	59164015	59224210	ENSGALG00000012934	protein coding	
1	177160927	177162801	ENSGALG00000027868	protein coding	AMER2
1	177430969	177493253	ENSGALG00000017118	protein coding	MIPEP
1	162382843	162527048	ENSGALG00000016937	protein coding	DIAPH3
1	179104456	179142555	ENSGALG00000043421	protein coding	
1	150234073	150532403	ENSGALG00000032339	lincRNA	
1	153246824	153303855	ENSGALG00000036877	lincRNA	
1	159526738	159744910	ENSGALG00000040093	lincRNA	
1	177505128	177506167	ENSGALG00000035746	lincRNA	
1	181770866	181805885	ENSGALG00000033716	lincRNA	
2	23387591	23424059	ENSGALG00000035994	protein coding	
2	20364201	20463104	ENSGALG00000008747	protein coding	ITGA8
2	104089460	104089532	ENSGALG00000025572	miRNA	gga-mir-1597
2	24156138	24250062	ENSGALG00000009728	protein coding	SLC25A13
2	144646756	144875068	ENSGALG00000038022	protein coding	COL22A1
2	22978146	23047300	ENSGALG00000009500	protein coding	VPS50
2	145815693	145960326	ENSGALG00000031741	protein coding	PTK2
2	132121027	132231350	ENSGALG00000030030	protein coding	RSPO2
2	21669403	21678883	ENSGALG00000009006	protein coding	
2	50150482	50280221	ENSGALG00000031758	protein coding	SUGCT
2	21710551	21734535	ENSGALG00000009026	protein coding	
2	31211304	31319341	ENSGALG00000010961	protein coding	IGF2BP3
2	21877225	22125099	ENSGALG00000009062	protein coding	CDK14
2	146149257	146178507	ENSGALG00000034971	protein coding	SLC45A4
2	17452004	17513814	ENSGALG00000007864	protein coding	ARMC3
2	49640512	49897096	ENSGALG00000031713	protein coding	POU6F2
2	49979496	49987966	ENSGALG00000043636	protein coding	YAE1D1
2	21736604	21737002	ENSGALG00000032592	protein coding	FAM237B
2	22162541	22164687	ENSGALG00000009064	protein coding	FZD1
2	22587398	22642927	ENSGALG00000031917	protein coding	ANKIB1
2	149141562	149141858	ENSGALG00000036414	protein coding	
2	49987976	50001040	ENSGALG00000037112	protein coding	
2	142197114	142221622	ENSGALG00000037773	protein coding	ST3GAL1
2	149145028	149145324	ENSGALG00000029325	protein coding	
2	147222471	147418330	ENSGALG00000037014	protein coding	TSNARE1
2	83340744	83708432	ENSGALG00000013124	protein coding	FHOD3
2	149148660	149148956	ENSGALG00000030191	protein coding	

Chromosome	Gene start (bp)	Gene end (bp)	Gene stable ID	Gene type	Gene name
2	23985830	24151767	ENSGALG00000009722	protein coding	DYNC1I1
2	149152445	149152741	ENSGALG00000034333	protein coding	
2	149228059	149229441	ENSGALG00000039346	protein coding	
2	30714422	30862920	ENSGALG00000034024	protein coding	RAPGEF5
2	20027818	20125211	ENSGALG00000040891	protein coding	RSU1
2	103906763	104138860	ENSGALG00000015112	protein coding	ZNF521
2	143191899	143269024	ENSGALG00000031519	protein coding	KHDRBS3
2	20693000	20781828	ENSGALG00000008912	protein coding	ABCB1
3	104621983	104668401	ENSGALG00000016500	protein coding	FKBP1B
3	12273168	12439182	ENSGALG00000009158	protein coding	CDC42BPA
3	79870059	79870168	ENSGALG00000025861	miRNA	gga-mir-6670
3	37916515	37937367	ENSGALG00000040000	protein coding	ERO1B
3	86406473	86714063	ENSGALG00000016276	protein coding	KHDRBS2
3	83576272	83636038	ENSGALG00000030872	protein coding	
3	78537400	78582981	ENSGALG00000015864	protein coding	IBTK
3	35235950	35336239	ENSGALG00000010713	protein coding	SDCCAG8
3	79785429	79884137	ENSGALG00000015889	protein coding	PHIP
3	83723661	83990345	ENSGALG00000016176	protein coding	
3	82215093	82512310	ENSGALG00000015944	protein coding	RIMS1
3	96512108	96596917	ENSGALG00000016419	protein coding	ASAP2
3	12614967	12687678	ENSGALG00000009057	protein coding	TASP1
3	5940896	6020972	ENSGALG00000035400	lincRNA	
4	83480038	83562645	ENSGALG00000015692	protein coding	POLN
4	20654247	20654356	ENSGALG00000027439	miRNA	
4	31172411	31172583	ENSGALG00000028077	misc_RNA	RF02271
4	19460437	19460523	ENSGALG00000042586	miRNA	
4	19548868	19548950	ENSGALG00000032953	miRNA	
4	2209876	2231355	ENSGALG00000005425	protein coding	OGT
4	39752033	39762452	ENSGALG00000020210	protein coding	CENPU
4	2232118	2260037	ENSGALG00000005464	protein coding	
4	19424229	19426802	ENSGALG00000009192	protein coding	SLITRK2
4	5049715	5062317	ENSGALG00000006513	protein coding	F9
4	2262230	2272389	ENSGALG00000005475	protein coding	RHOGL
4	5064752	5112915	ENSGALG00000006562	protein coding	MCF2
4	4097689	4105863	ENSGALG00000006108	protein coding	FAM122B
4	4107645	4121192	ENSGALG00000006127	protein coding	FAM122A
4	39762374	39778389	ENSGALG00000010636	protein coding	PRIMPOL
4	39713691	39752253	ENSGALG00000010628	protein coding	ACSL1
4	27095819	27127946	ENSGALG00000009719	protein coding	PCDH10
4	20559675	20561135	ENSGALG00000009276	protein coding	LRAT
4	31100895	31177614	ENSGALG00000009948	protein coding	HHIP
4	19392907	19563891	ENSGALG00000033107	lincRNA	
4	19504112	19511619	ENSGALG00000033380	lincRNA	

Chromosome	Gene start (bp)	Gene end (bp)	Gene stable ID	Gene type	Gene name
4	19541886	19542585	ENSGALG00000041824	lincRNA	
4	19819071	19857159	ENSGALG00000039736	lincRNA	
4	19873184	19873825	ENSGALG00000039492	lincRNA	
4	25900254	25900939	ENSGALG00000030400	lincRNA	
4	26689975	26702258	ENSGALG00000032689	lincRNA	
4	27043314	27051634	ENSGALG00000029613	lincRNA	
4	27396660	27628525	ENSGALG00000032527	lincRNA	
4	27600624	27601331	ENSGALG00000031625	lincRNA	
4	27788185	27825157	ENSGALG00000035886	lincRNA	
4	28160838	28173463	ENSGALG00000036104	lincRNA	
4	28904779	28987118	ENSGALG00000034709	lincRNA	
5	18540733	18648374	ENSGALG00000011609	protein coding	
5	16916541	17001110	ENSGALG00000007374	protein coding	YPEL4
5	25739631	25793114	ENSGALG00000041014	protein coding	
5	16823643	16830832	ENSGALG00000007217	protein coding	BEST1
5	25964150	26042047	ENSGALG00000009249	protein coding	UBR1
5	23667294	23667403	ENSGALG00000025785	miRNA	gga-mir-6706
5	21728195	21799637	ENSGALG00000031542	protein coding	EXT2
5	16777263	16794363	ENSGALG00000007178	protein coding	FADS2
5	14053799	14092907	ENSGALG00000006583	protein coding	LSP1
5	23428174	23428284	ENSGALG00000024631	snoRNA	RF00573
5	5522441	5536835	ENSGALG00000012109	protein coding	EIF3M
5	16919059	16920630	ENSGALG00000026207	protein coding	CNTF
5	26193022	26193130	ENSGALG00000026386	miRNA	gga-mir-6587
5	23698675	23739368	ENSGALG00000008393	protein coding	CREB3L1
5	27718429	27835276	ENSGALG00000009415	protein coding	SMOC1
5	16906936	16909098	ENSGALG00000028536	protein coding	MPEG1
5	18698547	18709078	ENSGALG00000035867	protein coding	ELF5
5	16921133	16935600	ENSGALG00000007287	protein coding	
5	26454626	26467002	ENSGALG00000009345	protein coding	
5	45129564	45133553	ENSGALG00000017387	protein coding	TMEM251
5	14921862	14996500	ENSGALG00000038950	protein coding	
5	27201732	27283175	ENSGALG00000000296	protein coding	PCNX1
5	2161580	2188356	ENSGALG00000003908	protein coding	SLC6A5
5	15151804	15252302	ENSGALG00000006830	protein coding	CHID1
5	44480201	44495004	ENSGALG00000010738	protein coding	TC2N
5	16740019	16749937	ENSGALG00000020485	protein coding	
5	16375981	16504146	ENSGALG00000029533	protein coding	LRP5
5	23347084	23385831	ENSGALG00000032181	protein coding	LRP4
5	16520186	16571864	ENSGALG00000007037	protein coding	PPP6R3
5	25967888	25978284	ENSGALG00000009185	protein coding	ROM1
5	25840267	25867905	ENSGALG00000009156	protein coding	CDAN1
5	21810345	21834715	ENSGALG00000032584	protein coding	ALX4

Chromosome	Gene start (bp)	Gene end (bp)	Gene stable ID	Gene type	Gene name
5	16323167	16343974	ENSGALG00000020488	protein coding	
5	15714417	15737602	ENSGALG00000006868	protein coding	
5	14163587	14184836	ENSGALG00000006647	protein coding	DUSP8
5	23771783	23893510	ENSGALG00000008403	protein coding	PHF21A
5	26043044	26063006	ENSGALG00000009260	protein coding	TMEM62
5	45136789	45147580	ENSGALG00000010842	protein coding	UBR7
5	14094429	14098832	ENSGALG00000006591	protein coding	TNNI2
5	25199152	25289469	ENSGALG00000008940	protein coding	SPTBN5
5	23170347	23190317	ENSGALG00000008231	protein coding	PACSIN3
5	2201059	2481132	ENSGALG00000003777	protein coding	NELL1
5	18522566	18531083	ENSGALG00000031889	protein coding	
5	22795462	22803111	ENSGALG00000008089	protein coding	KBTBD4
5	35109226	35715442	ENSGALG00000029022	protein coding	NPAS3
5	25432899	25445807	ENSGALG00000029454	protein coding	
5	16977551	16978970	ENSGALG00000007341	protein coding	MED19
5	16941486	16967936	ENSGALG00000007330	protein coding	CTNND1
5	22862958	22872275	ENSGALG00000008100	protein coding	RAPSN
5	13998219	14009090	ENSGALG00000006561	protein coding	MRPL23
5	26124345	26142266	ENSGALG00000009282	protein coding	ELMSAN1
5	2086559	2141355	ENSGALG00000003958	protein coding	PRMT3
5	26150108	26163720	ENSGALG00000028568	protein coding	DNAL1
5	14108059	14112076	ENSGALG00000006602	protein coding	SYT8
5	16802946	16816245	ENSGALG00000007203	protein coding	RAB3IL1
5	27987462	28003889	ENSGALG00000009431	protein coding	PLEKHD1
5	18493194	18514858	ENSGALG00000014573	protein coding	NAT10
5	23508006	23633040	ENSGALG00000008358	protein coding	AMBRA1
5	22127305	22175544	ENSGALG00000036901	protein coding	TSPAN18
5	25462299	25472633	ENSGALG00000028402	protein coding	
5	23399012	23435075	ENSGALG00000008325	protein coding	CKAP5
5	22351047	22362930	ENSGALG00000037220	protein coding	ASTL
5	5540164	5584404	ENSGALG00000012103	protein coding	CCDC73
5	16974079	16974902	ENSGALG00000031031	protein coding	SELENOH
5	26166529	26171162	ENSGALG00000023243	protein coding	
5	22949194	22970222	ENSGALG00000008127	protein coding	SPI1
5	22802580	22805146	ENSGALG00000008091	protein coding	PTPMT1
5	23648664	23650689	ENSGALG00000008367	protein coding	MDK
5	26171455	26176330	ENSGALG00000009292	protein coding	
5	25868235	25869978	ENSGALG00000030785	protein coding	
5	23651663	23689170	ENSGALG00000008380	protein coding	DGKZ
5	22981961	23039476	ENSGALG00000008148	protein coding	MYBPC3
5	27443194	27531009	ENSGALG00000009387	protein coding	
5	26425311	26448293	ENSGALG00000009338	protein coding	ZFYVE1
5	26192258	26194122	ENSGALG00000020454	protein coding	C5H14ORF169

Chromosome	Gene start (bp)	Gene end (bp)	Gene stable ID	Gene type	Gene name
5	15271751	15336034	ENSGALG00000006837	protein coding	TSPAN4
5	15851602	15855876	ENSGALG00000044313	protein coding	
5	15676801	15708216	ENSGALG00000006856	protein coding	CD151
5	26297611	26324915	ENSGALG00000009315	protein coding	PAPLN
5	22197736	22220666	ENSGALG00000008047	protein coding	
5	28008500	28025729	ENSGALG00000009438	protein coding	SLC39A9
5	22872406	22883540	ENSGALG00000008108	protein coding	PSMC3
5	25903704	25937422	ENSGALG00000009176	protein coding	TTBK2
5	16911791	16917496	ENSGALG00000010835	protein coding	DTX4
5	44965411	45115958	ENSGALG00000034898	protein coding	ITPK1
5	23204929	23293797	ENSGALG00000008255	protein coding	C11orf49
5	26200817	26293922	ENSGALG00000009300	protein coding	NUMB
5	14113198	14118876	ENSGALG00000006608	protein coding	
5	15451610	15451999	ENSGALG00000039066	protein coding	
5	16975014	16977341	ENSGALG00000007350	protein coding	
5	16832240	16836802	ENSGALG00000007220	protein coding	FTH1
5	22282853	22433771	ENSGALG00000008053	protein coding	
5	15859631	15880399	ENSGALG00000006873	protein coding	PHRF1
5	22804759	22852407	ENSGALG00000008097	protein coding	CELF1
5	23152839	23167347	ENSGALG00000008218	protein coding	DDB2
5	10434605	10509846	ENSGALG00000006035	protein coding	PDE3B
5	16980166	16989643	ENSGALG00000007362	protein coding	ZDHHC5
5	23437157	23447162	ENSGALG00000008332	protein coding	F2
5	24001629	24002515	ENSGALG00000022531	protein coding	
5	27618375	27715349	ENSGALG00000009400	protein coding	SLC8A3
5	22788881	22795997	ENSGALG00000008084	protein coding	NDUFS3
5	16761007	16770528	ENSGALG00000007127	protein coding	
5	16579760	16583124	ENSGALG00000032015	lincRNA	
5	16801352	16802718	ENSGALG00000041460	lincRNA	
5	16838668	16841925	ENSGALG00000029566	lincRNA	
5	16943053	16944982	ENSGALG00000042699	lincRNA	
5	16967524	16972137	ENSGALG00000030338	lincRNA	
5	21829440	21830894	ENSGALG00000042882	lincRNA	
5	23692085	23693892	ENSGALG00000040527	lincRNA	
5	23696085	23698539	ENSGALG00000032779	lincRNA	
5	25807073	25817072	ENSGALG00000041098	lincRNA	
5	25881336	25883509	ENSGALG00000041420	lincRNA	
5	26199697	26200631	ENSGALG00000034752	lincRNA	
5	26295526	26296764	ENSGALG00000038025	lincRNA	
5	37413460	37415830	ENSGALG00000043759	lincRNA	
7	31731614	31814126	ENSGALG00000012382	protein coding	
8	22275804	22536305	ENSGALG00000027655	protein coding	TRABD2B
10	2614900	2619795	ENSGALG00000001664	protein coding	PTPN9

Chromosome	Gene start (bp)	Gene end (bp)	Gene stable ID	Gene type	Gene name
10	2623651	2623758	ENSGALG00000026164	miRNA	gga-mir-6575
10	2590070	2610361	ENSGALG00000001644	protein coding	SIN3A
10	2621478	2630245	ENSGALG00000029537	protein coding	SNUPN
10	2630790	2634200	ENSGALG00000033110	protein coding	SNX33
10	623939	624280	ENSGALG00000039318	protein coding	
10	12413427	12483133	ENSGALG00000006445	protein coding	ARNT2
10	599661	601066	ENSGALG00000040159	protein coding	
10	621068	621409	ENSGALG00000029250	protein coding	
10	2637608	2655172	ENSGALG00000002678	protein coding	CSPG4
10	16697772	16838212	ENSGALG00000040651	protein coding	IGF1R
11	19086513	19089789	ENSGALG00000000059	protein coding	
11	19089858	19093054	ENSGALG00000025712	protein coding	DEF8
11	19064511	19086448	ENSGALG00000000129	protein coding	TCF25
11	12984674	13144905	ENSGALG00000005319	protein coding	CDH8
11	19022589	19054970	ENSGALG00000000516	protein coding	FANCA
11	19057727	19063586	ENSGALG00000000521	protein coding	SPIRE2
12	3752214	4001595	ENSGALG00000030908	protein coding	ATP2B2
13	13664069	13829628	ENSGALG00000032974	protein coding	ADAMTS2
14	3893187	3904532	ENSGALG00000004436	protein coding	CYP3A4
14	3530847	3889914	ENSGALG00000004420	protein coding	SDK1
17	2601746	2859437	ENSGALG00000008456	protein coding	CACNA1B
17	1071811	1124231	ENSGALG00000030263	protein coding	RABL6
27	5352969	5381707	ENSGALG00000003256	protein coding	ATP6V0A1
27	4095356	4096663	ENSGALG00000037179	protein coding	
27	4097144	4106102	ENSGALG00000040658	protein coding	
27	5260325	5272254	ENSGALG00000003359	protein coding	RAB5C
27	5296817	5306850	ENSGALG00000003282	protein coding	STAT5B
27	5271010	5279941	ENSGALG00000003354	protein coding	KCNH4
27	5381307	5386131	ENSGALG00000032610	protein coding	NAGLU
27	5280330	5281387	ENSGALG00000011485	protein coding	HCRT
27	5384974	5386409	ENSGALG00000027429	protein coding	HSD17B1
27	5282575	5292696	ENSGALG00000003345	protein coding	
27	5386659	5389962	ENSGALG00000028866	protein coding	COASY
27	5292832	5299192	ENSGALG00000003333	protein coding	GHDC

Table S 67. Overlapping Hp regions across populations.

Chromosome	Window start	Window end
1	32520000	32540000
1	32530000	32550000
1	162220000	1.62E+08
1	119520000	1.2E+08

Chromosome	Window start	Window end
1	32440000	32700000
1	32780000	32840000
1	103880000	1.04E+08
1	119500000	1.2E+08
2	147260000	1.47E+08
2	4520000	4540000
2	140500000	1.41E+08
2	9150000	9170000
2	9170000	9190000
2	74030000	74050000
3	82470000	82490000
3	103420000	1.03E+08
3	78100000	78120000
4	27810000	27830000
4	27840000	27860000
4	27850000	27870000
4	27860000	27880000
4	28610000	28630000
4	39490000	39510000
4	39500000	39520000
4	78130000	78150000
4	19920000	19980000
4	39450000	39470000
4	78110000	78140000
4	78170000	78200000
4	7940000	8030000
4	78020000	78040000
4	78090000	78150000
5	21380000	21400000
5	22480000	22500000
5	22490000	22510000
5	22530000	22550000
5	22540000	22560000
5	40830000	40850000
5	40840000	40860000
5	41880000	41900000
5	41020000	41070000
5	41870000	41900000
5	40850000	40870000
5	40860000	40880000
6	14980000	15000000
6	18320000	18360000

Chromosome	Window start	Window end
7	8580000	8600000
8	230000	250000
8	8800000	8880000
8	8990000	9020000
8	15220000	15310000
8	9130000	9190000
8	9200000	9220000
8	9520000	9540000
8	13100000	13120000
8	9160000	9180000
8	8830000	8850000
9	10410000	10430000
9	10150000	10220000
9	12400000	12430000
11	1610000	1630000
13	1650000	1670000
14	5300000	5320000
18	10270000	10310000

Table S 68. List of Ensemble Hp genes under selection across all populations.

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
1	ENSGALG00000027781	103899869	103900014	RF02271	misc_RNA
1	ENSGALG00000016936	162193513	162295112	TDRD3	protein coding
1	ENSGALG00000038179	32268154	32452343		lincRNA
1	ENSGALG00000042870	32603425	32604254		lincRNA
2	ENSGALG00000005710	4515467	4582669	CTDSPL	protein coding
2	ENSGALG00000030054	8821485	9397176	PTPRN2	protein coding
2	ENSGALG00000037014	147222471	147418330	TSNARE1	protein coding
3	ENSGALG00000015944	82215093	82512310	RIMS1	protein coding
3	ENSGALG00000015849	78041071	78198472	ME1	protein coding
4	ENSGALG00000014931	78013279	78074717	RAB28	protein coding
4	ENSGALG00000010596	39448857	39482459	TACR3	protein coding
4	ENSGALG00000035886	27788185	27825157		lincRNA
5	ENSGALG00000010576	40868271	40894704	GTF2A1	protein coding
5	ENSGALG00000010572	40811286	40858950	TSHR	protein coding
6	ENSGALG00000005035	14982062	15068657	KAT6B	protein coding
8	ENSGALG00000006237	15219523	15269342	PKN2	protein coding
8	ENSGALG00000033708	9019159	9019789		lincRNA
8	ENSGALG00000043258	9537043	9545093		lincRNA
9	ENSGALG00000002897	10142631	10150156	SLC16A14	protein coding
9	ENSGALG00000036543	10205227	10208808	ZBTB38	protein coding
9	ENSGALG00000038512	12398415	12430615	AGTR1	protein coding
9	ENSGALG00000002850	10213881	10256070	RASA2	protein coding

9	ENSGALG00000002729	10392753	10431361	GK5	protein coding
9	ENSGALG00000034946	10189098	10190468		lincRNA
11	ENSGALG00000002407	1604963	1708650	HYDIN	protein coding
13	ENSGALG00000040453	1649170	1650955	SRA1	protein coding
13	ENSGALG00000001132	1651000	1654407		protein coding
13	ENSGALG00000001099	1544222	1650955	ANKHD1	protein coding
14	ENSGALG00000005215	5264613	5339317	CACNA1H	protein coding
18	ENSGALG00000007522	10231908	10275081	ABCC3	protein coding
18	ENSGALG00000007623	10279329	10388753	CACNA1G	protein coding

Table S 69. Overlapping Fst windows across populations.

Chromosome	Window start	Window end
1	59230001	59250000
1	151610001	151630000
1	19380001	19400000
1	151620001	151640000
1	19340001	19360000
1	59250001	59270000
1	19370001	19390000
1	151630001	151650000
1	150300001	150320000
1	159520001	159540000
1	19320001	19340000
1	19430001	19450000
1	19330001	19350000
1	151540001	151560000
1	19460001	19480000
1	19360001	19380000
1	19310001	19330000
1	19410001	19430000
1	19450001	19470000
1	177170001	177190000
1	147080001	147100000
1	4410001	4430000
1	19420001	19440000
1	151550001	151570000
1	177160001	177180000
1	177180001	177200000
1	147070001	147090000
1	19300001	19320000
1	147090001	147110000
1	151680001	151700000
1	147050001	147070000
1	181790001	181810000
1	147060001	147080000
1	151690001	151710000
1	182720001	182740000
1	181310001	181330000
1	151700001	151720000
1	154530001	154550000
1	177550001	177570000
1	142940001	142960000

Chromosome	Window start	Window end
1	142920001	142940000
1	142930001	142950000
1	181840001	181860000
1	179050001	179070000
1	142910001	142930000
1	181850001	181870000
1	181800001	181820000
1	137450001	137470000
1	137510001	137530000
1	137440001	137460000
1	179020001	179040000
1	179030001	179050000
1	177330001	177350000
1	179040001	179060000
1	137500001	137520000
1	146780001	146800000
1	146770001	146790000
1	146790001	146810000
1	146810001	146830000
1	146760001	146780000
1	146800001	146820000
1	146820001	146840000
1	146990001	147010000
1	147110001	147130000
1	147100001	147120000
1	5210001	5230000
1	152810001	152830000
1	5220001	5240000
1	35320001	35340000
1	100540001	100560000
1	146980001	147000000
1	146830001	146850000
1	151670001	151690000
1	147010001	147030000
1	147020001	147040000
1	100530001	100550000
1	147000001	147020000
1	190910001	190930000
1	147030001	147050000
1	5390001	5410000
1	146140001	146160000
1	147040001	147060000

Chromosome	Window start	Window end
1	146900001	146920000
1	146750001	146770000
1	100520001	100540000
1	146920001	146940000
1	151750001	151770000
1	146130001	146150000
1	147120001	147140000
1	146970001	146990000
1	151660001	151680000
1	100510001	100530000
1	146910001	146930000
1	19540001	19560000
1	39050001	39070000
1	19700001	19720000
1	146840001	146860000
1	35330001	35350000
1	19620001	19640000
1	61340001	61360000
1	140930001	140950000
1	146880001	146900000
1	152820001	152840000
1	19400001	19420000
1	19570001	19590000
1	39040001	39060000
1	5380001	5400000
1	1610001	1630000
1	82330001	82350000
1	78270001	78290000
1	159080001	159100000
1	19690001	19710000
1	1210001	1230000
1	2140001	2160000
1	19350001	19370000
1	36360001	36380000
1	146960001	146980000
2	49890001	49910000
2	51260001	51280000
2	50210001	50230000
2	50200001	50220000
2	149230001	149250000
2	21230001	21250000
2	147350001	147370000

Chromosome	Window start	Window end
2	142900001	142920000
2	83420001	83440000
2	57730001	57750000
2	21260001	21280000
2	57720001	57740000
2	21960001	21980000
2	142800001	142820000
2	20090001	20110000
2	142290001	142310000
2	21950001	21970000
2	49990001	50010000
2	21270001	21290000
2	21240001	21260000
2	146070001	146090000
2	147360001	147380000
2	125510001	125530000
2	21990001	22010000
2	21970001	21990000
2	142330001	142350000
2	49960001	49980000
2	22140001	22160000
2	20080001	20100000
2	146060001	146080000
2	21220001	21240000
2	21980001	22000000
2	21250001	21270000
2	142270001	142290000
2	142210001	142230000
2	31300001	31320000
2	142320001	142340000
2	143190001	143210000
2	21880001	21900000
2	145960001	145980000
2	49980001	50000000
2	142280001	142300000
2	21210001	21230000
2	132120001	132140000
2	23010001	23030000
2	21890001	21910000
2	142470001	142490000
2	149220001	149240000
2	21280001	21300000

Chromosome	Window start	Window end
2	21170001	21190000
2	78330001	78350000
2	147390001	147410000
2	147380001	147400000
2	49970001	49990000
2	30810001	30830000
2	142260001	142280000
2	142460001	142480000
2	21830001	21850000
2	145990001	146010000
2	21810001	21830000
2	21820001	21840000
2	142540001	142560000
2	149150001	149170000
2	22610001	22630000
2	145980001	146000000
2	145970001	145990000
2	145940001	145960000
2	23510001	23530000
2	149210001	149230000
2	149160001	149180000
2	149200001	149220000
2	149190001	149210000
2	149180001	149200000
2	149170001	149190000
2	61580001	61600000
2	139700001	139720000
2	15340001	15360000
2	147310001	147330000
2	15330001	15350000
2	141780001	141800000
2	111910001	111930000
2	11690001	11710000
2	146180001	146200000
2	50050001	50070000
2	62440001	62460000
2	111900001	111920000
2	82350001	82370000
2	23780001	23800000
2	23770001	23790000
2	20120001	20140000
2	20110001	20130000

Chromosome	Window start	Window end
2	23790001	23810000
2	20100001	20120000
3	90950001	90970000
3	84170001	84190000
3	84040001	84060000
3	84130001	84150000
3	84160001	84180000
3	84050001	84070000
3	90990001	91010000
3	90980001	91000000
3	84150001	84170000
3	86440001	86460000
3	84140001	84160000
3	90970001	90990000
3	90800001	90820000
3	12410001	12430000
3	90820001	90840000
3	90810001	90830000
3	90620001	90640000
3	79800001	79820000
3	89680001	89700000
3	72010001	72030000
3	78560001	78580000
3	37920001	37940000
3	37910001	37930000
3	90520001	90540000
3	92220001	92240000
3	51270001	51290000
3	91460001	91480000
3	53590001	53610000
3	53610001	53630000
3	90510001	90530000
3	53600001	53620000
3	92190001	92210000
3	90360001	90380000
3	88840001	88860000
3	89840001	89860000
3	92200001	92220000
3	50060001	50080000
3	92210001	92230000
3	90350001	90370000
3	90530001	90550000

Chromosome	Window start	Window end
3	89330001	89350000
3	53580001	53600000
3	90500001	90520000
3	91380001	91400000
3	90960001	90980000
3	89690001	89710000
3	33110001	33130000
3	31730001	31750000
3	40200001	40220000
3	28500001	28520000
3	88320001	88340000
3	27560001	27580000
3	10690001	10710000
4	27980001	28000000
4	28160001	28180000
4	27950001	27970000
4	27740001	27760000
4	27780001	27800000
4	27730001	27750000
4	27970001	27990000
4	27960001	27980000
4	27770001	27790000
4	27990001	28010000
4	27900001	27920000
4	28000001	28020000
4	27750001	27770000
4	20290001	20310000
4	19550001	19570000
4	19530001	19550000
4	27720001	27740000
4	27810001	27830000
4	19440001	19460000
4	27760001	27780000
4	27790001	27810000
4	28010001	28030000
4	27800001	27820000
4	19840001	19860000
4	20300001	20320000
4	20280001	20300000
4	19790001	19810000
4	19850001	19870000
4	19830001	19850000

Chromosome	Window start	Window end
4	28020001	28040000
4	27940001	27960000
4	28460001	28480000
4	19860001	19880000
4	27820001	27840000
4	20260001	20280000
4	19600001	19620000
4	28130001	28150000
4	19560001	19580000
4	20310001	20330000
4	19800001	19820000
4	19770001	19790000
4	27840001	27860000
4	19610001	19630000
4	27830001	27850000
4	20320001	20340000
4	19520001	19540000
4	19590001	19610000
4	19820001	19840000
4	27850001	27870000
4	28490001	28510000
4	19780001	19800000
4	19870001	19890000
4	20270001	20290000
4	19670001	19690000
4	19470001	19490000
4	28510001	28530000
4	19510001	19530000
4	27710001	27730000
4	28440001	28460000
4	27890001	27910000
4	19660001	19680000
4	28450001	28470000
4	27400001	27420000
4	19940001	19960000
4	28520001	28540000
4	19580001	19600000
4	19950001	19970000
4	27390001	27410000
4	28410001	28430000
4	17970001	17990000
4	28530001	28550000

Chromosome	Window start	Window end
4	17980001	18000000
4	28430001	28450000
4	19680001	19700000
4	27930001	27950000
4	28370001	28390000
4	28170001	28190000
4	27610001	27630000
4	28420001	28440000
4	28400001	28420000
4	28540001	28560000
4	27860001	27880000
4	28030001	28050000
4	27620001	27640000
4	27500001	27520000
4	28360001	28380000
4	27910001	27930000
4	27520001	27540000
4	27370001	27390000
4	28660001	28680000
4	27410001	27430000
4	27700001	27720000
4	28120001	28140000
4	27600001	27620000
4	17960001	17980000
4	28350001	28370000
4	26780001	26800000
4	27570001	27590000
4	28380001	28400000
4	17950001	17970000
4	26010001	26030000
4	26040001	26060000
4	28770001	28790000
4	26120001	26140000
4	27580001	27600000
4	27870001	27890000
4	27690001	27710000
4	27880001	27900000
4	27920001	27940000
4	28730001	28750000
4	27040001	27060000
4	28390001	28410000
4	28340001	28360000

Chromosome	Window start	Window end
4	28050001	28070000
4	28710001	28730000
4	28240001	28260000
4	28040001	28060000
4	28110001	28130000
4	26680001	26700000
4	27590001	27610000
4	27160001	27180000
4	27550001	27570000
4	28740001	28760000
4	27510001	27530000
4	26470001	26490000
4	26560001	26580000
4	28180001	28200000
4	28600001	28620000
4	28060001	28080000
4	28590001	28610000
4	28580001	28600000
4	28670001	28690000
4	26080001	26100000
4	28720001	28740000
4	26770001	26790000
4	27260001	27280000
4	28230001	28250000
4	26030001	26050000
4	27120001	27140000
4	27360001	27380000
4	26050001	26070000
4	28190001	28210000
4	26130001	26150000
4	26020001	26040000
4	26090001	26110000
4	26500001	26520000
4	28100001	28120000
4	28780001	28800000
4	25900001	25920000
4	28200001	28220000
4	28610001	28630000
4	28700001	28720000
4	26480001	26500000
4	28910001	28930000
4	28070001	28090000

Chromosome	Window start	Window end
4	26720001	26740000
4	28680001	28700000
4	27020001	27040000
4	27030001	27050000
4	26110001	26130000
4	26690001	26710000
4	27250001	27270000
4	26710001	26730000
4	26100001	26120000
4	26490001	26510000
4	28690001	28710000
4	26440001	26460000
4	28220001	28240000
4	28210001	28230000
4	26430001	26450000
4	27420001	27440000
4	26700001	26720000
4	20650001	20670000
4	28810001	28830000
4	25970001	25990000
4	28090001	28110000
4	26070001	26090000
4	28760001	28780000
4	27010001	27030000
4	28790001	28810000
4	28080001	28100000
4	28920001	28940000
4	25950001	25970000
4	26060001	26080000
4	25960001	25980000
4	25930001	25950000
4	28750001	28770000
4	28800001	28820000
4	25940001	25960000
4	25880001	25900000
4	25910001	25930000
4	25840001	25860000
4	25850001	25870000
4	25870001	25890000
4	25790001	25810000
4	25780001	25800000
4	2230001	2250000

Chromosome	Window start	Window end
4	25770001	25790000
4	39720001	39740000
4	49170001	49190000
4	39740001	39760000
4	39730001	39750000
4	2240001	2260000
4	2250001	2270000
4	26340001	26360000
4	26350001	26370000
4	26280001	26300000
4	26310001	26330000
4	41780001	41800000
4	39700001	39720000
4	39710001	39730000
4	41790001	41810000
4	41770001	41790000
4	41830001	41850000
4	41820001	41840000
4	26170001	26190000
4	41850001	41870000
4	41840001	41860000
4	37810001	37830000
4	26320001	26340000
4	39690001	39710000
4	27660001	27680000
4	41810001	41830000
4	42060001	42080000
4	87460001	87480000
4	27670001	27690000
4	27650001	27670000
4	26160001	26180000
4	27680001	27700000
4	41860001	41880000
4	26180001	26200000
4	26150001	26170000
4	25260001	25280000
4	27540001	27560000
4	26450001	26470000
4	27490001	27510000
4	25270001	25290000
4	16450001	16470000
4	25190001	25210000

Chromosome	Window start	Window end
4	27530001	27550000
4	37720001	37740000
4	25180001	25200000
4	26460001	26480000
4	7580001	7600000
4	37700001	37720000
4	7570001	7590000
4	37730001	37750000
4	16460001	16480000
4	27270001	27290000
4	27480001	27500000
4	37710001	37730000
4	19810001	19830000
4	6620001	6640000
4	20030001	20050000
4	6610001	6630000
4	5860001	5880000
4	20610001	20630000
4	25750001	25770000
4	20620001	20640000
4	21000001	21020000
5	2320001	2340000
5	2130001	2150000
5	14990001	15010000
5	2280001	2300000
5	2270001	2290000
5	2200001	2220000
5	2310001	2330000
5	2150001	2170000
5	2100001	2120000
5	23390001	23410000
5	5530001	5550000
5	24030001	24050000
5	24000001	24020000
5	21120001	21140000
5	18560001	18580000
5	25240001	25260000
5	23810001	23830000
5	15310001	15330000
5	18570001	18590000
5	21780001	21800000
5	25250001	25270000

Chromosome	Window start	Window end
5	16730001	16750000
5	23820001	23840000
5	15280001	15300000
5	25920001	25940000
5	15290001	15310000
5	21110001	21130000
5	10460001	10480000
5	15450001	15470000
5	15270001	15290000
5	5540001	5560000
5	27150001	27170000
5	15440001	15460000
5	26190001	26210000
5	14150001	14170000
5	15320001	15340000
5	15260001	15280000
5	15460001	15480000
5	15170001	15190000
5	15700001	15720000
5	15180001	15200000
5	15560001	15580000
5	23170001	23190000
5	15210001	15230000
5	16790001	16810000
5	15350001	15370000
5	15200001	15220000
5	15190001	15210000
5	15480001	15500000
5	5550001	5570000
5	15430001	15450000
5	15360001	15380000
5	5560001	5580000
5	15490001	15510000
5	15570001	15590000
5	15220001	15240000
5	15550001	15570000
5	16740001	16760000
5	15420001	15440000
5	16550001	16570000
5	15500001	15520000
5	16560001	16580000
5	15540001	15560000

Chromosome	Window start	Window end
5	16750001	16770000
5	15530001	15550000
5	15510001	15530000
5	15520001	15540000
5	26640001	26660000
5	1900001	1920000
5	520001	540000
5	12690001	12710000
5	1830001	1850000
5	1890001	1910000
5	32450001	32470000
5	29440001	29460000
5	29420001	29440000
5	29450001	29470000
5	29430001	29450000
5	31240001	31260000
5	14780001	14800000
5	14770001	14790000
5	4810001	4830000
5	32830001	32850000
5	14890001	14910000
5	32840001	32860000
5	32580001	32600000
6	13810001	13830000
6	13800001	13820000
6	5760001	5780000
6	13340001	13360000
7	2620001	2640000
7	6580001	6600000
7	9640001	9660000
7	11300001	11320000
7	6440001	6460000
7	9360001	9380000
7	4670001	4690000
8	1970001	1990000
8	1590001	1610000
9	10340001	10360000
9	4490001	4510000
9	13790001	13810000
9	9490001	9510000
9	12420001	12440000
9	12430001	12450000

Chromosome	Window start	Window end
9	12390001	12410000
10	12440001	12460000
10	12460001	12480000
10	12450001	12470000
10	12470001	12490000
10	12480001	12500000
11	13530001	13550000
11	13520001	13540000
11	19070001	19090000
11	19060001	19080000
11	19050001	19070000
11	4650001	4670000
11	19040001	19060000
12	3850001	3870000
12	3860001	3880000
12	3880001	3900000
12	3870001	3890000
12	3710001	3730000
12	3720001	3740000
12	3700001	3720000
12	3690001	3710000
12	3730001	3750000
12	3740001	3760000
14	4590001	4610000
20	4800001	4820000
20	4790001	4810000
23	4540001	4560000
23	90001	110000
23	100001	120000
23	4930001	4950000
24	5470001	5490000
24	5820001	5840000
24	5830001	5850000
24	5770001	5790000
24	6040001	6060000
24	6060001	6080000
25	2830001	2850000
25	2820001	2840000
27	5280001	5300000

Table S 70. List of candidate genes using Fst from overlapping regions across populations.

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
1	ENSGALG00000044624	59245579	59246586		protein coding
1	ENSGALG00000017119	177513346	177560920	TNFRSF19	protein coding
1	ENSGALG00000038995	181192418	181414573	GRIA4	protein coding
1	ENSGALG00000008477	1421469	1841500	EXOC4	protein coding
1	ENSGALG00000009945	35315781	35347355	CPM	protein coding
1	ENSGALG00000006489	2002525	2187486	CHCHD3	protein coding
1	ENSGALG00000038154	182684536	182765393	YAP1	protein coding
1	ENSGALG00000016896	146127088	146275409	ABCC4	protein coding
1	ENSGALG00000032978	1213840	1214346	UCN3	protein coding
1	ENSGALG00000029270	4402132	4591692	GATA3	protein coding
1	ENSGALG00000017139	179051034	179094239		protein coding
1	ENSGALG00000045031	59237872	59238879		protein coding
1	ENSGALG00000044524	59241726	59242732		protein coding
1	ENSGALG00000046372	137439551	137445352		protein coding
1	ENSGALG00000037697	137487513	137505777	LAMP1	protein coding
1	ENSGALG00000016900	146527090	147094328	GPC6	protein coding
1	ENSGALG00000016830	137511432	137545754	CUL4A	protein coding
1	ENSGALG00000010177	36351342	36388496	ZFC3H1	protein coding
1	ENSGALG00000016908	159096610	159285693	PCDH9	protein coding
1	ENSGALG00000016828	137458314	137486611	GRTP1	protein coding
1	ENSGALG00000044959	59249433	59250440		protein coding
1	ENSGALG00000046239	59253286	59254293		protein coding
1	ENSGALG00000045433	59257140	59258147		protein coding
1	ENSGALG00000027868	177160927	177162801	AMER2	protein coding
1	ENSGALG00000031514	146892901	146893485		lincRNA
1	ENSGALG00000032339	150234073	150532403		lincRNA
1	ENSGALG00000040093	159526738	159744910		lincRNA
1	ENSGALG00000033716	181770866	181805885		lincRNA
1	ENSGALG00000035278	39036722	39056354		lincRNA
1	ENSGALG00000032654	78268586	78290816		lincRNA
2	ENSGALG00000012732	62437754	62509972	PHACTR1	protein coding
2	ENSGALG00000009500	22978146	23047300	VPS50	protein coding
2	ENSGALG00000031741	145815693	145960326	PTK2	protein coding
2	ENSGALG00000030030	132121027	132231350	RSPO2	protein coding
2	ENSGALG00000031758	50150482	50280221	SUGCT	protein coding
2	ENSGALG00000010961	31211304	31319341	IGF2BP3	protein coding
2	ENSGALG00000009062	21877225	22125099	CDK14	protein coding
2	ENSGALG00000031713	49640512	49897096	POU6F2	protein coding
2	ENSGALG00000043636	49979496	49987966	YAE1D1	protein coding
2	ENSGALG00000042548	141751641	141782032	LRRC6	protein coding
2	ENSGALG00000031917	22587398	22642927	ANKIB1	protein coding
2	ENSGALG00000035281	15342791	15398782	WAC	protein coding
2	ENSGALG00000037112	49987976	50001040		protein coding
2	ENSGALG00000037773	142197114	142221622	ST3GAL1	protein coding
2	ENSGALG00000037014	147222471	147418330	TSNARE1	protein coding
2	ENSGALG00000044996	141791891	141797962	TMEM71	protein coding

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
2	ENSGALG00000013124	83340744	83708432	FHOD3	protein coding
2	ENSGALG00000034333	149152445	149152741		protein coding
2	ENSGALG00000039346	149228059	149229441		protein coding
2	ENSGALG00000009686	23744767	23815855		protein coding
2	ENSGALG00000034024	30714422	30862920	RAPGEF5	protein coding
2	ENSGALG00000043243	50062031	50120197	CDK13	protein coding
2	ENSGALG00000040891	20027818	20125211	RSU1	protein coding
2	ENSGALG00000031519	143191899	143269024	KHDRBS3	protein coding
3	ENSGALG00000032937	91386688	91473055	DLGAP2	protein coding
3	ENSGALG00000025589	92233115	92233218	RF00026	snRNA
3	ENSGALG00000009158	12273168	12439182	CDC42BPA	protein coding
3	ENSGALG00000016329	88826113	88881081	AGPAT5	protein coding
3	ENSGALG00000010541	31572475	31748573	BIRC6	protein coding
3	ENSGALG00000010039	27486112	27649822	BRE	protein coding
3	ENSGALG00000035230	90162525	90533217	CSMD1	protein coding
3	ENSGALG00000040000	37916515	37937367	ERO1B	protein coding
3	ENSGALG00000016276	86406473	86714063	KHDRBS2	protein coding
3	ENSGALG00000015864	78537400	78582981	IBTK	protein coding
3	ENSGALG00000015889	79785429	79884137	PHIP	protein coding
3	ENSGALG00000011098	40214428	40230986	TAF5L	protein coding
3	ENSGALG00000029553	28447222	28667979		lincRNA
3	ENSGALG00000036544	28450739	28526039		lincRNA
3	ENSGALG00000034684	33116938	33125450		lincRNA
3	ENSGALG00000036112	50058811	50161705		lincRNA
4	ENSGALG00000009361	20960961	21000658	GUCY1B1	protein coding
4	ENSGALG00000027439	20654247	20654356		miRNA
4	ENSGALG00000038140	25162884	25180520		protein coding
4	ENSGALG00000032953	19548868	19548950		miRNA
4	ENSGALG00000005425	2209876	2231355	OGT	protein coding
4	ENSGALG00000025212	21010293	21010422	RF00548	snRNA
4	ENSGALG00000009639	25181859	25200923		protein coding
4	ENSGALG00000030791	5837514	5995090	DIAPH2	protein coding
4	ENSGALG00000020210	39752033	39762452	CENPU	protein coding
4	ENSGALG00000005464	2232118	2260037		protein coding
4	ENSGALG00000009207	19996054	20033183	TRIM2	protein coding
4	ENSGALG00000005475	2262230	2272389	RHOGL	protein coding
4	ENSGALG00000006851	6599257	7006957		protein coding
4	ENSGALG00000009212	20040123	20078631	MND1	protein coding
4	ENSGALG00000009714	25756022	25763028	CBR4	protein coding
4	ENSGALG00000010628	39713691	39752253	ACSL1	protein coding
4	ENSGALG00000009719	27095819	27127946	PCDH10	protein coding
4	ENSGALG00000008517	16449974	16457382	MCTS1	protein coding
4	ENSGALG00000008559	16458726	16479086	CUL4B	protein coding
4	ENSGALG00000042912	5862686	5863323		lincRNA
4	ENSGALG00000031591	16479446	16482772		lincRNA
4	ENSGALG00000033107	19392907	19563891		lincRNA
4	ENSGALG00000033380	19504112	19511619		lincRNA

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
4	ENSGALG00000041824	19541886	19542585		lincRNA
4	ENSGALG00000039736	19819071	19857159		lincRNA
4	ENSGALG00000039492	19873184	19873825		lincRNA
4	ENSGALG00000030400	25900254	25900939		lincRNA
4	ENSGALG00000032689	26689975	26702258		lincRNA
4	ENSGALG00000029613	27043314	27051634		lincRNA
4	ENSGALG00000032527	27396660	27628525		lincRNA
4	ENSGALG00000031625	27600624	27601331		lincRNA
4	ENSGALG00000035886	27788185	27825157		lincRNA
4	ENSGALG00000036104	28160838	28173463		lincRNA
4	ENSGALG00000034709	28904779	28987118		lincRNA
5	ENSGALG00000011609	18540733	18648374		protein coding
5	ENSGALG00000031542	21728195	21799637	EXT2	protein coding
5	ENSGALG00000007178	16777263	16794363	FADS2	protein coding
5	ENSGALG00000012109	5522441	5536835	EIF3M	protein coding
5	ENSGALG00000026386	26193022	26193130	gga-mir-6587	miRNA
5	ENSGALG00000025793	1896796	1896969	RF02271	misc_RNA
5	ENSGALG00000038950	14921862	14996500		protein coding
5	ENSGALG00000003908	2161580	2188356	SLC6A5	protein coding
5	ENSGALG00000006830	15151804	15252302	CHID1	protein coding
5	ENSGALG00000020485	16740019	16749937		protein coding
5	ENSGALG00000007037	16520186	16571864	PPP6R3	protein coding
5	ENSGALG00000006868	15714417	15737602		protein coding
5	ENSGALG00000006647	14163587	14184836	DUSP8	protein coding
5	ENSGALG00000008403	23771783	23893510	PHF21A	protein coding
5	ENSGALG00000003999	1910717	1996488	NAV2	protein coding
5	ENSGALG00000008940	25199152	25289469	SPTBN5	protein coding
5	ENSGALG00000008231	23170347	23190317	PACSIN3	protein coding
5	ENSGALG00000003777	2201059	2481132	NELL1	protein coding
5	ENSGALG00000009847	32441311	32495180	STXBP6	protein coding
5	ENSGALG00000040761	520312	526176	DRD4	protein coding
5	ENSGALG00000003958	2086559	2141355	PRMT3	protein coding
5	ENSGALG00000037020	533877	538465	SCT	protein coding
5	ENSGALG00000007203	16802946	16816245	RAB3IL1	protein coding
5	ENSGALG00000006368	12685002	12717134	PTPN5	protein coding
5	ENSGALG00000008325	23399012	23435075	CKAP5	protein coding
5	ENSGALG00000012103	5540164	5584404	CCDC73	protein coding
5	ENSGALG00000039118	31240857	31409344	MEIS2	protein coding
5	ENSGALG00000020454	26192258	26194122	C5H14ORF169	protein coding
5	ENSGALG00000006837	15271751	15336034	TSPAN4	protein coding
5	ENSGALG00000006856	15676801	15708216	CD151	protein coding
5	ENSGALG00000009176	25903704	25937422	TTBK2	protein coding
5	ENSGALG00000009300	26200817	26293922	NUMB	protein coding
5	ENSGALG00000039066	15451610	15451999		protein coding
5	ENSGALG00000009352	26488837	26646463	DPF3	protein coding
5	ENSGALG00000006035	10434605	10509846	PDE3B	protein coding
5	ENSGALG00000022531	24001629	24002515		protein coding

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
5	ENSGALG00000006717	14871236	14911577		protein coding
5	ENSGALG00000007127	16761007	16770528		protein coding
5	ENSGALG00000014537	29410988	29430989	BMF	protein coding
5	ENSGALG00000031737	14760117	14805890		protein coding
5	ENSGALG00000032015	16579760	16583124		lincRNA
5	ENSGALG00000041460	16801352	16802718		lincRNA
5	ENSGALG00000034752	26199697	26200631		lincRNA
5	ENSGALG00000033973	26652505	26660856		lincRNA
6	ENSGALG00000004980	13362771	13800472	KCNMA1	protein coding
6	ENSGALG00000034133	13321781	13363451		lincRNA
7	ENSGALG00000025571	6580437	6580522	gga-mir-1845	miRNA
7	ENSGALG00000020876	11289758	11332344	AOX2	protein coding
7	ENSGALG00000042117	4668050	4670981		protein coding
7	ENSGALG00000007777	9564789	9679908	SLC39A10	protein coding
7	ENSGALG00000003862	4682652	4717918		protein coding
7	ENSGALG00000041563	2614780	2681771		protein coding
7	ENSGALG00000023742	6580483	6603208	AHR2	protein coding
7	ENSGALG00000033329	9273897	9443440		lincRNA
7	ENSGALG00000035909	9641479	9643660		lincRNA
8	ENSGALG00000002182	1592876	1687096	NR5A2	protein coding
9	ENSGALG00000006488	4479194	4530082	RYK	protein coding
9	ENSGALG00000038512	12398415	12430615	AGTR1	protein coding
9	ENSGALG00000006843	12448872	12485514	NCBP2	protein coding
9	ENSGALG00000025759	10338213	10382351	TFDP2	protein coding
9	ENSGALG00000003052	9475461	9510946	AGFG1	protein coding
9	ENSGALG00000030000	10355033	10369237		lincRNA
10	ENSGALG00000006445	12413427	12483133	ARNT2	protein coding
11	ENSGALG00000000059	19086513	19089789		protein coding
11	ENSGALG00000025712	19089858	19093054	DEF8	protein coding
11	ENSGALG00000000129	19064511	19086448	TCF25	protein coding
11	ENSGALG00000000516	19022589	19054970	FANCA	protein coding
11	ENSGALG00000000521	19057727	19063586	SPIRE2	protein coding
12	ENSGALG00000030908	3752214	4001595	ATP2B2	protein coding
14	ENSGALG00000029817	4588547	4676355		protein coding
23	ENSGALG00000018302	4947355	4947443	gga-mir-30c-1	miRNA
23	ENSGALG00000018301	4946132	4946227	gga-mir-30e	miRNA
23	ENSGALG00000037136	117566	147202	RPS6KA1L	protein coding
23	ENSGALG00000003189	4927211	4955061	NFYC	protein coding
24	ENSGALG00000007438	5484062	5488400		protein coding
24	ENSGALG00000007833	5765420	5775028		protein coding
24	ENSGALG00000007430	5475477	5483503	ARCN1	protein coding
24	ENSGALG00000007839	5780707	5862536	NCAM1	protein coding
24	ENSGALG00000040155	5460918	5470400	ZW10	protein coding
25	ENSGALG00000028478	2848558	2856046		protein coding
25	ENSGALG00000040687	2829873	2845968	SNX27	protein coding
25	ENSGALG00000032955	2816337	2828064	TUFT1	protein coding
27	ENSGALG00000003282	5296817	5306850	STAT5B	protein coding

Chr	Gene stable ID	Gene start (bp)	Gene end (bp)	Gene name	Gene type
27	ENSGALG00000011485	5280330	5281387	HCRT	protein coding
27	ENSGALG00000003345	5282575	5292696		protein coding
27	ENSGALG00000003333	5292832	5299192	GHDC	protein coding

Chr = Chromosome

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